

PLANT GENES INVOLVED IN DEFENSE AGAINST PATHOGENS

Cross-Reference to Related Applications

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5 Serial No. 60/213,634, filed on June 23, 2000, U.S. application Serial
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35 U.S.C. § 119(e).

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Field of the Invention

The present invention generally relates to the field of plant molecular
biology, and more specifically to the regulation of gene expression in plants in
response to pathogen exposure.

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Background of the Invention

Plants are capable of activating a large array of defense mechanisms in
response to pathogen attack, some of which are preexisting and others are inducible.
Pathogens must specialize to circumvent the defense mechanisms of the host,
20 especially those biotrophic pathogens that derive their nutrition from an intimate
association with living plant cells. If the pathogen can cause disease, the interaction
is said to be compatible, but if the plant is resistant, the interaction is said to be
incompatible. A crucial factor determining the success of these mechanisms is the
speed of their activation. Consequently, there is considerable interest in
25 understanding how plants recognize pathogen attack and control expression of
defense mechanisms.

Some potential pathogens trigger a very rapid resistance response called
gene-for-gene resistance. This occurs when the pathogen carries an avirulence (*avr*)
gene that triggers specific recognition by a corresponding host resistance (*R*) gene.
30 *R* gene specificity is generally quite narrow, in most cases only pathogens carrying a
particular *avr* gene are recognized. Recognition is thought to be mediated by ligand-

receptor binding. *R* genes have been studied extensively in recent years. For a review of *R* genes, see Ellis et al. (1998); Jones et al. (1997); and Ronald (1998).

One of the defense mechanisms triggered by gene-for-gene resistance is programmed cell death at the infection site. This is called the hypersensitive response, or HR. Pathogens that induce the HR, or cause cell death by other means, activate a systemic resistance response called systemic acquired resistance (SAR). During SAR, levels of salicylic acid (SA) rise throughout the plant, defense genes such as pathogenesis related (PR) genes are expressed, and the plant becomes more resistant to pathogen attack. SA is a crucial component of this response. Plants that cannot accumulate SA due to the presence of a transgene that encodes an SA-degrading enzyme (*nahG*), develop a HR in response to challenge by avirulent pathogens, but do not exhibit systemic expression of defense genes and do not develop resistance to subsequent pathogen attack (Ryals et al., 1996). The nature of the systemic signal that triggers SAR is a subject of debate (Shulaev et al., 1995; Vernooji et al., 1994). SA clearly moves from the site of the HR to other parts of the plant, but if this is the signal, it must be effective at extremely low concentration (Willits et al., 1998).

SAR is quite similar to some reactions that occur locally in response to attack by virulent (those that cause disease) or avirulent (those that trigger gene-for-gene resistance) pathogens. In general, activation of defense gene expression occurs more slowly in response to virulent pathogens than in response to avirulent pathogens. Some pathogens trigger expression of defense genes through a different signaling pathway that requires components of the jasmonic acid (JA) and ethylene signaling pathways (Creelman et al., 1997).

One approach to understanding the signal transduction networks that control defense mechanisms is to use genetic methods to identify signaling components and determine their roles within the network. Considerable progress has been made using this approach in *Arabidopsis*-pathogen model systems.

R gene signal transduction

Genes such as *NDR1* and *EDS1*, as well as *DND1* and the lesion-mimic genes, likely act in signal transduction pathways downstream from *R-avr*

recognition. *NDR1* and *EDS1* are required for gene-for-gene mediated resistance to avirulent strains of the bacterial pathogen *Pseudomonas syringae* and the oomycete pathogen *Peronospora parasitica*. Curiously, *ndr1* mutants are susceptible to one set of avirulent pathogens, whereas *eds1* mutants are susceptible to a non-overlapping set (Aarts et al., 1998). The five cloned *R* genes that require *EDS1* all belong to the subset of the nucleotide binding site-leucine rich repeat (NBS-LRR) class of *R* genes that contain sequences similar to the cytoplasmic domains of *Drosophila* Toll and mammalian interleukin 1 transmembrane receptors (TIR-NBS-LRR). The two genes that require *NDR1* belong to the leucine-zipper (LZ-NBS-LRR) subclass of NBS-LRR genes. There is another LZ-NBS-LRR gene, *RPP8*, that does not require *EDS1* or *NDR1*, so the correlation between *R* gene structure and requirement for *EDS1* or *NDR1* is not perfect. Nevertheless, these results show that *R* genes differ in their requirements for downstream factors and that these differences are correlated with *R* gene structural type.

NDR1 encodes a protein with two predicted transmembrane domains (Century et al. 1997). RPM1, which requires *NDR1* to mediate resistance, is membrane-associated, despite the fact that its primary sequence does not include any likely membrane-integral stretches (Boyes et al., 1998). It is possible that part of the function of *NDR1* is to hold *R* proteins close to the membrane. *EDS1* encodes a protein with blocks of homology to triacyl glycerol lipases (Falk et al., 1999). The significance of this homology is not known, but it is tempting to speculate that *EDS1* is involved in synthesis or degradation of a signal molecule. *EDS1* expression is inducible by SA and pathogen infection, suggesting that *EDS1* may be involved in signal amplification (Falk et al., 1999).

It has been extremely difficult to isolate mutations in genes other than the *R* genes that are required for gene-for-gene resistance. A selection procedure was devised (McNellis et al., 1998) on the basis of precisely controlled inducible expression of the *avr* gene *avrRpt2* in plants carrying the corresponding resistance gene *RPS2*. Expression of *avrRpt2* in this background is lethal, as it triggers a systemic HR. It is now possible to select for mutants with subtle defects in gene-

for-gene signaling by requiring growth on a concentration of inducer slightly higher than the lethal dose.

Putative plant receptor proteins encoded by *RPP* genes (recognition of *P. parasitica*) mediate specific recognition of *Peronospora* isolates and trigger defense reactions. Recently, McDowell et al. (2000) reported that two members of this class, *RPP7* and *RPP8* (the latter of which encodes a LZ-NBS-LRR type R protein) were not significantly suppressed by mutations in either *EDS1* or *NDRI*, and that *RPP7* resistance was also not compromised by mutations in *EIN2*, *JAR1* or *COII*, which affect ethylene or jasmonic acid signaling, or in *coil/npr1* or *coil/NahG* backgrounds. The authors suggested that *RPP7* initiates resistance through a novel signaling pathway that is independent of salicylic acid accumulation or jasmonic acid response components.

SA-dependent signaling

SA levels increase locally in response to pathogen attack, and systemically in response to the SAR-inducing signal. SA is necessary and sufficient for activation of PR gene expression and enhanced disease resistance. Physiological analyses and characterization of certain lesion-mimic mutants strongly suggest that there is a positive autoregulatory loop affecting SA concentrations (Shirasu et al., 1997; Hunt et al., 1997; Weymann et al., 1995). Several mutants with defects in SA signaling have been characterized. These include *npr1*, in which expression of PR genes in response to SA is blocked; *cpr1*, *cpr5*, and *cpr6*, which constitutively express PR genes; the *npr1* suppressor *ssi1*; *pad4*, which has a defect in SA accumulation; and *eds5*, which has a defect in *PR1* expression.

Expression of the defense genes *PR1*, *BG2*, and *PR5* in response to SA treatment requires a gene called *NPR1* or *NIM1*. Mutations in *npr1* abolish SAR, and cause enhanced susceptibility to infection by various pathogens (Cao et al., 1994; Delaney et al., 1995; Glazebrook et al., 1996; Shah et al., 1997). *NPR1* appears to be a positive regulator of PR gene expression that acts downstream from SA. *NPR1* encodes a novel protein that contains ankyrin repeats (which are often involved in protein-protein interactions (Cao et al., 1997; Ryals et al., 1997), and that is localized to the nucleus in the presence of SA (Dong et al., 1998).

Consequently, it is unlikely that NPR1 acts as a transcription factor to directly control *PR* gene expression, but its nuclear localization suggests that it may interact with such transcription factors.

PAD4 appears to act upstream from SA. In *pad4* plants infected with a virulent *P. syringae* strain, SA levels, synthesis of the antimicrobial compound camalexin, and *PR1* expression are all reduced (Zhou et al., 1998). SA is necessary, but not sufficient, for activation of camalexin synthesis (Zhou et al., 1998; Zhao et al., 1996). The camalexin defect in *pad4* plants is reversible by exogenous SA (Zhou et al., 1998). Mutations in *pad4* do not affect SA levels, camalexin synthesis, or *PR1* when plants are infected with an avirulent *P. syringae* strain (Zhou et al., 1998). Taken together, these results suggest that PAD4 is required for signal amplification to activate the SA pathway in response to pathogens that do not elicit a strong defense response (Zhou et al., 1998).

JA-dependent signaling

JA signaling affects diverse processes including fruit ripening, pollen development, root growth, and response to wounding (Creelman et al., 1997). The *jar1* and *coil* mutants fail to respond to JA (Feys et al., 1994; Staswick et al., 1992). *COI1* has been cloned, and found to encode protein containing leucine-rich repeats and a degenerate F-box motif (Xie et al., 1998). These features are characteristic of proteins that function in complexes that ubiquitinate protein targeted for degradation.

In the past few years it has become apparent that JA plays an important role in regulation of pathogen defenses. For example, the induction of the defensin gene *PDF1.2* after inoculation of *Arabidopsis* with the avirulent pathogen *Alternaria brassicicola* does not require SA or NPR1, but does require ethylene and JA signaling (Penninck et al., 1996).

SA signaling and JA signaling pathways are interconnected in complicated ways. Studies in other systems have shown that SA signaling and JA signaling are mutually inhibitory (Creelman et al., 1997; Harms et al., 1998). However, synthesis of camalexin in response to *P. syringae* infection is blocked in *nahG* (Zhou et al.,

1998; Zhao et al., 1996) and *coi1* (Glazebrook, 1999) plants, strongly suggesting that camalexin synthesis requires both SA and JA signaling.

Induced systemic resistance (ISR)

Some rhizosphere-associated bacteria promote disease resistance (van Loon et al., 1998). This phenomenon, called ISR, has been studied using *Pseudomonas fluorescens* strain WCS417r to colonize *Arabidopsis* roots (Pieterse et al., 1996). Colonized plants are more resistant to infection by the fungal pathogen *Fusarium oxysporum* f sp *raphani* and *P. syringae* (Pieterse et al., 1996). ISR occurs in *nahG* plants, indicating that it is not a SA-dependent phenomenon (Pieterse et al., 1996). Rather, ISR appears to be JA- and ethylene-dependent. The observation that ethylene can induce ISR in *jar1* mutants led to the hypothesis that ISR requires a JA signal followed by an ethylene signal (Pieterse et al., 1998). No changes in gene expression associated with ISR have been detected (Pieterse et al., 1998), suggesting that it is different from activation of *PDF1.2* expression by *A. brassicicola*.

Curiously, ISR requires *NPR1* (Pieterse et al., 1996). This was unexpected in light of the fact that *NPR1* was previously known to be involved only in SA-dependent processes and ISR is SA-independent. If the SA-dependent signal is received, *NPR1* mediates a resistance response characterized by *PR1* expression, whereas if the ISR signal is received, *NPR1* mediates a different resistance response. It is difficult to imagine how this could occur, unless *NPR1* is interacting with different 'adapter' molecules to mediate the different signals. The ankyrin repeats found in *NPR1* could function in protein-protein interactions between *NPR1* and adapter proteins. Identification of proteins that interact with *NPR1*, and characterization of plants with loss-of-function mutations affecting those proteins, would be very helpful for understanding how *NPR1* acts in each pathway. It would also be worthwhile to determine if the *ssi1* or *cpr6* mutations suppress the ISR defect of *npr1* mutants.

Relevance to disease resistance

Characterization of the effects of various mutations on resistance to different pathogens has revealed that there is considerable variation in the extent to which pathogens are affected by defense mechanisms. SAR is known to confer resistance

to a wide array of pathogens, including bacteria, fungi, oomycetes, and viruses. JA signaling is important for limiting the growth of certain fungal pathogens. In *Arabidopsis*, the SA pathway mutants *npr1* and *pad4* show enhanced susceptibility to *P. syringae* and *P. parasitica* (Cao et al., 1994; Delaney et al., 1995; Shah et al., 1997; Zhou et al., 1998; Glazebrook et al., 1997).

Overexpression of rate-limiting defense response regulators may cause the signaling network to respond faster or more strongly to pathogen attack, thereby improving resistance. For example, overexpression of *NPR1* caused increased resistance to *P. syringae* and *P. parasitica* in a dosage dependent manner (Cao et al., 1998). Moreover, *NPR1*-overexpression had no obvious deleterious effects on plant growth, in contrast to mutations that lead to constitutive overexpression of defense responses, which generally cause dwarfism.

Promoters for gene expression of plant pathogen defense genes

Promoters (and other regulatory components) from bacteria, viruses, fungi and plants have been used to control gene expression in plant cells. Numerous plant transformation experiments using DNA constructs comprising various promoter sequences fused to various foreign genes (for example, bacterial marker genes) have led to the identification of useful promoter sequences. It has been demonstrated that sequences up to 500-1,000 bases in most instances are sufficient to allow for the regulated expression of foreign genes. However, it has also been shown that sequences much longer than 1 kb may have useful features which permit high levels of gene expression in transgenic plants. The expression of genes encoding proteins that are useful for protecting plants from pathogen attack may have deleterious effects on plant growth if expressed constitutively. Consequently, it is desirable to have promoter sequences that control expression of these gene(s) in such a way that expression is absent or very low in the absence of pathogens, and high in the presence of pathogens.

Thus, what is needed is the identification of plant genes useful to confer resistance to a pathogen(s) and plant promoters, the expression of which is altered in response to pathogen attack.

Summary of the Invention

The invention generally provides an isolated nucleic acid molecule (polynucleotide) comprising a plant nucleotide sequence obtained or isolatable from a gene, the expression of which is altered, either increased or decreased, in response to pathogen infection. In one embodiment, the plant nucleotide sequence comprises an open reading frame, while in another embodiment, the plant nucleotide sequence comprises a promoter. A promoter sequence of the invention directs transcription of a linked nucleic acid segment, e.g., a linked plant DNA comprising an open reading frame for a structural or regulatory gene, in a host cell, such as a plant cell, in response to pathogen infection of that cell. As used herein, a "pathogen" includes bacteria, fungi, oomycetes, viruses, nematodes and insects, e.g., aphids (see Hammond-Kosack and Jones, 1997). Moreover, the expression of a plant nucleotide sequence of the invention comprising a promoter may be altered in response to one or more species of bacteria, nematode, fungi, oomycete, virus, or insect. Likewise, the expression of a plant nucleotide sequence of the invention comprising an open reading frame may be useful to confer tolerance or resistance of a plant to one or more species of bacteria, nematode, fungi, oomycete, virus or insect.

The nucleotide sequence preferably is obtained or isolatable from plant DNA. In particular, the nucleotide sequence is obtained or isolatable from a gene encoding a polypeptide which is substantially similar, and preferably has at least 70%, e.g., 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, and even 90% or more, e.g., 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, and 99%, amino acid sequence identity, to a polypeptide encoded by an *Arabidopsis* gene comprising any one of SEQ ID NOs: 1-953 and 2137-2661 or a fragment (portion) thereof which encodes a partial length polypeptide having substantially the same activity of the full-length polypeptide, a rice gene comprising one of SEQ ID NOs: 2000-2129 and 2662-6813, or a *Chenopodium* gene comprising one of SEQ ID NOs: 1954-1966.

The present invention also provides an isolated nucleic acid molecule comprising a plant nucleotide sequence that directs transcription of a linked nucleic acid segment in a host cell, e.g., a plant cell. The nucleotide sequence preferably is

obtained or isolatable from plant genomic DNA. In particular, the nucleotide sequence is obtained or isolatable from a gene encoding a polypeptide which is substantially similar, and preferably has at least 70%, e.g., 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, and even 90% or more, e.g., 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, and 99%, amino acid sequence identity, to a polypeptide encoded by an *Arabidopsis* gene comprising any one of SEQ ID NOs:1-953 and 2137-2661, a rice gene comprising one of SEQ ID NOs:2000-2129 and 2662-6813, or a *Chenopodium* gene comprising any one of SEQ ID NOs:1954-1966, the expression of which is increased or decreased in response to pathogen infection. Preferred promoters comprise DNA obtained or isolatable from a gene encoding a polypeptide which is substantially similar, and preferably has at least 70%, e.g., 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, and even 90% or more, e.g., 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, and 99%, amino acid sequence identity, to a polypeptide encoded by an *Arabidopsis* gene comprising a promoter according to SEQ ID NOs:1001-1095 and 2137-2661, a rice gene comprising a promoter according to SEQ IN NOs:4738-6813, or a fragment thereof (i.e., promoters isolatable from any one of SEQ ID NOs:1001-1095, 2137-2661 and 4738-6813) which increases or decreases transcription of a linked nucleic acid segment in response to pathogen infection.

The invention also provides uses for an isolated nucleic acid molecule, e.g., DNA or RNA, comprising a plant nucleotide sequence comprising an open reading frame encoding a polypeptide which is substantially similar, and preferably has at least 70%, e.g., 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, and even 90% or more, e.g., 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, and 99%, amino acid sequence identity, to a polypeptide encoded by an *Arabidopsis*, *Chenopodium* or rice gene comprising an open reading frame comprising any one of SEQ ID NOs:1-953, 1954-1966, 2000-2129, 2662-4737 or the complement thereof. For example, these open reading frames may be useful to prepare plants that over- or under-express the encoded product or to prepare knockout plants.

The promoters and open reading frames of the invention can be identified by any method. For example, they can be identified by employing an array of nucleic acid samples, e.g., each sample having a plurality of oligonucleotides, and each plurality corresponding to a different plant gene, on a solid substrate, e.g., a DNA chip, and probes corresponding to nucleic acid which is up- or down-regulated in response to pathogen infection in one or more ecotypes or species of plant relative to a control (e.g., a water control, nucleic acid from an uninfected plant or nucleic acid from a mutant plant). Thus, genes that are upregulated or downregulated in response to pathogen infection can be systematically identified.

As described herein, GeneChip® technology was utilized to discover a plurality of genes, the expression of which is altered after pathogen infection. The *Arabidopsis* oligonucleotide probe array consists of probes from about 8,100 unique *Arabidopsis* genes, which covers approximately one third of the genome. This genome array permits a broader, more complete and less biased analysis of gene expression. Using labeled cRNA probes, expression levels were determined by laser scanning and genes generally selected for expression levels that were > 2 fold over the control.

For example, using this approach, 953 genes were identified, the expression of which was altered after infection of wild-type *Arabidopsis* plants with a pathogen (SEQ ID NOs:1-953). In addition, 745 genes were identified, the expression which was increased after infection of wild-type *Arabidopsis* with *Pseudomonas syringae* (SEQ ID NOs: 2-6, 8-13, 16, 18, 22-23, 25, 28-29, 31-32, 35-37, 39-43, 45-47, 49-50, 52, 54-55, 57-58, 60-66, 70-72, 74, 76-77, 79, 81, 83, 85, 87-90, 92, 94, 97, 100-107, 111-115, 117-125, 127-135, 138-140, 142-153, 156-158, 160, 162-165, 168-170, 173-181, 183-184, 186-188, 190-198, 200-201, 203-211, 214-215, 218-224, 227-232, 234-249, 251-262, 264, 266-268, 270, 272-275, 277-281, 283, 286-294, 297-298, 302, 304-306, 308-326, 328-339, 341, 344-345, 347, 350-351, 353-358, 361-371, 373-377, 379-386, 388-390, 392, 394-400, 402-406, 408-410, 412-417, 419-427, 429-433, 435-443, 445-452, 454-457, 459-460, 462-464, 466-470, 473-475, 478-479, 481-482, 484-187, 489-494, 496-498, 500-501, 503-506, 508, 510, 512-515, 517-523, 526, 528-529, 531-538, 540, 544-548, 550-558, 560, 563-568,

570, 572-577, 579-580, 582-585, 588-594, 596, 598-600, 602-603, 605-606, 608-612, 614-617, 619-624, 626-630, 632-639, 642, 644, 646-651, 653-657, 659-665, 667-671, 673-678, 681-689, 691-693, 695-713, 715-717, 719, 721-727, 729-733, 736-738, 740, 742, 744, 746, 748-752, 755-756, 758-760, 762-769, 771, 774, 776-781, 783-788, 790-796, 798-799, 802, 804-808, 810-815, 817-831, 833-848, 850-855, 857-869, 871-880, 882-900, 903-907, 909, 911-915, 918-920, 922-925, 927, 929, 931-938, 940, 943-945, 947, and 950-953). Of the 745 genes, the expression of 530 of those genes was altered in at least one mutant *Arabidopsis* after infection with *Pseudomonas syringae* (SEQ ID NOs: 2, 4-6, 11-13, 18, 22-23, 28, 31, 36, 39-43, 45, 47, 49-50, 52, 54-55, 57-58, 60-61, 63-66, 71-72, 74, 77, 81, 83, 85, 87-89, 92, 97, 100-107, 111-112, 114-115, 117-120, 122, 125, 127-128, 134, 128-140, 143-144, 148-151, 153, 156-157, 160, 165, 168-170, 173-174, 176-180, 183, 187-188, 191, 193-194, 197-198, 200, 203-210, 214, 219-224, 227, 230-232, 235-237, 239-240, 243-246, 248-249, 251-254, 256-258, 261, 264, 266-268, 270, 272-275, 277-278, 280, 283, 286-287, 290-293, 297, 302, 305-306, 308-310, 312-316, 321-326, 328-331, 333, 336-339, 341, 345, 351, 353, 355-358, 361-363, 365-366, 368-371, 373, 375, 377, 379-381, 384-385, 388-390, 392, 394-400, 402-406, 410, 412, 415-416, 419-420, 422-425, 429-433, 435-439, 441-443, 445-452, 454, 459-460, 463, 466, 468-470, 473, 481-482, 485-486, 489, 491-494, 497-498, 500-501, 503, 505-506, 508, 510, 513-515, 517, 520-521, 523, 528-529, 531, 533-538, 540, 545-548, 550-551, 553-554, 556-558, 560, 566-567, 575, 580, 582-584, 588-593, 596, 598-600, 602-603, 605-606, 608-610, 612, 614, 616, 620-622, 627-629, 633-634, 636-639, 644, 646, 648-651, 654-657, 659, 661-663, 667, 669, 673-674, 677, 682, 684-687, 689, 691-693, 697, 699, 701, 703-708, 713, 717, 719, 721-727, 730-733, 736, 740, 744, 746, 749-752, 755-756, 758-760, 762-764, 766-769, 774, 776-778, 780-781, 786, 788, 791-796, 799, 802, 804-808, 810-812, 815, 818-821, 823-825, 827-829, 831, 833-836, 838-843, 845, 847-848, 852-853, 855, 858, 860-869, 871-874, 876, 878-880, 884-887, 889, 892-894, 896-900, 904-907, 911-915, 918-920, 922-924, 931, 933, 938, 943-945, 947, and 950-952). Of the 530, 81 encode regulatory factors (SEQ ID NOs: 39, 52, 60, 63, 81, 83, 106, 107, 115, 117, 118, 168, 174, 176, 179, 204, 207, 208, 220, 221, 248, 258, 268, 275, 280, 309, 323, 326, 329, 351, 419,

422, 429, 430, 432, 459, 460, 468, 469, 473, 500, 505, 506, 508, 529, 531, 533, 535, 538, 545, 553, 602, 606, 608, 610, 614, 616, 634, 654, 655, 684, 686, 687, 691, 717, 751, 752, 766, 777, 815, 831, 834, 835, 839, 841, 847, 876, 884, 906, 920, and 924).

As also described herein, 333 genes were identified that are useful to confer improved resistance to plants to bacterial infection (SEQ ID NOs: 12-13, 18, 23, 36, 39-40, 43, 45, 50, 52, 57-58, 60-61, 64, 71-72, 81, 87-89, 97, 100, 102-105, 107, 111-112, 115, 119-120, 122, 125, 127-128, 140, 144, 148-150, 153, 165, 168-169, 176-177, 179, 183, 188, 191, 193-194, 197-198, 203-206, 208-209, 214, 219-222, 227, 230, 232, 237, 244-246, 248-249, 251-253, 258, 261, 264, 266, 268, 273-275, 283, 287, 290, 293, 297, 302, 305-306, 308, 312-315, 321-322, 324, 326, 330, 333, 338, 341, 345, 353, 356-358, 362-363, 366, 369, 371, 375, 377, 380, 384-385, 389, 392, 394-395, 398-399, 402-404, 406, 410, 415, 419, 422, 425, 429-430, 433, 435-439, 443, 445-452, 454, 463, 466, 468-470, 473, 486, 489, 491-492, 4894, 498, 500-501, 503, 508, 513-514, 517, 529, 533-538, 548, 550, 553-554, 4556-558, 566, 575, 580, 582-583, 590-591, 593, 600, 602, 609-610, 612, 614, 620-622, 627-629, 637-638, 644, 649, 654-657, 659, 663, 667, 669, 673-674, 677, 684-685, 689, 691-693, 699, 703-705, 708, 719, 721, 724-726, 730-732, 744, 746, 749-750, 752, 755-756, 758, 760, 762-764, 767, 769, 774, 780-781, 786, 788, 791-792, 794-796, 799, 804-808, 810-812, 815, 818-819, 823, 828-829, 833, 840841, 843, 847, 852-853, 858, 860, 862-865, 867-868, 872-874, 876, 885-887, 889, 892-894, 896-900, 904-905, 907, 911-914, 918-920, 922-924, 931, 933, 938, 947, 950, and 952).

Further, 296 genes were identified that are useful to confer improved resistance to plants to fungal infection (SEQ ID NOs: 2, 4, 6, 11-13, 18, 22-23, 31, 41-43, 49-50, 54, 57-58, 61, 64-66, 71-72, 74, 77, 85, 87, 89, 92, 97, 101, 103, 106-107, 112, 114, 117-119, 125, 128, 134, 138, 143, 149, 151, 156-157, 165, 169-170, 174, 176-180, 187-188, 191, 193, 206, 208, 219-220, 222, 224, 231, 236, 239, 243-245, 251-254, 256-257, 267, 272, 287, 290, 292, 297, 302, 312-313, 315-316, 321-322, 324-325, 328, 330, 345, 351, 353, 355-357, 362-363, 366, 368-371, 373, 375, 379, 381, 384, 388-390, 392, 395-400, 405, 410, 415-416, 419, 422, 424, 431-432, 435-436, 438-439, 447, 459-460, 470, 473, 481-482, 489, 491, 493-494, 500-501, 505-506, 513-514, 517, 520-521, 523, 528-529, 531, 535, 537-538, 540, 545-548,

551, 553-554, 557-558, 566, 575, 580, 582, 584, 589, 591, 593, 596, 598-599, 603, 605, 608-609, 612, 628, 633-634, 636-637, 639, 646, 648, 650-651, 656, 661, 663, 667, 674, 685-687, 689, 691, 693, 697, 699, 701, 705, 707, 713, 723-724, 726, 736, 740, 749, 751-752, 756, 758-759, 764, 766-768, 774, 776, 778, 780, 792-796, 799, 802, 806, 810-812, 818, 820-821, 825, 827-829, 833-836, 838-839, 841-843, 848, 855, 860-861, 866, 868-869, 871, 873-874, 876, 878-880, 889, 892, 898-900, 904-905, 907, 915, 918, 922, 924, 933, 943-945, 947, and 951).

In addition, 288 genes were identified that are useful to confer improved resistance to plants to infection with more than one pathogen, e.g., pathogens that include bacteria, oomycetes and viruses (SEQ ID NOs: 12-13, 18, 23, 36, 39-40, 43, 45, 50, 52, 57-58, 60-61, 64, 71-72, 81, 87-88, 100, 102-105, 107, 111-112, 115, 119-120, 122, 125, 127-128, 140, 148-150, 153, 168-169, 176-177, 188, 191, 193-194, 197-198, 203-206, 209, 219-222, 227, 232, 237, 244-246, 248-249, 251-253, 258, 261, 264, 266, 268, 273-275, 283, 287, 290, 293, 297, 302, 305-306, 308, 312-315, 324, 326, 330, 333, 341, 345, 353, 356, 358, 366, 371, 375, 377, 380, 385, 389, 392, 394, 398, 402-404, 406, 410, 415, 419, 425, 429-430, 433, 435-438, 443, 445-447, 449-452, 454, 463, 466, 468-470, 473, 486, 489, 492, 494, 498, 500-501, 503, 508, 513-514, 517, 533-538, 548, 550, 553-554, 57-558, 566, 575, 582-583, 590-591, 593, 600, 602, 609-610, 612, 620-622, 627-629, 637-638, 644, 649, 654-657, 659, 667, 669, 673, 677, 684, 689, 692-693, 703-705, 719, 721, 724-726, 730-732, 744, 746, 749-750, 752, 755-756, 760, 762-764, 767, 769, 774, 780-781, 786, 788, 791-792, 795-796, 805-808, 810-812, 815, 818-819, 823, 828, 833, 840-841, 843, 852-853, 858, 860, 862-865, 867-868, 872-874, 876, 887, 889, 893-894, 896-898, 900, 905, 907, 911-914, 918-920, 922-923, 931, 933, 938, 947, 950, and 952).

Using the same approach described above, 25 genes were identified (SEQ ID NOs: 1, 15, 19, 20, 24, 26, 27, 34, 38, 51, 56, 59, 67-69, 99, 116, 155, 159, 182, 212, 284, 372, 444, and 789), the expression of which was decreased at 6 hours in an *avr2* plant. Also identified were 33 genes (SEQ ID NOs: 17, 70, 76, 81, 84, 109, 123, 144, 160, 230, 265, 268, 269, 271, 323, 333, 385, 427, 428, 430, 457, 505, 569, 597, 602, 606, 616, 708, 730, 741, 812, 862, and 942), the expression of which was elevated in an incompatible or a compatible interaction in four *Arabidopsis* ecotypes

infected with bacteria. Eight of the genes were upregulated by 3 hours in an incompatible interaction, 18 of the genes were upregulated by 6 hours, but not at 3 hours, in an incompatible interaction, and 6 of the genes were upregulated in a compatible interaction.

5 Further identified were 33 genes, the expression of which was induced early after infection (SEQ ID NOs:17, 21, 80, 81, 156, 174, 176, 221, 227, 296, 302, 303, 306, 333, 340, 360, 500, 505, 524, 575, 601, 602, 614, 628, 687, 733, 782, 811, 835, 862, 900, 905, and 912), 10 genes, the expression of which was decreased early after infection (SEQ ID NOs:30, 73, 282, 541, 640, 679, 761, 870, 917, and 930), and 135
10 genes, 107 of which were induced at 3 and/or 6 hours after infection, and 28 of which were decreased after infection (SEQ ID NOs:7, 21, 33, 44, 46, 60, 82, 86, 91, 93, 106, 110, 119, 122, 130, 131, 136, 141, 154, 161, 166-168, 171, 176, 185, 189, 199, 200, 202, 203, 213, 225, 227, 248, 261, 262, 266, 274, 285, 300, 301, 302, 320, 326, 341, 345, 348, 349, 360, 366, 378, 406, 409, 422, 425, 434, 441, 443, 446, 449,
15 454, 461, 471, 475, 476, 483, 485, 499, 500, 511, 512, 516, 527, 530, 533, 543, 545, 549, 550, 552, 567, 575, 578, 586, 590, 608, 611, 615, 618, 625, 631, 643, 656, 658, 659, 666, 668, 671, 680, 690, 694, 704, 706, 711, 714, 718, 721, 728, 734, 738, 757, 770, 772, 791, 807, 811, 813, 816, 827, 857, 864, 868, 875, 881, 893, 901, 905, 908, 912, 916, 939, 941, 951, and 952).

20 In a similar approach, 48 genes that were upregulated in response to infection, e.g., bacterial or fungal infection, as well as 46 of the corresponding promoter containing regions, were identified. Thirty-six of the genes were upregulated in response to bacterial, e.g., *Pseudomonas*, infection (the promoters for genes corresponding to SEQ ID NOs: 104-106, 119, 123, 129, 131, 151-152, 183,
25 191, 198, 200, 227, 249, 274, 302, 358, 415, 481, 547, 566, 582, 628, 633, 639, 656, 673, 793, 818, 827, 864, 874, 880, and 904-905), while 23 of the genes were upregulated in response to fungal, e.g., *Botrytis*, infection (SEQ ID NOs: 18, 71, 119, 123, 129, 151, 191, 244, 245, 302, 545, 547, 562, 566, 637, 653, 747, 756, 774, 793, 842, 864, and 905). Twenty-five of the genes were upregulated only in
30 response to bacterial, e.g., *Pseudomonas*, infection (the promoters for genes corresponding to SEQ ID NOs: 104-106, 131, 152, 183, 198, 200, 227, 249, 274,

358, 415, 481, 582, 628, 633, 639, 656, 673, 818, 827, 874, 880, and 904 are provided in SEQ ID NOs:1001-1025), 10 of the genes were upregulated only in response to fungal, e.g., *Botrytis*, infection (the promoters for genes corresponding to SEQ ID NOs:18, 71, 244, 245, 545, 562, 637, 653, 747, 756, 774, and 842 are provided in SEQ ID NOs:1026-1035), and 11 genes were upregulated in response to both bacterial and fungal infection (the promoters for genes corresponding to SEQ ID NOs:119, 123, 129, 151, 191, 302, 547, 566, 793, 864, and 905 are provided in SEQ ID NOs:1036-1046).

As also described hereinbelow, 129 *Arabidopsis* genes (SEQ ID NOs: 3, 51, 54, 60, 61, 66, 75, 76, 78, 88, 95, 96, 101, 106, 108, 123, 126, 128, 129, 131, 137, 145-147, 150, 158, 169, 170, 172, 173, 197, 200, 216, 219, 224, 230, 233, 237, 249, 250, 263, 274, 275, 276, 299, 307, 323, 333, 342, 346, 359, 382, 383, 387, 391, 393, 401, 411, 415, 427, 442, 455, 459, 466, 477, 481, 485, 487, 502, 511, 515, 525, 534, 539, 542, 560, 571, 577, 579, 584, 587, 595, 600, 627, 638, 645, 654, 659, 668, 681, 688, 695, 696, 706, 708, 730, 742, 753, 775, 785, 786, 791, 797, 800, 801, 809, 817, 819, 820, 823, 827, 847, 856, 875, 885, 896, 902, 910, 921, 922, 923, 925, 926, 928, 946, and 952) were identified that were upregulated in response to viral infection, and 46 *Arabidopsis* genes were identified that were downregulated in response to viral infection (SEQ ID NOs: 14, 48, 53, 98, 217, 226, 295, 327, 343, 352, 369, 404, 407, 418, 453, 458, 465, 472, 480, 488, 495, 507, 509, 513, 514, 559, 561, 581, 604, 607, 613, 641, 652, 672, 720, 735, 739, 743, 745, 754, 773, 803, 832, 849, 948, and 949).

Also provided are nucleic acid molecules comprising a nucleotide sequence comprising an open reading frame expressed in response to pathogen infection comprising SEQ ID NOs:209, 216, 262, 267, 317, 386, 425, 440 and 800. These sequences are useful to over- or under-express the encoded product, or prepare knock-out plants which have an altered response to pathogen infection.

The invention therefore provides a method in which the open reading frame of a plant pathogen resistance gene, e.g., a gene that is associated with a response to pathogen infection, which is altered in a plant in response to infection is identified and isolated. A transgene comprising the isolated open reading frame may be

introduced to and expressed in a transgenic plant, e.g., prior to infection, e.g., constitutively, or early and/or rapidly after infection, or in regulatable (inducible) fashion, e.g., after exposure to a chemical or using a promoter that is upregulated after infection, so as to confer resistance to that transgenic plant to the pathogen relative to a corresponding plant which does not have the transgene. The expression of the transgene is preferably at higher than normal levels, and under the regulation of a promoter that allows very fast and high induction in response to the presence of a pathogen or under cycling promoters (e.g., circadian clock regulated promoters), such that the encoded gene product(s) is maintained at sufficiently high levels to provide enhanced resistance or tolerance. The invention further provides a method in which a gene in a plant which is downregulated in response to infection, is disrupted or the expression of that gene is further downregulated, e.g., using antisense expression, so as to result in a plant that has enhanced resistance to infection, and which disruption or downregulation preferably has little or no detrimental effect(s) on the host plant.

As also described herein, it was found that the early incompatible response was similar to the late compatible response, suggesting that early expression of plant pathogen-resistance genes is important for resistance. Also, various plant strains were found to respond differently to the same pathogen, but there was also an identifiable global pattern of response. Thus, the comparison of the expression patterns in incompatible and compatible interactions in one or more ecotypes can lead to identifying subsets of key responding genes and clusters of genes that are key (early) responders. In addition, the observed global expression pattern indicated that the least resistant strain tested (Ws) had a low basal level of pathogen-upregulated genes and a high level of pathogen-downregulated genes compared to the most resistant strain (Ler). Thus, plant strains that are more resistant to pathogens have a gene expression phenotype in which genes that are upregulated in response to infection are already expressed at a higher than normal basal level, and those genes that are downregulated are expressed at a lower than normal basal level.

Thus, further provided herein is a method to identify at least one gene involved in plant (dicot or monocot) resistance or response to infection by at least

one pathogen, e.g., a bacterium, fungus or virus, which method involves determining or detecting plant gene expression in an incompatible interaction and identifying at least one gene whose expression is significantly altered, e.g., upregulated or downregulated in response to infection, in the incompatible interaction relative to expression of the at least one gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to infection by a pathogen, or in a corresponding compatible interaction. Also provided is a method to identify at least one gene involved in plant (dicot or monocot) resistance or response to infection by at least one pathogen, e.g., bacterium, fungus or virus, which method involves determining or detecting plant gene expression in a compatible interaction; and identifying at least one gene whose expression is significantly altered, e.g., upregulated or downregulated in response to infection, in the compatible interaction relative to expression of the at least one gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to infection by a pathogen, or in a corresponding incompatible interaction. A compatible interaction can be, for example, between a plant having a resistance gene and a pathogen lacking a corresponding avirulence gene, a plant lacking a resistance gene to a pathogen having a corresponding avirulence gene, or a plant lacking a resistance gene and a pathogen lacking a corresponding avirulence gene. For example, the gene identified by such a method can encode a polypeptide that is substantially similar to a polypeptide encoded by an open reading frame comprising one of SEQ ID NOs: 50, 139, 609, 2699, 3311, 3463, 3584, 3791, 4210, 4451 or 4595, or has an open reading frame comprising one of SEQ ID NOs: 50, 139, 609, 2699, 3311, 3463, 3584, 3791, 4210, 4451 or 4595. In such a method, gene expression can be detected or determined using, for example, a gene chip, a cDNA array, cDNA-AFLP or differential display PCR. Such a method can further involve isolating the at least one gene or a portion thereof which includes the open reading frame or promoter for the gene.

Further provided is a method to identify at least one gene, the expression of which is altered by pathogen infection in a wild-type plant relative to a plant having a mutation that decreases jasmonic acid or ethylene-dependent signaling, which

method involves contacting a plurality of isolated nucleic acid samples on a solid substrate each comprising isolated nucleic acid with a probe comprising plant nucleic acid corresponding to RNA from a wild-type plant infected with the pathogen, so as to form a complex, wherein each sample comprises a plurality of

5 oligonucleotides corresponding to at least a portion of one plant gene; and comparing complex formation in a) with complex formation between a second plurality of isolated nucleic acid samples on a solid substrate with a second probe comprising nucleic acid corresponding to RNA from the plant having the mutation and infected with the pathogen, so as to identify a gene, the expression of which is

10 altered by pathogen infection in a wild-type plant relative to the mutant plant. Also provided herein is a method to identify at least one gene, the expression of which is altered by pathogen infection in a wild-type plant relative to a plant having a mutation in a gene that interferes with salicylic acid dependent signaling, which method involves contacting a plurality of isolated nucleic acid samples on a solid

15 substrate each comprising isolated nucleic acid with a probe comprising plant nucleic acid corresponding to RNA from a wild-type plant infected with the pathogen, so as to form a complex, wherein each sample comprises a plurality of oligonucleotides corresponding to at least a portion of one plant gene; and comparing complex formation in a) with complex formation between a second

20 plurality of isolated nucleic acid samples on a solid substrate with a second probe comprising nucleic acid corresponding to RNA from the plant having a mutation and infected with the pathogen, so as to identify a gene, the expression of which is altered by pathogen infection in a wild-type plant relative to the mutant plant. Also provided herein is a method to identify at least one gene, the expression of which is

25 altered by pathogen infection in a wild-type plant relative to a plant having a mutation that results in enhanced susceptibility to bacterial infection, which method involves contacting a plurality of isolated nucleic acid samples on a solid substrate each comprising isolated nucleic acid with a probe comprising plant nucleic acid corresponding to RNA from a wild-type plant infected with the pathogen, so as to

30 form a complex, wherein each sample comprises a plurality of oligonucleotides corresponding to at least a portion of one plant gene; and comparing complex

formation in a) with complex formation between a second plurality of isolated
 nucleic acid samples on a solid substrate with a second probe comprising nucleic
 acid corresponding to RNA from the plant having a mutation and infected with the
 pathogen, so as to identify a gene, the expression of which is altered by pathogen
 5 infection in a wild-type plant relative to the mutant plant. In addition, provided
 herein is a method to identify at least one gene, the expression of which is altered by
 infection with at least one virus, which method comprises contacting a plurality of
 isolated nucleic acid samples on a solid substrate each comprising isolated nucleic
 acid with a probe comprising plant nucleic acid corresponding to RNA from a wild-
 10 type plant infected with a virus, so as to form a complex, wherein each sample
 comprises a plurality of oligonucleotides corresponding to at least a portion of one
 plant gene; and comparing complex formation in a) with complex formation
 between a second plurality of isolated nucleic acid samples on a solid substrate with
 a second probe comprising nucleic acid corresponding to RNA from an uninfected
 15 plant, so as to identify a gene, the expression of which is altered by virus infection.
 Also provided is a method to identify at least one gene, the expression of which is
 altered by infection with at least one pathogen, which involves contacting a plurality
 of isolated nucleic acid samples on a solid substrate each comprising isolated
 nucleic acid with a probe comprising plant nucleic acid corresponding to RNA from
 20 an incompatible interaction so as to form a complex, wherein each sample
 comprises a plurality of oligonucleotides corresponding to at least a portion of one
 plant gene; and comparing complex formation in a) with complex formation
 between a second plurality of isolated nucleic acid samples on a solid substrate with
 a second probe comprising nucleic acid corresponding to RNA from a
 25 corresponding compatible interaction so as to identify a gene, the expression of
 which is altered by the pathogen. In any of the methods described herein, the probes
 can have nucleic acid, for example, from a dicot, a cereal plant, or a monocot.
 Further, the methods can additionally involve identifying the promoter for the at
 least one gene.
 30 The genes and promoters described hereinabove can be used to identify
 orthologous genes and their promoters which are also likely useful to enhance

resistance of plants to pathogens. Moreover, the orthologous promoters are useful to express linked open reading frames. In addition by aligning the promoters of these orthologs, novel *cis* elements can be identified that are useful to generate synthetic promoters.

5 Hence, the isolated nucleic acid molecules of the invention include the orthologs (homologs) of the *Arabidopsis*, *Chenopodium* and rice sequences disclosed herein, i.e., the corresponding nucleic acid molecules in organisms other than *Arabidopsis*, *Chenopodium* and rice, including, but not limited to, plants other than *Arabidopsis*, *Chenopodium* and rice, preferably cereal plants, e.g., corn, wheat,
10 rye, turfgrass, sorghum, millet, sugarcane, soybean, barley, alfalfa, sunflower, canola, soybean, cotton, peanut, tobacco, sugarbeet, or rice. An ortholog is a gene from a different species that encodes a product having the same function as the product encoded by a gene from a reference organism. Databases such GenBank or one found at <http://bioserver.myongji.ac.kr/rjce.html> (for rice) may be employed to
15 identify sequences related to the *Arabidopsis* or *Chenopodium* sequences, e.g., orthologs in cereal crops such as rice. Alternatively, recombinant DNA techniques such as hybridization or PCR may be employed to identify sequences related to the *Arabidopsis* sequences. The encoded ortholog products likely have at least 70% sequence identity to each other. Hence, the invention includes an isolated nucleic
20 acid molecule comprising a nucleotide sequence encoding a polypeptide having at least 70% identity to a polypeptide encoded by one or more of the *Arabidopsis*, *Chenopodium* or rice sequences disclosed herein. For example, promoter sequences within the scope of the invention are those which direct expression of an open reading frame which encodes a polypeptide that is substantially similar to an
25 *Arabidopsis* polypeptide encoded by a gene comprising SEQ ID NOs:1-953.

 The genes and promoters described hereinabove can be used to identify orthologous genes and their promoters which are also likely expressed in a particular tissue and/or development manner. Moreover, the orthologous promoters are useful to express linked open reading frames. In addition, by aligning the promoters of
30 these orthologs, novel *cis* elements can be identified that are useful to generate synthetic promoters. Hence, the isolated nucleic acid molecules of the invention

include the orthologs of the *Arabidopsis* sequences disclosed herein, i.e., the corresponding nucleotide sequences in organisms other than *Arabidopsis*, including, but not limited to, plants other than *Arabidopsis*, preferably cereal plants, e.g., corn, wheat, rye, turfgrass, sorghum, millet, sugarcane, soybean, barley, alfalfa, sunflower, canola, soybean, cotton, peanut, tobacco, sugarbeet, or rice. An orthologous gene is a gene from a different species that encodes a product having the same or similar function, e.g., catalyzing the same reaction as a product encoded by a gene from a reference organism. Thus, an ortholog includes polypeptides having less than, e.g., 65% amino acid sequence identity, but which ortholog encodes a polypeptide having the same or similar function. Databases such as GenBank or one found at <http://bioserver.myongji.ac.kr/rjce.html> (for rice) may be employed to identify sequences related to the *Arabidopsis* sequences, e.g., orthologs in cereal crops such as rice, wheat, sunflower or alfalfa. SEQ ID NOs: 6286, 4210 and for example, are the rice promoter and open reading frame for rice peroxidase, the ortholog of the *Arabidopsis* gene comprising SEQ ID NO: 50. SEQ ID NOs: 3311, 5387, 3791 and 5867 are rice orthologs of the *Arabidopsis* gene comprising SEQ ID NO:609; SEQ ID NOs: 2699, 4775, 3463, 5539, 3584, 5660, 4451, 6527, 4595 and 6671 are rice orthologs of the *Arabidopsis* gene comprising SEQ ID NO: 139.

Preferably, the promoters of the invention include a consecutive stretch of about 25 to 2000, including 50 to 500 or 100 to 250, and up to 1000 or 1500, contiguous nucleotides, e.g., 40 to about 743, 60 to about 743, 125 to about 743, 250 to about 743, 400 to about 743, 600 to about 743, of any one of SEQ ID NOs:1001-1095, 2137-2661, 4738-6813 or the promoter orthologs thereof, which include the minimal promoter region. Preferably, the nucleotide sequence that includes the promoter region includes at least one copy of a TATA box. Thus, the invention provides plant promoters, including orthologs of *Arabidopsis* promoters corresponding to genes comprising any one of SEQ ID NOs: 1-953. The present invention further provides a composition, an expression cassette or a recombinant vector containing the nucleic acid molecule of the invention, and host cells comprising the expression cassette or vector, e.g., comprising a plasmid. In particular, the present invention provides an expression cassette or a recombinant

vector comprising a promoter of the invention linked to a nucleic acid segment which, when present in a plant, plant cell or plant tissue, results in transcription of the linked nucleic acid segment.

In its broadest sense, the term "substantially similar" when used herein with respect to a nucleotide sequence means that the nucleotide sequence is part of a gene which encodes a polypeptide having substantially the same structure and function as a polypeptide encoded by a gene for the reference nucleotide sequence, e.g., the nucleotide sequence comprises a promoter from a gene that is the ortholog of the gene corresponding to the reference nucleotide sequence, as well as promoter sequences that are structurally related the promoter sequences particularly exemplified herein, i.e., the substantially similar promoter sequences hybridize to the complement of the promoter sequences exemplified herein under high or very high stringency conditions. The term "substantially similar" thus includes nucleotide sequences wherein the sequence has been modified, for example, to optimize expression in particular cells, as well as nucleotide sequences encoding a variant polypeptide comprising one or more amino acid substitutions relative to the (unmodified) polypeptide encoded by the reference sequence, which substitution(s) does not alter the activity of the variant polypeptide relative to the unmodified polypeptide. In its broadest sense, the term "substantially similar" when used herein with respect to polypeptide means that the polypeptide has substantially the same structure and function as the reference polypeptide. The percentage of amino acid sequence identity between the substantially similar and the reference polypeptide is at least 65%, 66%, 67%, 68%, 69%, 70%, e.g., 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, and even 90% or more, e.g., 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, up to at least 99%, wherein the reference polypeptide is a polypeptide encoded by an *Arabidopsis* gene comprising any one of SEQ ID NOs:1-953, a *Chenopodium* gene comprising any one of SEQ ID NOs:1954-1966, or a rice gene comprising any one of SEQ ID NOs:2000-2129 and 2662-4737. One indication that two polypeptides are substantially similar to each other, besides having substantially the same function, is

that an agent, e.g., an antibody, which specifically binds to one of the polypeptides, specifically binds to the other.

Sequence comparisons may be carried out using a Smith-Waterman sequence alignment algorithm (see e.g., Waterman (1995) or <http://www>

- 5 [.uto.usc.edu/software/seqaln/index.html](http://www.uto.usc.edu/software/seqaln/index.html)). The localS program, version 1.16, is preferably used with following parameters: match: 1, mismatch penalty: 0.33, open-gap penalty: 2, extended-gap penalty: 2. Further, a nucleotide sequence that is "substantially similar" to a reference nucleotide sequence hybridizes to the reference nucleotide sequence in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM
- 10 EDTA at 50°C with washing in 2X SSC, 0.1% SDS at 50°C, more desirably in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 1X SSC, 0.1% SDS at 50°C, more desirably still in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 0.5X SSC, 0.1% SDS at 50°C, preferably in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM
- 15 EDTA at 50°C with washing in 0.1X SSC, 0.1% SDS at 50°C, more preferably in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 0.1X SSC, 0.1% SDS at 65°C.

- Hence, the present invention further provides an expression cassette or a vector containing the nucleic acid molecule comprising an open reading frame of the
- 20 invention operably linked to a promoter, or comprising a promoter of the invention operably linked to an open reading frame or portion thereof, and the vector may be a plasmid. Such cassettes or vectors, when present in a plant, plant cell or plant tissue result in transcription of the linked nucleic acid fragment in the plant. The expression cassettes or vectors of the invention may optionally include other
- 25 regulatory sequences, e.g., transcription terminator sequences, operator, repressor binding site, transcription factor binding site, and/or an enhancer and may be contained in a host cell. The expression cassette or vector may augment the genome of a transformed plant or may be maintained extrachromosomally. The expression cassette or vector may further have a Ti plasmid and be contained in an
- 30 *Agrobacterium tumefaciens* cell; it may be carried on a microparticle, wherein the microparticle is suitable for ballistic transformation of a plant cell; or it may be

contained in a plant cell or protoplast. Further, the expression cassette can be contained in a transformed plant or cells thereof and the plant may be a dicot or a monocot. In particular, the plant may be a cereal plant.

The invention also provides sense and anti-sense nucleic acid molecules corresponding to the open reading frames identified herein as well as their orthologs. Also provided are expression cassettes, e.g., recombinant vectors, and host cells, comprising the nucleic acid molecule of the invention, e.g., one which comprises a nucleotide sequence which encodes a polypeptide the expression of which is altered in response to pathogen infection.

The present invention further provides a method of augmenting a plant genome by contacting plant cells with a nucleic acid molecule of the invention, e.g., one isolatable or obtained from a plant gene encoding a polypeptide that is substantially similar to a polypeptide encoded by an *Arabidopsis*, *Chenopodium* or rice gene comprising a sequence comprising any one of SEQ ID NOs: 1-953, 1954-1966, 2000-2129 or 2662-4737 so as to yield transformed plant cells; and regenerating the transformed plant cells to provide a differentiated transformed plant, wherein the differentiated transformed plant expresses the nucleic acid molecule in the cells of the plant. The nucleic acid molecule may be present in the nucleus, chloroplast, mitochondria and/or plastid of the cells of the plant. The present invention also provides a transgenic plant prepared by this method, a seed from such a plant and progeny plants from such a plant including hybrids and inbreds. Preferred transgenic plants are transgenic maize, soybean, barley, alfalfa, sunflower, canola, soybean, cotton, peanut, sorghum, tobacco, sugarbeet, rice, wheat, rye, turfgrass, millet, sugarcane, tomato, or potato.

The invention also provides a method of plant breeding, e.g., to prepare a crossed fertile transgenic plant. The method comprises crossing a fertile transgenic plant comprising a particular nucleic acid molecule of the invention with itself or with a second plant, e.g., one lacking the particular nucleic acid molecule, to prepare the seed of a crossed fertile transgenic plant comprising the particular nucleic acid molecule. The seed is then planted to obtain a crossed fertile transgenic plant. The

plant may be a monocot or a dicot. In a particular embodiment, the plant is a cereal plant.

The crossed fertile transgenic plant may have the particular nucleic acid molecule inherited through a female parent or through a male parent. The second
5 plant may be an inbred plant. The crossed fertile transgenic may be a hybrid. Also included within the present invention are seeds of any of these crossed fertile transgenic plants.

The various breeding steps are characterized by well-defined human intervention such as selecting the lines to be crossed, directing pollination of the
10 parental lines, or selecting appropriate progeny plants. Depending on the desired properties different breeding measures are taken. The relevant techniques are well known in the art and include but are not limited to hybridization, inbreeding, backcross breeding, multiline breeding, variety blend, interspecific hybridization, aneuploid techniques, etc. Hybridization techniques also include the sterilization of
15 plants to yield male or female sterile plants by mechanical, chemical or biochemical means. Cross pollination of a male sterile plant with pollen of a different line assures that the genome of the male sterile but female fertile plant will uniformly obtain properties of both parental lines. Thus, the transgenic plants according to the invention can be used for the breeding of improved plant lines that for example
20 increase the effectiveness of conventional methods such as herbicide or pesticide treatment or allow to dispense with said methods due to their modified genetic properties. Alternatively new crops with improved stress tolerance can be obtained that, due to their optimized genetic “equipment”, yield harvested product of better quality than products that were not able to tolerate comparable adverse
25 developmental conditions.

The nucleic acid molecules of the invention, their encoded polypeptides and compositions thereof, are: for open reading frames, useful to provide resistance to pathogens to alter expression of a particular gene corresponding to the open reading frame by decreasing or eliminating expression of that plant gene or by
30 overexpressing a particular gene product, and as a diagnostic for the presence or absence of the pathogen by correlating the expression level or pattern of expression

of one or more of the nucleic acid molecules or polypeptides of the invention; and for promoters, useful to alter the expression of a linked open reading frame in response to pathogen infection. As one embodiment of the invention includes isolated nucleic acid molecules that have increased expression in response to

5 pathogen infection, the invention further provides compositions and methods for enhancing resistance to pathogen infection. The compositions of the invention include plant nucleic acid sequences and the amino acid sequences for the polypeptides or partial-length polypeptides encoded thereby which are described herein, or other plant nucleic acid sequences and the amino acid sequences for the

10 polypeptides or partial-length polypeptides encoded thereby which are operably linked to a promoters are useful to provide tolerance or resistance to a plant to a pathogen, preferably by preventing or inhibiting pathogen infection. Methods of the invention involve stably transforming a plant with one or more of at least a portion of these nucleotide sequences which confer tolerance or resistance operably linked

15 to a promoter capable of driving expression of that nucleotide sequence in a plant cell. By "portion" or "fragment", as it relates to a nucleic acid molecule, sequence or segment of the invention, when it is linked to other sequences for expression, is meant a sequence comprising at least 80 nucleotides, more preferably at least 150 nucleotides, and still more preferably at least 400 nucleotides. If not employed for

20 expressing, a "portion" or "fragment" means at least 9, preferably 12, more preferably 15, even more preferably at least 20, consecutive nucleotides, e.g., probes and primers (oligonucleotides), corresponding to the nucleotide sequence of the nucleic acid molecules of the invention. By "resistant" is meant a plant which exhibits substantially no phenotypic changes as a consequence of infection with the

25 pathogen. By "tolerant" is meant a plant which, although it may exhibit some phenotypic changes as a consequence of infection, does not have a substantially decreased reproductive capacity or substantially altered metabolism.

A method of combating a pathogen in an agricultural crop is also provided. The method comprises introducing to a plant, plant cell, or plant tissue an

30 expression cassette comprising a nucleic acid molecule of the invention comprising an open reading frame so as to yield a transformed differentiated plant, transformed

cell or transformed tissue. Transformed cells or tissue can be regenerated to provide a transformed differentiated plant. The transformed differentiated plant preferably expresses the nucleic acid molecule in an amount that confers resistance to the transformed plant to pathogen infection relative to a corresponding nontransformed plant. The present invention also provides a transformed plant prepared by the method, progeny and seed thereof. Examples of plant viruses which may be combated by the present invention include single stranded RNA viruses (with and without envelope), double stranded RNA viruses, and single and double stranded DNA viruses such as (but not limited to) tobacco mosaic virus, cucumber mosaic virus, turnip mosaic virus, turnip vein clearing virus, oilseed rape mosaic virus, tobacco rattle virus, pea enation mosaic virus, barley stripe mosaic virus, potato viruses X and Y, carnation latent virus, beet yellows virus, maize chlorotic virus, tobacco necrosis virus, turnip yellow mosaic virus, tomato bushy stunt virus, southern bean mosaic virus, barley yellow dwarf virus, tomato spotted wilt virus, lettuce necrotic yellows virus, wound tumor virus, maize streak virus, and cauliflower mosaic virus. Other pathogens within the scope of the invention include, but are not limited to, fungi such as *Cochliobolus carbonum*, *Phytophthora infestans*, *Phytophthora sojae*, *Colletesichum*, *Melampsora lini*, *cladosporium fulvum*, *Heminthosporium maydia*, *Peronospora parasitica*, *Puccinia sorghi*, and *Puccinia polysora*; bacteria such as *Phynchosporium secalis*, *Pseudomonas glycinea*, *Xanthomonas oryzae* and, *Fusarium oxyaporium*; and nematodes such as *Globodera rostochiensis*.

For example, the invention provides a nucleic acid molecule comprising a plant nucleotide sequence comprising at least a portion of a key effector gene(s) responsible for host resistance to particular pathogens. To provide resistance or tolerance to a pathogen in a plant, this sequence may be overexpressed individually, in the sense or antisense orientation, or in combination with other sequences to confer improved disease resistance or tolerance to a plant relative to a plant that does not comprise and/or express the sequence. The overexpression may be constitutive, or it may be preferable to express the effector gene(s) in a tissue-specific manner or from an inducible promoter including a promoter which is

responsive to external stimuli, such as chemical application, or to pathogen infection, e.g., so as to avoid possible deleterious effects on plant growth if the effector gene(s) was constitutively expressed. In one embodiment of the invention, the promoter employed may be one that is rapidly and transiently and/or highly transcribed after pathogen infection.

A transformed (transgenic) plant of the invention includes plants, for example, a plant the cells of which have an expression cassette of the invention, i.e., an expression cassette having a polynucleotide of the invention operatively linked to an open reading frame, or, the genome of which is augmented by a nucleic acid molecule of the invention, or in which the corresponding gene has been disrupted, e.g., to result in a loss, a decrease or an alteration, in the function of the product encoded by the gene, which plant may also have increased yields, e.g., under conditions of pathogen infection, and/or produce a better-quality product than the corresponding wild-type plant. The nucleic acid molecules of the invention are thus useful for targeted gene disruption, as well as markers and probes.

For example, the invention includes a pathogen, e.g., virus, tolerant or resistant plant and seed thereof having stably integrated and expressed within its genome, a nucleic acid molecule of the invention. The normal fertile transformed (transgenic) plant may be selfed to yield a substantially homogenous line with respect to viral resistance or tolerance. Individuals of the line, or the progeny thereof, may be crossed with plants which optionally exhibit the trait. In a particular embodiment of the method, the selfing and selection steps are repeated at least five times in order to obtain the homogenous (isogenic) line. Thus, the invention also provides transgenic plants and the products of the transgenic plants.

The invention further includes a nucleotide sequence which is complementary to one (hereinafter "test" sequence) which hybridizes under low, moderate or stringent conditions with the nucleic acid molecules of the invention as well as RNA which is encoded by the nucleic acid molecule. When the hybridization is performed under stringent conditions, either the test or nucleic acid molecule of invention is preferably supported, e.g., on a membrane or DNA chip. Thus, either a denatured test or nucleic acid molecule of the invention is preferably

first bound to a support and hybridization is effected for a specified period of time at a temperature of, e.g., between 55 and 70°C, in double strength citrate buffered saline (SC) containing 0.1% SDS followed by rinsing of the support at the same temperature but with a buffer having a reduced SC concentration. Depending upon
5 the degree of stringency required such reduced concentration buffers are typically single strength SC containing 0.1% SDS, half strength SC containing 0.1% SDS and one-tenth strength SC containing 0.1% SDS.

The invention further provides a method to identify an open reading frame in the genome of a plant cell, the expression of which is altered by pathogen infection
10 of that cell. The method comprises contacting a solid substrate comprising a plurality of samples comprising isolated plant nucleic acid of a probe comprising plant nucleic acid, e.g., cRNA, isolated from a pathogen infected plant so as to form a complex. Each individual sample comprises one or more nucleic acid sequences (e.g., oligonucleotides) corresponding to at least a portion of a plant gene. The
15 method may be employed with nucleic acid samples and probes from any organism, e.g., any prokaryotic or eukaryotic organism. Preferably, the nucleic acid sample and probes are from a plant, such as a dicot or monocot. More preferably the nucleic acid samples and probes are from a cereal plant. Even more preferably the nucleic acids and probes are from a crop plant. A second plurality of samples on a
20 solid substrate, i.e., a DNA chip, each comprising a plurality of samples comprising isolated plant nucleic acid is contacted with a probe comprising plant nucleic acid isolated from an uninfected or infected control (mutant) plant so as to form a complex. Then complex formation between the samples and probes comprising nucleic acid from infected or control cells compared. For example, potato virus X,
25 tobacco mosaic virus, tobnavirus, cucumber mosaic virus and gemnivirus are known to infect *Arabidopsis*. Thus, *Arabidopsis* genes, the expression of which is altered in response to infection by any of these viruses, can be identified. Regions that are 5' to the start codon for the gene can then be identified and/or isolated.

The invention further provides a method for identifying a plant cell infected
30 with a pathogen. The method comprises contacting nucleic acid obtained from a plant cell suspected of being infected with a pathogen with oligonucleotides

corresponding to a portion of a plurality of sequences selected from SEQ ID NOs:1-953, 1954-1966, 2000-2129 or 2662-4737 under conditions effective to amplify those sequences. Then the presence of the amplified product is detected or determined. The presence of two or more amplified products, e.g., in an amount that is different than the amount of the corresponding amplified products from an uninfected plant, each corresponding to two or more SEQ ID NOs: 1-953, 1954-1966, 2000-2129 or 2662-4737 is indicative of pathogen infection.

The invention further provides a method for identifying a plant cell infected with a pathogen. The method comprises contacting a protein sample obtained from a plant cell suspected of being infected with a pathogen with an agent that specifically binds a polypeptide encoded by an open reading frame comprising SEQ ID NOs:1-953, 1954-1966, 2000-2129 or 2662-4737 so as to form a complex. Then the presence or amount of complex formation is detected or determined.

The invention provides an additional method for identifying a plant cell infected with a pathogen. The method comprises hybridizing a probe selected from SEQ ID NOs:1-953, 1954-1966, 2000-2129 or 2662-4737 to nucleic acid obtained from a plant cell suspected of being infected with a pathogen. The amount of the probe hybridized to nucleic acid obtained from a cell suspected of being infected with a virus is compared to hybridization of the probe to nucleic acid isolated from an uninfected cell. A change in the amount of at least two probes that hybridize to nucleic acid isolated from a cell suspected of being infected by a virus relative to hybridization of at least two probes to nucleic acid isolated from an uninfected cell is indicative of viral infection.

A method to shuffle the nucleic acids of the invention is provided. This method involves fragmentation of a nucleic acid corresponding to a nucleic acid sequence listed in SEQ ID NOs: 1-953, 1954-1966, 2000-2129 or 2662-4737, the orthologs thereof, and the corresponding genes, followed by religation. This method allows for the production of polypeptides having altered activity relative to the native form of the polypeptide. Accordingly, the invention provides cells and transgenic plants containing nucleic acid segments produced through shuffling that

encode polypeptides having altered activity relative to the corresponding native polypeptide.

A computer readable medium, e.g., a magnetic tape, optical disk, CD-ROM, random access memory, volatile memory, non-volatile memory, or bubble memory, containing the nucleic acid sequences of the invention as well as methods of use for the computer readable medium are provided. For example, a computer readable medium can contain a nucleic acid molecule that has at least 70% nucleic acid sequence identity to SEQ ID NOs: 50, 139, 609, 4210, 6286, 3311, 5387, 3791, 5867, 2699, 4775, 3463, 5539, 3584, 5660, 4451, 6527, 4595, 6671 or the complement thereof. This medium allows a nucleic acid segment corresponding to a nucleic acid sequence listed in SEQ ID NOs:1-953, 1001-1095, 1954-1966, 2000-2129 or 2662-4737 to be used as a reference sequence to search against databases. This medium also allows for computer-based manipulation of a nucleic acid sequence corresponding to a nucleic acid sequence listed in SEQ ID NOs :1-953, 1001-1095, 1954-1966, 2000-2129 or 2662-4737, and the corresponding gene and polypeptide encoded by the nucleic acid sequence.

The invention also provides a method for marker-assisted breeding to select for plants having altered resistance to a pathogen. The method involves contacting plant DNA or cDNA with a probe corresponding to a nucleic acid sequence listed in SEQ ID NOs. 1-953, 1954-1966, 2000-2129 or 2662-4737, the orthologs thereof, and the corresponding genes, or a portion thereof which hybridizes under moderate stringency conditions to a gene corresponding to one of of SEQ ID Nos. 1-953, 1954-1966, 2000-2129 or 2662-4737 so as to form a duplex and detecting or determining the presence or amount of the duplex. The amount or presence of the duplex is indicative of the presence of a gene, the expression of which alters the resistance of the plant to a pathogen.

Therefore, another embodiment of the present invention provides a method of using known inducers or inhibitors of genes identified as being important in plant-pathogen interactions to induce genes that are important in resistance, or to inhibit genes that are downregulated in resistance.

Thus, some of the isolated nucleic acid molecules of the invention are useful in a method of combating a pathogen in an agricultural crop. The method comprises introducing to a plant an expression cassette comprising a nucleic acid molecule of the invention so as to yield a transformed differentiated plant. The transformed differentiated plant expresses the nucleic acid molecule in an amount that confers resistance to the transformed plant to infection relative to a corresponding nontransformed plant.

Detailed Description of the Invention

I. Definitions

The term "gene" is used broadly to refer to any segment of nucleic acid associated with a biological function. Thus, genes include coding sequences and/or the regulatory sequences required for their expression. For example, gene refers to a nucleic acid fragment that expresses mRNA or functional RNA, or encodes a specific protein, and which includes regulatory sequences. Genes also include nonexpressed DNA segments that, for example, form recognition sequences for other proteins. Genes can be obtained from a variety of sources, including cloning from a source of interest or synthesizing from known or predicted sequence information, and may include sequences designed to have desired parameters.

The term "native" or "wild type" gene refers to a gene that is present in the genome of an untransformed cell, i.e., a cell not having a known mutation.

A "marker gene" encodes a selectable or screenable trait.

The term "chimeric gene" refers to any gene that contains 1) DNA sequences, including regulatory and coding sequences, that are not found together in nature, or 2) sequences encoding parts of proteins not naturally adjoined, or 3) parts of promoters that are not naturally adjoined. Accordingly, a chimeric gene may comprise regulatory sequences and coding sequences that are derived from different sources, or comprise regulatory sequences and coding sequences derived from the same source, but arranged in a manner different from that found in nature.

A "transgene" refers to a gene that has been introduced into the genome by transformation and is stably maintained. Transgenes may include, for example,

genes that are either heterologous or homologous to the genes of a particular plant to be transformed. Additionally, transgenes may comprise native genes inserted into a non-native organism, or chimeric genes. The term "endogenous gene" refers to a native gene in its natural location in the genome of an organism. A "foreign" gene
5 refers to a gene not normally found in the host organism but that is introduced by gene transfer.

An "oligonucleotide" corresponding to a nucleotide sequence of the invention, e.g., for use in probing or amplification reactions, may be about 30 or fewer nucleotides in length (e.g., 9, 12, 15, 18, 20, 21 or 24, or any number between
10 9 and 30). Generally specific primers are upwards of 14 nucleotides in length. For optimum specificity and cost effectiveness, primers of 16 to 24 nucleotides in length may be preferred. Those skilled in the art are well versed in the design of primers for use processes such as PCR. If required, probing can be done with entire restriction fragments of the gene disclosed herein which may be 100's or even 1000's
15 of nucleotides in length.

The terms "protein," "peptide" and "polypeptide" are used interchangeably herein.

The nucleotide sequences of the invention can be introduced into any plant. The genes to be introduced can be conveniently used in expression cassettes for
20 introduction and expression in any plant of interest. Such expression cassettes will comprise the transcriptional initiation region of the invention linked to a nucleotide sequence of interest. Preferred promoters include constitutive, tissue-specific, developmental-specific, inducible and/or viral promoters. Such an expression cassette is provided with a plurality of restriction sites for insertion of the gene of
25 interest to be under the transcriptional regulation of the regulatory regions. The expression cassette may additionally contain selectable marker genes. The cassette will include in the 5'-3' direction of transcription, a transcriptional and translational initiation region, a DNA sequence of interest, and a transcriptional and translational termination region functional in plants. The termination region may be native with
30 the transcriptional initiation region, may be native with the DNA sequence of interest, or may be derived from another source. Convenient termination regions are

available from the Ti-plasmid of *A. tumefaciens*, such as the octopine synthase and nopaline synthase termination regions. See also, Guerineau et al., 1991; Proudfoot, 1991; Sanfacon et al., 1991; Mogen et al., 1990; Munroe et al., 1990; Ballas et al., 1989; Joshi et al., 1987.

5 "Coding sequence" refers to a DNA or RNA sequence that codes for a specific amino acid sequence and excludes the non-coding sequences. It may constitute an "uninterrupted coding sequence", i.e., lacking an intron, such as in a cDNA or it may include one or more introns bounded by appropriate splice junctions. An "intron" is a sequence of RNA which is contained in the primary
10 transcript but which is removed through cleavage and re-ligation of the RNA within the cell to create the mature mRNA that can be translated into a protein.

The terms "open reading frame" and "ORF" refer to the amino acid sequence encoded between translation initiation and termination codons of a coding sequence. The terms "initiation codon" and "termination codon" refer to a unit of three
15 adjacent nucleotides ('codon') in a coding sequence that specifies initiation and chain termination, respectively, of protein synthesis (mRNA translation).

A "functional RNA" refers to an antisense RNA, ribozyme, or other RNA that is not translated.

The term "RNA transcript" refers to the product resulting from RNA
20 polymerase catalyzed transcription of a DNA sequence. When the RNA transcript is a perfect complementary copy of the DNA sequence, it is referred to as the primary transcript or it may be a RNA sequence derived from posttranscriptional processing of the primary transcript and is referred to as the mature RNA. "Messenger RNA" (mRNA) refers to the RNA that is without introns and that can be translated into
25 protein by the cell. "cDNA" refers to a single- or a double-stranded DNA that is complementary to and derived from mRNA.

"Regulatory sequences" and "suitable regulatory sequences" each refer to nucleotide sequences located upstream (5' non-coding sequences), within, or downstream (3' non-coding sequences) of a coding sequence, and which influence
30 the transcription, RNA processing or stability, or translation of the associated coding sequence. Regulatory sequences include enhancers, promoters, translation leader

sequences, introns, and polyadenylation signal sequences. They include natural and synthetic sequences as well as sequences which may be a combination of synthetic and natural sequences. As is noted above, the term "suitable regulatory sequences" is not limited to promoters.

5 "5' non-coding sequence" refers to a nucleotide sequence located 5' (upstream) to the coding sequence. It is present in the fully processed mRNA upstream of the initiation codon and may affect processing of the primary transcript to mRNA, mRNA stability or translation efficiency (Turner et al., 1995).

"3' non-coding sequence" refers to nucleotide sequences located 3' (downstream) to a coding sequence and include polyadenylation signal sequences and other sequences encoding regulatory signals capable of affecting mRNA processing or gene expression. The polyadenylation signal is usually characterized by affecting the addition of polyadenylic acid tracts to the 3' end of the mRNA precursor. The use of different 3' non-coding sequences is exemplified by

The term "translation leader sequence" refers to that DNA sequence portion of a gene between the promoter and coding sequence that is transcribed into RNA and is present in the fully processed mRNA upstream (5') of the translation start codon. The translation leader sequence may affect processing of the primary transcript to mRNA, mRNA stability or translation efficiency.

The term "mature" protein refers to a post-translationally processed polypeptide without its signal peptide. "Precursor" protein refers to the primary product of translation of an mRNA. "Signal peptide" refers to the amino terminal extension of a polypeptide, which is translated in conjunction with the polypeptide forming a precursor peptide and which is required for its entrance into the secretory pathway. The term "signal sequence" refers to a nucleotide sequence that encodes the signal peptide.

The term "intracellular localization sequence" refers to a nucleotide sequence that encodes an intracellular targeting signal. An "intracellular targeting signal" is an amino acid sequence that is translated in conjunction with a protein and directs it to a particular sub-cellular compartment. "Endoplasmic reticulum (ER)

stop transit signal" refers to a carboxy-terminal extension of a polypeptide, which is translated in conjunction with the polypeptide and causes a protein that enters the secretory pathway to be retained in the ER. "ER stop transit sequence" refers to a nucleotide sequence that encodes the ER targeting signal. Other intracellular
5 targeting sequences encode targeting signals active in seeds and/or leaves and vacuolar targeting signals.

"Pathogen" as used herein includes but is not limited to bacteria, fungi, yeast, oomycetes and virus, e.g., American wheat striate mosaic virus mosaic (AWSMV), barley stripe mosaic virus (BSMV), barley yellow dwarf virus (BYDV),
10 Brome mosaic virus (BMV), cereal chlorotic mottle virus (CCMV), corn chlorotic vein banding virus (CCVBV), maize chlorotic mottle virus (MCMV), maize dwarf mosaic virus (MDMV), A or B, wheat streak mosaic virus (WSMV), cucumber mosaic virus (CMV), cynodon chlorotic streak virus (CCSV), Johnsongrass mosaic virus (JGMV), maize bushy stunt or mycoplasma-like organism (NJILO), maize
15 chlorotic dwarf virus (MCDV), maize chlorotic mottle virus (MCMV), maize dwarf mosaic virus (MDMV) strains A, D, E and F, maize leaf fleck virus (MLFV), maize line virus (NELV), maize mosaic virus (MMV), maize mottle and chlorotic stunt virus, maize pellucid ringspot virus (MPRV), maize raya gruesa virus (MRGV), maize rayado fino virus (MRFV), maize red leaf and red stripe virus (MRSV), maize
20 ring mottle virus (MRMV), maize rio cuarto virus (MRCV), maize rough dwarf virus (MRDV), maize sterile stunt virus (strains of barley yellow striate virus), maize streak virus (MSV), maize chlorotic stripe, maize hoja Maize stripe virus blanca, maize stunting virus, maize tassel abortion virus (MTAV), maize vein enation virus (MVEV), maize wallaby ear virus (MAVEV), maize white leaf virus,
25 maize white line mosaic virus (NTVVL MV), millet red leaf virus (NMV), Northern cereal mosaic virus (NCMV), oat pseudorosette virus, oat sterile dwarf virus (OSDV), rice black-streaked dwarf virus (RBSDV), rice stripe virus (RSV), sorghum mosaic virus (SrMV), formerly sugarcane mosaic virus (SCMV) strains H, I and M, sugarcane Fiji disease virus (FDV), sugarcane mosaic virus (SCMV)
30 strains A, B, D, E, SC, BC, Sabi and NM vein enation virus, and wheat spot mosaic virus (WSMV).

Bacterial pathogens include but are not limited to *Pseudomonas avenae* subsp. *avenae*, *Xanthomonas campestris* pv. *holcicola*, *Enterobacter dissolvens*, *Erwinia dissolvens*, *Erwinia carotovora* subsp. *carotovora*, *Erwinia chrysanthemi* pv. *zeae*, *Pseudomonas andropogonis*, *Pseudomonas syringae* pv. *coronafaciens*,
 5 *Clavibacter michiganensis* subsp., *Corynebacterium michiganense* pv. *nebraskense*, *Pseudomonas syringae* pv. *syringae*, Hemiparasitic bacteria (see under fungi), *Bacillus subtilis*, *Erwinia stewartii*, and *Spiroplasma kunkelii*.

Fungal pathogens include but are not limited to *Collelotrichum graminicola*, *Glomerella graminicola* Politis, *Glomerella lucumanensis*, *Aspergillus flavus*,
 10 *Rhizoctonia solani* Kuhn, *Thanatephorus cucumeris*, *Acremonium strictum* W. Gams, *Cephalosporium acremonium* Auct. non Corda Black *Lasiodiplodia theobromae* = *BoIr odiplochia y theobromae* Borde blanco *Marasmiellus* sp., *Physoderma maydis*, *Cephalosporium Corticium sasakii*, *Curvularia clavata*, *C. maculans*, *Cochhobolus eragrostidis*, *Curvularia inaequahs*, *C. intermedia*
 15 (teleomorph *Cochhobolus intermedius*), *Curvularia lunata* (teleomorph: *Cochliobolus lunatus*), *Curvularia pallescens* (teleomorph - *Cochliobolus pallescens*), *Curvularia senegalensis*, *C. huberculata* (teleomorph: *Cochliobolus tuberculatus*), *Didymella exitalis* *Diplodiaftumenti* (teleomorph - *Botryosphaeria festucae*), *Diplodia maydis* = *Stenocarpella maydis*, *Stenocarpella*
 20 *macrospora* = *Diplodia macrospora*, *Sclerophthora rayssiae* var. *zeae*, *Sclerophthora macrospora* = *Sclerospora macrospora*, *Sclerospora graminicola*, *Peronosclerospora maydis* = *Sclerospora maydis*, *Peronosclerospora philippinensis*, *Sclerospora philippinensis*, *Peronosclerospora sorghi* = *Sclerospora sorghi*, *Peronosclerospora spontanea* = *Sclerospora spontanea*, *Peronosclerospora*
 25 *sacchari* = *Sclerospora sacchari*, *Nigrospora oryzae* (teleomorph: *Khuskia oryzae*) *A. Iternaria alternata* = *A. tenuis*, *Aspergillus glaucus*, *A. niger*, *Aspergillus* spp., *Botrytis cinerea*, *Cunninghamella* sp., *Curvularia pallescens*, *Doratomyces slemonitis* = *Cephalotrichum slemonitis*, *Fusarium culmorum*, *Gonatobotrys simplex*, *Pithomyces maydicus*, *Rhizopus microsporus* Tiegh., *R. stolonifer* = *R.*
 30 *nigricans*, *Scopulariopsis brumptii*, *Claviceps gigantea* (anamorph: *Sphacelia* sp.) *Aureobasidium zeae* = *Kabatiella zeae*, *Fusarium subglutinans* = *F. moniliforme*

- var. *subglutinans*, *Fusarium moniliforme*, *Fusarium avenaceum* (teleomorph - *Gibberella avenacea*), *Botryosphaeria zeae* = *Physalospora zeae* (anamorph: *Allacrophoma zeae*), *Cercospora sorghi* = *C. sorghi* var. *maydis*, *Helminthosporium pedicellatum* (teleomorph: *Selosphaerapedicellata*), *Cladosporium cladosporioides*
- 5 = *Hormodendrum cladosporioides*, *C. herbarum* (teleomorph - *Mycosphaerella tassiana*), *Cephalosporium maydis*, *A. Iternaria alternata*, *A. scochyta maydis*, *A. tritici*, *A. zeicola*, *Bipolaris victoriae*, *Helminthosporium victoriae* (teleomorph *Cochhoholus victoriae*), *C sativus* (anamorph: *Bipolaris sorokiniana* = *H. sorokinianum* = *H. sativum*), *Epicoccum nigrum*, *Exserohilum prolatum* =
- 10 *Drechslera prolata* (teleomorph: *Setosphaeriaprolata*), *Graphium penicillioides*, *Leptosphaeria maydis*, *Leptothyrium zeae*, *Ophiosphaerella herpotricha* (anamorph - *Scolecosporella* sp.), *Pataphaeosphaeria michotii*, *Phoma* sp., *Septoria zeae*, *S. zeicola*, *S. zeina* *Setosphaeria turcica*, *Exserohilum turcicum* = *Helminthosporium furcicum*, *Cochhoholus carbonum*, *Bipolaris zeicola* = *Helminthosporium*
- 15 *carbonum*, *Penicilium* spp., *P. chrysogenum*, *P. expansum*, *P. oxalicum*, *Phaeocystostroma ambiguum*, *Phaeocylosporella zeae*, *Phaeosphaeria maydis* = *Sphaerulina maydis*, *Botryosphaeria festucae* = *Physalospora zeicola* (anamorph: *Diplodia fumenfi*), *Herniparasitic bacteria and fungi* *Pyrenochaeta Phoma terrestris* = *Pyrenochaeta terrestris*, *Pythium* spp., *P. arrhenomanes*, *P.*
- 20 *graminicola*, *Pythium aphanidermatum* = *P. hutleri* L., *Rhizoctonia zeae* (teleomorph: *Waitea circinata*), *Rhizoctonia solani*, minor *A Iternaria alternata*, *Cercospora sorghi*, *Dictochaeta frtilis*, *Fusarium acuminatum* (teleomorph *Gibberella acuminata*), *E. equiseti* (teleomorph: *G. intricans*), *E. oxysporum*, *E. pallidoroseum*, *E. poae*, *E. roseum*, *G. cyanogena* (anamorph: *E. sulphureum*),
- 25 *Microdochium holleyi*, *Mucor* sp., *Periconia circinata*, *Phytophthora cactorum*, *P. drechsleri*, *P. nicotianae* var. *parasitica*, *Rhizopus arrhizus*, *Setosphaeria rostrata*, *Exserohilum rostratum* = *Helminthosporium rostratum*, *Puccinia sorghi*, *Physopella pallescens*, *P. zeae*, *Sclerotium rofsii* Sacc. (teleomorph- *Athelia rofsii*), *Bipolaris sorokiniana*, *B. zeicola* = *Helminthosporium carbonum*, *Diplodia maydis*,
- 30 *Exserohilum pedicellatum*, *Exserohilum furcicum* = *Helminthosporium turcicum*, *Fusarium avenaceum*, *E. culmorum*, *E. moniliforme*, *Gibberella zeae* (anamorph - *E.*

- graminearum), *Macrophomina phaseolina*, *Penicillium* spp., *Phomopsis* sp., *Pythium* spp., *Rhizoctonia solani*, *R. zeae*, *Sclerotium rolfsii*, *Spicaria* sp., *Selenophoma* sp., *Gaeumannomyces graminis*, *Myrothecium gramineum*, *Monascus purpureus*, *M. ruber* Smut, *Ustilago zeae* = *U. maydis* Smut, *Ustilaginoidea virens* Smut, *Sphacelotheca reiliana* = *Sporisorium holci*, *Cochliobolus heterostrophus* (anamorph: *Bipolaris maydis* = *Helminthosporium maydis*), *Stenocarpella macrospora* = *Diplodia macrospora*, *Cercospora sorghi*, *Fusarium episphaeria*, *E. merismoides*, *F. oxysporum* Schlechtend, *E. poae*, *E. roseum*, *E. solani* (teleomorph: *Nectria haematococca*), *F. tricinctum*, *Mariannaea elegans*, *Mucor* sp.,
- 10 *Rhopoglyphus zeae*, *Spicaria* sp., *Aspergillus* spp., *Penicillium* spp., *Trichoderma viride* = *T. lignorum* teleomorph: *Hypocrea* sp., *Stenocarpella maydis* = *Diplodia zeae*, *Ascochyta ischaemi*, *Phyllosticta maydis* (telomorph: *Mycosphaerella zeae-maydis*), and *Gloeocercospora sorghi*.

- Parasitic nematodes include but are not limited to *Awl Dolichodorus* spp., *D.*
- 15 *heterocephalus* Bulb and stem (Europe), *Ditylenchus dipsaci* Burrowing Radopholus similis Cyst Heterodera avenae, *H. zeae*, *Punctodera chalconensis* Dagger Xiphinema spp., *X. americanum*, *X. mediterraneum* False root-knot *Nacobbus dorsalis* Lance, *Columbia* *Hoplolaimus columbus* Lance *Hoplolaimus* spp., *H. galeatus* Lesion *Pratylenchus* spp., *P. brachyurus*, *P. crenatus*, *P. hexincisus*, *P. neglectus*, *P.*
- 20 *penetrans*, *P. scribneri*, *P. thornei*, *P. zeae* Needle Longidorus spp., *L. breviannulatus* Ring Criconemella spp., *C. ornata* Root-knot Meloidogyne spp., *M. chitwoodi*, *M. incognita*, *M. javanica* Spiral Helicotylenchus spp., *Belonolaimus* spp., *B. longicaudatus* Stubby-root Paratrichodorus spp., *P. christiei*, *P. minor*, *Ouinisulcius aculus*, and *Trichodorus* spp.

- 25 "Promoter" refers to a nucleotide sequence, usually upstream (5') to its coding sequence, which controls the expression of the coding sequence by providing the recognition for RNA polymerase and other factors required for proper transcription. "Promoter" includes a minimal promoter that is a short DNA sequence comprised of a TATA box and other sequences that serve to specify the site of
- 30 transcription initiation, to which regulatory elements are added for control of expression. "Promoter" also refers to a nucleotide sequence that includes a minimal

reading frame (ORF) that it controls in all or nearly all of the plant tissues during all or nearly all developmental stages of the plant. Each of the transcription-activating elements do not exhibit an absolute tissue-specificity, but mediate transcriptional activation in most plant parts at a level of $\geq 1\%$ of the level reached in the part of the plant in which transcription is most active.

"Regulated promoter" refers to promoters that direct gene expression not constitutively, but in a temporally- and/or spatially-regulated manner, and includes both tissue-specific and inducible promoters. It includes natural and synthetic sequences as well as sequences which may be a combination of synthetic and natural sequences. Different promoters may direct the expression of a gene in different tissues or cell types, or at different stages of development, or in response to different environmental conditions. New promoters of various types useful in plant cells are constantly being discovered, numerous examples may be found in the compilation by Okamuro et al. (1989). Typical regulated promoters useful in plants include but are not limited to safener-inducible promoters, promoters derived from the tetracycline-inducible system, promoters derived from salicylate-inducible systems, promoters derived from alcohol-inducible systems, promoters derived from glucocorticoid-inducible system, promoters derived from pathogen-inducible systems, and promoters derived from ecdysone-inducible systems.

"Tissue-specific promoter" refers to regulated promoters that are not expressed in all plant cells but only in one or more cell types in specific organs (such as leaves or seeds), specific tissues (such as embryo or cotyledon), or specific cell types (such as leaf parenchyma or seed storage cells). These also include promoters that are temporally regulated, such as in early or late embryogenesis, during fruit ripening in developing seeds or fruit, in fully differentiated leaf, or at the onset of senescence.

"Inducible promoter" refers to those regulated promoters that can be turned on in one or more cell types by an external stimulus, such as a chemical, light, hormone, stress, or a pathogen.

"Operably-linked" refers to the association of nucleic acid sequences on single nucleic acid fragment so that the function of one is affected by the other. For

example, a regulatory DNA sequence is said to be "operably linked to" or "associated with" a DNA sequence that codes for an RNA or a polypeptide if the two sequences are situated such that the regulatory DNA sequence affects expression of the coding DNA sequence (i.e., that the coding sequence or functional RNA is under the transcriptional control of the promoter). Coding sequences can be operably-linked to regulatory sequences in sense or antisense orientation.

"Expression" refers to the transcription and/or translation of an endogenous gene, ORF or portion thereof, or a transgene in plants. For example, in the case of antisense constructs, expression may refer to the transcription of the antisense DNA only. In addition, expression refers to the transcription and stable accumulation of sense (mRNA) or functional RNA. Expression may also refer to the production of protein.

"Specific expression" is the expression of gene products which is limited to one or a few plant tissues (spatial limitation) and/or to one or a few plant developmental stages (temporal limitation). It is acknowledged that hardly a true specificity exists: promoters seem to be preferably switch on in some tissues, while in other tissues there can be no or only little activity. This phenomenon is known as leaky expression. However, with specific expression in this invention is meant preferable expression in one or a few plant tissues.

The "expression pattern" of a promoter (with or without enhancer) is the pattern of expression levels which shows where in the plant and in what developmental stage transcription is initiated by said promoter. Expression patterns of a set of promoters are said to be complementary when the expression pattern of one promoter shows little overlap with the expression pattern of the other promoter. The level of expression of a promoter can be determined by measuring the 'steady state' concentration of a standard transcribed reporter mRNA. This measurement is indirect since the concentration of the reporter mRNA is dependent not only on its synthesis rate, but also on the rate with which the mRNA is degraded. Therefore, the steady state level is the product of synthesis rates and degradation rates.

The rate of degradation can however be considered to proceed at a fixed rate when the transcribed sequences are identical, and thus this value can serve as a

measure of synthesis rates. When promoters are compared in this way techniques available to those skilled in the art are hybridization S1-RNase analysis, northern blots and competitive RT-PCR. This list of techniques in no way represents all available techniques, but rather describes commonly used procedures used to
5 analyze transcription activity and expression levels of mRNA.

The analysis of transcription start points in practically all promoters has revealed that there is usually no single base at which transcription starts, but rather a more or less clustered set of initiation sites, each of which accounts for some start points of the mRNA. Since this distribution varies from promoter to promoter the
10 sequences of the reporter mRNA in each of the populations would differ from each other. Since each mRNA species is more or less prone to degradation, no single degradation rate can be expected for different reporter mRNAs. It has been shown for various eukaryotic promoter sequences that the sequence surrounding the initiation site ('initiator') plays an important role in determining the level of RNA
15 expression directed by that specific promoter. This includes also part of the transcribed sequences. The direct fusion of promoter to reporter sequences would therefore lead to suboptimal levels of transcription.

A commonly used procedure to analyze expression patterns and levels is through determination of the 'steady state' level of protein accumulation in a cell.
20 Commonly used candidates for the reporter gene, known to those skilled in the art are β -glucuronidase (GUS), chloramphenicol acetyl transferase (CAT) and proteins with fluorescent properties, such as green fluorescent protein (GFP) from *Aequora victoria*. In principle, however, many more proteins are suitable for this purpose, provided the protein does not interfere with essential plant functions. For
25 quantification and determination of localization a number of tools are suited. Detection systems can readily be created or are available which are based on, e.g., immunochemical, enzymatic, fluorescent detection and quantification. Protein levels can be determined in plant tissue extracts or in intact tissue using *in situ* analysis of protein expression.

30 Generally, individual transformed lines with one chimeric promoter reporter construct will vary in their levels of expression of the reporter gene. Also frequently

observed is the phenomenon that such transformants do not express any detectable product (RNA or protein). The variability in expression is commonly ascribed to 'position effects', although the molecular mechanisms underlying this inactivity are usually not clear.

5 The term "average expression" is used here as the average level of expression found in all lines that do express detectable amounts of reporter gene, so leaving out of the analysis plants that do not express any detectable reporter mRNA or protein.

 "Root expression level" indicates the expression level found in protein
10 extracts of complete plant roots. Likewise, leaf, and stem expression levels, are determined using whole extracts from leaves and stems. It is acknowledged however, that within each of the plant parts just described, cells with variable functions may exist, in which promoter activity may vary.

 "Non-specific expression" refers to constitutive expression or low level,
15 basal ('leaky') expression in undesired cells or tissues from a 'regulated promoter'.

 "Altered levels" refers to the level of expression in transgenic organisms that differs from that of normal or untransformed organisms.

 "Overexpression" refers to the level of expression in transgenic cells or organisms that exceeds levels of expression in normal or untransformed
20 (nontransgenic) cells or organisms.

 "Antisense inhibition" refers to the production of antisense RNA transcripts capable of suppressing the expression of protein from an endogenous gene or a transgene.

 "Co-suppression" and "transwitch" each refer to the production of sense
25 RNA transcripts capable of suppressing the expression of identical or substantially similar transgene or endogenous genes (U.S. Patent No. 5,231,020).

 "Gene silencing" refers to homology-dependent suppression of viral genes, transgenes, or endogenous nuclear genes. Gene silencing may be transcriptional, when the suppression is due to decreased transcription of the affected genes, or post-
30 transcriptional, when the suppression is due to increased turnover (degradation) of

RNA species homologous to the affected genes (English et al., 1996). Gene silencing includes virus-induced gene silencing (Ruiz et al. 1998).

"Silencing suppressor" gene refers to a gene whose expression leads to counteracting gene silencing and enhanced expression of silenced genes. Silencing suppressor genes may be of plant, non-plant, or viral origin. Examples include, but are not limited to HC-Pro, P1-HC-Pro, and 2b proteins. Other examples include one or more genes in TGMV-B genome.

The terms "heterologous DNA sequence," "exogenous DNA segment" or "heterologous nucleic acid," as used herein, each refer to a sequence that originates from a source foreign to the particular host cell or, if from the same source, is modified from its original form. Thus, a heterologous gene in a host cell includes a gene that is endogenous to the particular host cell but has been modified through, for example, the use of DNA shuffling. The terms also include non-naturally occurring multiple copies of a naturally occurring DNA sequence. Thus, the terms refer to a DNA segment that is foreign or heterologous to the cell, or homologous to the cell but in a position within the host cell nucleic acid in which the element is not ordinarily found. Exogenous DNA segments are expressed to yield exogenous polypeptides. A "homologous" DNA sequence is a DNA sequence that is naturally associated with a host cell into which it is introduced.

"Homologous to" in the context of nucleotide sequence identity refers to the similarity between the nucleotide sequence of two nucleic acid molecules or between the amino acid sequences of two protein molecules. Estimates of such homology are provided by either DNA-DNA or DNA-RNA hybridization under conditions of stringency as is well understood by those skilled in the art (as described in Haines and Higgins (eds.), Nucleic Acid Hybridization, IRL Press, Oxford, U.K.), or by the comparison of sequence similarity between two nucleic acids or proteins.

The term "substantially similar" refers to nucleotide and amino acid sequences that represent functional and/or structural equivalents of *Arabidopsis* sequences disclosed herein. For example, altered nucleotide sequences which simply reflect the degeneracy of the genetic code but nonetheless encode amino acid

sequences that are identical to a particular amino acid sequence are substantially similar to the particular sequences. In addition, amino acid sequences that are substantially similar to a particular sequence are those wherein overall amino acid identity is at least 65% or greater to the instant sequences. Modifications that result in equivalent nucleotide or amino acid sequences are well within the routine skill in the art. Moreover, the skilled artisan recognizes that equivalent nucleotide sequences encompassed by this invention can also be defined by their ability to hybridize, under low, moderate and/or stringent conditions (e.g., 0.1X SSC, 0.1% SDS, 65°C), with the nucleotide sequences that are within the literal scope of the instant claims.

"Target gene" refers to a gene on the replicon that expresses the desired target coding sequence, functional RNA, or protein. The target gene is not essential for replicon replication. Additionally, target genes may comprise native non-viral genes inserted into a non-native organism, or chimeric genes, and will be under the control of suitable regulatory sequences. Thus, the regulatory sequences in the target gene may come from any source, including the virus. Target genes may include coding sequences that are either heterologous or homologous to the genes of a particular plant to be transformed. However, target genes do not include native viral genes. Typical target genes include, but are not limited to genes encoding a structural protein, a seed storage protein, a protein that conveys herbicide resistance, and a protein that conveys insect resistance. Proteins encoded by target genes are known as "foreign proteins". The expression of a target gene in a plant will typically produce an altered plant trait.

The term "altered plant trait" means any phenotypic or genotypic change in a transgenic plant relative to the wild-type or non-transgenic plant host.

"Transcription Stop Fragment" refers to nucleotide sequences that contain one or more regulatory signals, such as polyadenylation signal sequences, capable of terminating transcription. Examples include the 3' non-regulatory regions of genes encoding nopaline synthase and the small subunit of ribulose biphosphate carboxylase.

"Replication gene" refers to a gene encoding a viral replication protein. In addition to the ORF of the replication protein, the replication gene may also contain other overlapping or non-overlapping ORF(s), as are found in viral sequences in nature. While not essential for replication, these additional ORFs may enhance replication and/or viral DNA accumulation. Examples of such additional ORFs are AC3 and AL3 in ACMV and TGMV geminiviruses, respectively.

"Chimeric *trans*-acting replication gene" refers either to a replication gene in which the coding sequence of a replication protein is under the control of a regulated plant promoter other than that in the native viral replication gene, or a modified native viral replication gene, for example, in which a site specific sequence(s) is inserted in the 5' transcribed but untranslated region. Such chimeric genes also include insertion of the known sites of replication protein binding between the promoter and the transcription start site that attenuate transcription of viral replication protein gene.

"Chromosomally-integrated" refers to the integration of a foreign gene or DNA construct into the host DNA by covalent bonds. Where genes are not "chromosomally integrated" they may be "transiently expressed." Transient expression of a gene refers to the expression of a gene that is not integrated into the host chromosome but functions independently, either as part of an autonomously replicating plasmid or expression cassette, for example, or as part of another biological system such as a virus.

"Production tissue" refers to mature, harvestable tissue consisting of non-dividing, terminally-differentiated cells. It excludes young, growing tissue consisting of germline, meristematic, and not-fully-differentiated cells.

"Germline cells" refer to cells that are destined to be gametes and whose genetic material is heritable.

"*Trans*-activation" refers to switching on of gene expression or replicon replication by the expression of another (regulatory) gene in *trans*.

The term "transformation" refers to the transfer of a nucleic acid fragment into the genome of a host cell, resulting in genetically stable inheritance. Host cells containing the transformed nucleic acid fragments are referred to as "transgenic"

cells, and organisms comprising transgenic cells are referred to as "transgenic organisms". Examples of methods of transformation of plants and plant cells include *Agrobacterium*-mediated transformation (De Blaere et al., 1987) and particle bombardment technology (Klein et al. 1987; U.S. Patent No. 4,945,050). Whole
5 plants may be regenerated from transgenic cells by methods well known to the skilled artisan (see, for example, Fromm et al., 1990).

"Transformed," "transgenic," and "recombinant" refer to a host organism such as a bacterium or a plant into which a heterologous nucleic acid molecule has been introduced. The nucleic acid molecule can be stably integrated into the
10 genome generally known in the art and are disclosed in Sambrook et al., 1989. See also Innis et al., 1995 and Gelfand, 1995; and Innis and Gelfand, 1999. Known methods of PCR include, but are not limited to, methods using paired primers, nested primers, single specific primers, degenerate primers, gene-specific primers, vector-specific primers, partially mismatched primers, and the like. For example,
15 "transformed," "transformant," and "transgenic" plants or calli have been through the transformation process and contain a foreign gene integrated into their chromosome. The term "untransformed" refers to normal plants that have not been through the transformation process.

"Transiently transformed" refers to cells in which transgenes and foreign
20 DNA have been introduced (for example, by such methods as *Agrobacterium*-mediated transformation or biolistic bombardment), but not selected for stable maintenance.

"Stably transformed" refers to cells that have been selected and regenerated on a selection media following transformation.

25 "Transient expression" refers to expression in cells in which a virus or a transgene is introduced by viral infection or by such methods as *Agrobacterium*-mediated transformation, electroporation, or biolistic bombardment, but not selected for its stable maintenance.

"Genetically stable" and "heritable" refer to chromosomally-integrated
30 genetic elements that are stably maintained in the plant and stably inherited by progeny through successive generations.

"Primary transformant" and "T0 generation" refer to transgenic plants that are of the same genetic generation as the tissue which was initially transformed (i.e., not having gone through meiosis and fertilization since transformation).

5 "Secondary transformants" and the "T1, T2, T3, etc. generations" refer to transgenic plants derived from primary transformants through one or more meiotic and fertilization cycles. They may be derived by self-fertilization of primary or secondary transformants or crosses of primary or secondary transformants with other transformed or untransformed plants.

10 "Wild-type" refers to a virus or organism found in nature without any known mutation.

"Genome" refers to the complete genetic material of an organism.

The term "nucleic acid" refers to deoxyribonucleotides or ribonucleotides and polymers thereof in either single- or double-stranded form, composed of monomers (nucleotides) containing a sugar, phosphate and a base which is either a
15 purine or pyrimidine. Unless specifically limited, the term encompasses nucleic acids containing known analogs of natural nucleotides which have similar binding properties as the reference nucleic acid and are metabolized in a manner similar to naturally occurring nucleotides. Unless otherwise indicated, a particular nucleic acid sequence also implicitly encompasses conservatively modified variants thereof
20 (e.g., degenerate codon substitutions) and complementary sequences as well as the sequence explicitly indicated. Specifically, degenerate codon substitutions may be achieved by generating sequences in which the third position of one or more selected (or all) codons is substituted with mixed-base and/or deoxyinosine residues (Batzer et al., 1991; Ohtsuka et al., 1985; Rossolini et al. 1994). A "nucleic acid
25 fragment" is a fraction of a given nucleic acid molecule. In higher plants, deoxyribonucleic acid (DNA) is the genetic material while ribonucleic acid (RNA) is involved in the transfer of information contained within DNA into proteins. The term "nucleotide sequence" refers to a polymer of DNA or RNA which can be single- or double-stranded, optionally containing synthetic, non-natural or altered
30 nucleotide bases capable of incorporation into DNA or RNA polymers. The terms

"nucleic acid" or "nucleic acid sequence" may also be used interchangeably with gene, cDNA, DNA and RNA encoded by a gene.

The invention encompasses isolated or substantially purified nucleic acid or protein compositions. In the context of the present invention, an "isolated" or "purified" DNA molecule or an "isolated" or "purified" polypeptide is a DNA molecule or polypeptide that, by the hand of man, exists apart from its native environment and is therefore not a product of nature. An isolated DNA molecule or polypeptide may exist in a purified form or may exist in a non-native environment such as, for example, a transgenic host cell. For example, an "isolated" or "purified" nucleic acid molecule or protein, or biologically active portion thereof, is substantially free of other cellular material, or culture medium when produced by recombinant techniques, or substantially free of chemical precursors or other chemicals when chemically synthesized. Preferably, an "isolated" nucleic acid is free of sequences (preferably protein encoding sequences) that naturally flank the nucleic acid (i.e., sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated nucleic acid molecule can contain less than about 5 kb, 4 kb, 3 kb, 2 kb, 1 kb, 0.5 kb, or 0.1 kb of nucleotide sequences that naturally flank the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived. A protein that is substantially free of cellular material includes preparations of protein or polypeptide having less than about 30%, 20%, 10%, 5%, (by dry weight) of contaminating protein. When the protein of the invention, or biologically active portion thereof, is recombinantly produced, preferably culture medium represents less than about 30%, 20%, 10%, or 5% (by dry weight) of chemical precursors or non-protein of interest chemicals.

The nucleotide sequences of the invention include both the naturally occurring sequences as well as mutant (variant) forms. Such variants will continue to possess the desired activity, i.e., either promoter activity or the activity of the product encoded by the open reading frame of the non-variant nucleotide sequence.

Thus, by "variants" is intended substantially similar sequences. For nucleotide sequences comprising an open reading frame, variants include those

sequences that, because of the degeneracy of the genetic code, encode the identical amino acid sequence of the native protein. Naturally occurring allelic variants such as these can be identified with the use of well-known molecular biology techniques, as, for example, with polymerase chain reaction (PCR) and hybridization techniques. Variant nucleotide sequences also include synthetically derived nucleotide sequences, such as those generated, for example, by using site-directed mutagenesis and for open reading frames, encode the native protein, as well as those that encode a polypeptide having amino acid substitutions relative to the native protein. Generally, nucleotide sequence variants of the invention will have at least 40, 50, 60, to 70%, e.g., preferably 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, to 79%, generally at least 80%, e.g., 81%-84%, at least 85%, e.g., 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, to 98% and 99% nucleotide sequence identity to the native (wild type or endogenous) nucleotide sequence.

“Conservatively modified variations” of a particular nucleic acid sequence refers to those nucleic acid sequences that encode identical or essentially identical amino acid sequences, or where the nucleic acid sequence does not encode an amino acid sequence, to essentially identical sequences. Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids encode any given polypeptide. For instance the codons CGT, CGC, CGA, CGG, AGA, and AGG all encode the amino acid arginine. Thus, at every position where an arginine is specified by a codon, the codon can be altered to any of the corresponding codons described without altering the encoded protein. Such nucleic acid variations are “silent variations” which are one species of “conservatively modified variations.” Every nucleic acid sequence described herein which encodes a polypeptide also describes every possible silent variation, except where otherwise noted. One of skill will recognize that each codon in a nucleic acid (except ATG, which is ordinarily the only codon for methionine) can be modified to yield a functionally identical molecule by standard techniques. Accordingly, each “silent variation” of a nucleic acid which encodes a polypeptide is implicit in each described sequence.

The nucleic acid molecules of the invention can be “optimized” for enhanced expression in plants of interest. See, for example, EPA 035472; WO 91/16432;

Perlak et al., 1991; and Murray et al., 1989. In this manner, the open reading frames in genes or gene fragments can be synthesized utilizing plant-preferred codons. See, for example, Campbell and Gowri, 1990 for a discussion of host-preferred codon usage. Thus, the nucleotide sequences can be optimized for expression in any plant.

5 It is recognized that all or any part of the gene sequence may be optimized or synthetic. That is, synthetic or partially optimized sequences may also be used. Variant nucleotide sequences and proteins also encompass sequences and protein derived from a mutagenic and recombinogenic procedure such as DNA shuffling. With such a procedure, one or more different coding sequences can be manipulated
10 to create a new polypeptide possessing the desired properties. In this manner, libraries of recombinant polynucleotides are generated from a population of related sequence polynucleotides comprising sequence regions that have substantial sequence identity and can be homologously recombined *in vitro* or *in vivo*. Strategies for such DNA shuffling are known in the art. See, for example, Stemmer,
15 1994; Stemmer, 1994; Cramer et al., 1997; Moore et al., 1997; Zhang et al., 1997; Cramer et al., 1998; and U.S. Patent Nos. 5,605,793 and 5,837,458.

By "variant" polypeptide is intended a polypeptide derived from the native protein by deletion (so-called truncation) or addition of one or more amino acids to the N-terminal and/or C-terminal end of the native protein; deletion or addition of
20 one or more amino acids at one or more sites in the native protein; or substitution of one or more amino acids at one or more sites in the native protein. Such variants may result from, for example, genetic polymorphism or from human manipulation. Methods for such manipulations are generally known in the art.

Thus, the polypeptides may be altered in various ways including amino acid
25 substitutions, deletions, truncations, and insertions. Methods for such manipulations are generally known in the art. For example, amino acid sequence variants of the polypeptides can be prepared by mutations in the DNA. Methods for mutagenesis and nucleotide sequence alterations are well known in the art. See, for example, Kunkel, 1985; Kunkel et al., 1987; U. S. Patent No. 4,873,192; Walker and Gastra,
30 1983 and the references cited therein. Guidance as to appropriate amino acid substitutions that do not affect biological activity of the protein of interest may be

found in the model of Dayhoff et al. (1978). Conservative substitutions, such as exchanging one amino acid with another having similar properties, are preferred.

Individual substitutions deletions or additions that alter, add or delete a single amino acid or a small percentage of amino acids (typically less than 5%, more typically less than 1%) in an encoded sequence are “conservatively modified variations,” where the alterations result in the substitution of an amino acid with a chemically similar amino acid. Conservative substitution tables providing functionally similar amino acids are well known in the art. The following five groups each contain amino acids that are conservative substitutions for one another:

10 Aliphatic: Glycine (G), Alanine (A), Valine (V), Leucine (L), Isoleucine (I); Aromatic: Phenylalanine (F), Tyrosine (Y), Tryptophan (W); Sulfur-containing: Methionine (M), Cysteine (C); Basic: Arginine (R), Lysine (K), Histidine (H); Acidic: Aspartic acid (D), Glutamic acid (E), Asparagine (N), Glutamine (Q). See also, Creighton, 1984. In addition, individual substitutions, deletions or additions which

15 alter, add or delete a single amino acid or a small percentage of amino acids in an encoded sequence are also “conservatively modified variations.”

“Expression cassette” as used herein means a DNA sequence capable of directing expression of a particular nucleotide sequence in an appropriate host cell, comprising a promoter operably linked to the nucleotide sequence of interest which

20 is operably linked to termination signals. It also typically comprises sequences required for proper translation of the nucleotide sequence. The coding region usually codes for a protein of interest but may also code for a functional RNA of interest, for example antisense RNA or a nontranslated RNA, in the sense or antisense direction. The expression cassette comprising the nucleotide sequence of

25 interest may be chimeric, meaning that at least one of its components is heterologous with respect to at least one of its other components. The expression cassette may also be one which is naturally occurring but has been obtained in a recombinant form useful for heterologous expression. The expression of the nucleotide sequence in the expression cassette may be under the control of a

30 constitutive promoter or of an inducible promoter which initiates transcription only when the host cell is exposed to some particular external stimulus. In the case of a

multicellular organism, the promoter can also be specific to a particular tissue or organ or stage of development.

"Vector" is defined to include, inter alia, any plasmid, cosmid, phage or *Agrobacterium* binary vector in double or single stranded linear or circular form which may or may not be self transmissible or mobilizable, and which can transform prokaryotic or eukaryotic host either by integration into the cellular genome or exist extrachromosomally (e.g. autonomous replicating plasmid with an origin of replication).

Specifically included are shuttle vectors by which is meant a DNA vehicle capable, naturally or by design, of replication in two different host organisms, which may be selected from actinomycetes and related species, bacteria and eukaryotic (e.g. higher plant, mammalian, yeast or fungal cells).

Preferably the nucleic acid in the vector is under the control of, and operably linked to, an appropriate promoter or other regulatory elements for transcription in a host cell such as a microbial, e.g. bacterial, or plant cell. The vector may be a bi-functional expression vector which functions in multiple hosts. In the case of genomic DNA, this may contain its own promoter or other regulatory elements and in the case of cDNA this may be under the control of an appropriate promoter or other regulatory elements for expression in the host cell.

"Cloning vectors" typically contain one or a small number of restriction endonuclease recognition sites at which foreign DNA sequences can be inserted in a determinable fashion without loss of essential biological function of the vector, as well as a marker gene that is suitable for use in the identification and selection of cells transformed with the cloning vector. Marker genes typically include genes that provide tetracycline resistance, hygromycin resistance or ampicillin resistance.

A "transgenic plant" is a plant having one or more plant cells that contain an expression vector.

"Plant tissue" includes differentiated and undifferentiated tissues or plants, including but not limited to roots, stems, shoots, leaves, pollen, seeds, tumor tissue and various forms of cells and culture such as single cells, protoplast, embryos, and callus tissue. The plant tissue may be in plants or in organ, tissue or cell culture.

The following terms are used to describe the sequence relationships between two or more nucleic acids or polynucleotides: (a) "reference sequence", (b) "comparison window", (c) "sequence identity", (d) "percentage of sequence identity", and (e) "substantial identity".

5 (a) As used herein, "reference sequence" is a defined sequence used as a basis for sequence comparison. A reference sequence may be a subset or the entirety of a specified sequence; for example, as a segment of a full length cDNA or gene sequence, or the complete cDNA or gene sequence.

10 (b) As used herein, "comparison window" makes reference to a contiguous and specified segment of a polynucleotide sequence, wherein the polynucleotide sequence in the comparison window may comprise additions or deletions (i.e., gaps) compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. Generally, the comparison window is at least 20 contiguous nucleotides in length, and optionally can be 30, 40,
15 50, 100, or longer. Those of skill in the art understand that to avoid a high similarity to a reference sequence due to inclusion of gaps in the polynucleotide sequence a gap penalty is typically introduced and is subtracted from the number of matches.

Methods of alignment of sequences for comparison are well known in the art. Thus, the determination of percent identity between any two sequences can be
20 accomplished using a mathematical algorithm. Preferred, non-limiting examples of such mathematical algorithms are the algorithm of Myers and Miller, 1988; the local homology algorithm of Smith et al. 1981; the homology alignment algorithm of Needleman and Wunsch 1970; the search-for-similarity-method of Pearson and Lipman 1988; the algorithm of Karlin and Altschul, 1990, modified as in Karlin and
25 Altschul, 1993.

Computer implementations of these mathematical algorithms can be utilized for comparison of sequences to determine sequence identity. Such implementations include, but are not limited to: CLUSTAL in the PC/Gene program (available from Intelligenetics, Mountain View, California); the ALIGN program (Version 2.0) and
30 GAP, BESTFIT, BLAST, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Version 8 (available from Genetics Computer Group (GCG), 575

Science Drive, Madison, Wisconsin, USA). Alignments using these programs can be performed using the default parameters. The CLUSTAL program is well described by Higgins et al. 1988; Higgins et al. 1989; Corpet et al. 1988; Huang et al. 1992; and Pearson et al. 1994. The ALIGN program is based on the algorithm of
5 Myers and Miller, *supra*. The BLAST programs of Altschul et al., 1990, are based on the algorithm of Karlin and Altschul *supra*.

Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>). This algorithm involves first identifying high scoring sequence pairs (HSPs) by
10 identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul et al., 1990). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are then
15 extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score.
20 Extension of the word hits in each direction are halted when the cumulative alignment score falls off by the quantity X from its maximum achieved value, the cumulative score goes to zero or below due to the accumulation of one or more negative-scoring residue alignments, or the end of either sequence is reached.

In addition to calculating percent sequence identity, the BLAST algorithm
25 also performs a statistical analysis of the similarity between two sequences (see, e.g., Karlin & Altschul (1993). One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a test nucleic acid sequence is considered
30 similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid sequence to the reference nucleic acid sequence is less than

about 0.1, more preferably less than about 0.01, and most preferably less than about 0.001.

To obtain gapped alignments for comparison purposes, Gapped BLAST (in BLAST 2.0) can be utilized as described in Altschul et al. 1997. Alternatively, PSI-
5 BLAST (in BLAST 2.0) can be used to perform an iterated search that detects distant relationships between molecules. See Altschul et al., *supra*. When utilizing BLAST, Gapped BLAST, PSI-BLAST, the default parameters of the respective programs (e.g. BLASTN for nucleotide sequences, BLASTX for proteins) can be used. The BLASTN program (for nucleotide sequences) uses as defaults a
10 wordlength (W) of 11, an expectation (E) of 10, a cutoff of 100, M=5, N=-4, and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength (W) of 3, an expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff & Henikoff, 1989). See <http://www.ncbi.nlm.nih.gov>. Alignment may also be performed manually by inspection.

15 For purposes of the present invention, comparison of nucleotide sequences for determination of percent sequence identity to the promoter sequences disclosed herein is preferably made using the BlastN program (version 1.4.7 or later) with its default parameters or any equivalent program. By "equivalent program" is intended any sequence comparison program that, for any two sequences in question, generates
20 an alignment having identical nucleotide or amino acid residue matches and an identical percent sequence identity when compared to the corresponding alignment generated by the preferred program.

(c) As used herein, "sequence identity" or "identity" in the context of two nucleic acid or polypeptide sequences makes reference to the residues in the two
25 sequences that are the same when aligned for maximum correspondence over a specified comparison window. When percentage of sequence identity is used in reference to proteins it is recognized that residue positions which are not identical often differ by conservative amino acid substitutions, where amino acid residues are substituted for other amino acid residues with similar chemical properties (e.g.,
30 charge or hydrophobicity) and therefore do not change the functional properties of the molecule. When sequences differ in conservative substitutions, the percent

sequence identity may be adjusted upwards to correct for the conservative nature of the substitution. Sequences that differ by such conservative substitutions are said to have "sequence similarity" or "similarity." Means for making this adjustment are well known to those of skill in the art. Typically this involves scoring a conservative substitution as a partial rather than a full mismatch, thereby increasing the percentage sequence identity. Thus, for example, where an identical amino acid is given a score of 1 and a non-conservative substitution is given a score of zero, a conservative substitution is given a score between zero and 1. The scoring of conservative substitutions is calculated, e.g., as implemented in the program PC/GENE (Intelligenetics, Mountain View, California).

(d) As used herein, "percentage of sequence identity" means the value determined by comparing two optimally aligned sequences over a comparison window, wherein the portion of the polynucleotide sequence in the comparison window may comprise additions or deletions (i.e., gaps) as compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid base or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison, and multiplying the result by 100 to yield the percentage of sequence identity.

(e)(i) The term "substantial identity" of polynucleotide sequences means that a polynucleotide comprises a sequence that has at least 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, or 79%, preferably at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, or 89%, more preferably at least 90%, 91%, 92%, 93%, or 94%, and most preferably at least 95%, 96%, 97%, 98%, or 99% sequence identity, compared to a reference sequence using one of the alignment programs described using standard parameters. One of skill in the art will recognize that these values can be appropriately adjusted to determine corresponding identity of proteins encoded by two nucleotide sequences by taking into account codon degeneracy, amino acid similarity, reading frame positioning, and the like. Substantial identity

of amino acid sequences for these purposes normally means sequence identity of at least 70%, more preferably at least 80%, 90%, and most preferably at least 95%.

Another indication that nucleotide sequences are substantially identical is if two molecules hybridize to each other under stringent conditions (see below).

5 Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH.

However, stringent conditions encompass temperatures in the range of about 1°C to about 20°C, depending upon the desired degree of stringency as otherwise qualified herein. Nucleic acids that do not hybridize to each other under stringent conditions
10 are still substantially identical if the polypeptides they encode are substantially identical. This may occur, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code. One indication that two nucleic acid sequences are substantially identical is when the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the polypeptide
15 encoded by the second nucleic acid.

(e)(ii) The term "substantial identity" in the context of a peptide indicates that a peptide comprises a sequence with at least 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, or 79%, preferably 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, or 89%, more preferably at least 90%, 91%, 92%, 93%, or 94%, or even more
20 preferably, 95%, 96%, 97%, 98% or 99%, sequence identity to the reference sequence over a specified comparison window. Preferably, optimal alignment is conducted using the homology alignment algorithm of Needleman and Wunsch (1970). An indication that two peptide sequences are substantially identical is that one peptide is immunologically reactive with antibodies raised against the second
25 peptide. Thus, a peptide is substantially identical to a second peptide, for example, where the two peptides differ only by a conservative substitution.

For sequence comparison, typically one sequence acts as a reference sequence to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are input into a computer,
30 subsequence coordinates are designated if necessary, and sequence algorithm program parameters are designated. The sequence comparison algorithm then

calculates the percent sequence identity for the test sequence(s) relative to the reference sequence, based on the designated program parameters.

As noted above, another indication that two nucleic acid sequences are substantially identical is that the two molecules hybridize to each other under stringent conditions. The phrase "hybridizing specifically to" refers to the binding, duplexing, or hybridizing of a molecule only to a particular nucleotide sequence under stringent conditions when that sequence is present in a complex mixture (e.g., total cellular) DNA or RNA. "Bind(s) substantially" refers to complementary hybridization between a probe nucleic acid and a target nucleic acid and embraces minor mismatches that can be accommodated by reducing the stringency of the hybridization media to achieve the desired detection of the target nucleic acid sequence.

"Stringent hybridization conditions" and "stringent hybridization wash conditions" in the context of nucleic acid hybridization experiments such as Southern and Northern hybridization are sequence dependent, and are different under different environmental parameters. The T_m is the temperature (under defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly matched probe. Specificity is typically the function of post-hybridization washes, the critical factors being the ionic strength and temperature of the final wash solution. For DNA-DNA hybrids, the T_m can be approximated from the equation of Meinkoth and Wahl, 1984; $T_m = 81.5^\circ\text{C} + 16.6 (\log M) + 0.41 (\%GC) - 0.61 (\% \text{ form}) - 500/L$; where M is the molarity of monovalent cations, %GC is the percentage of guanosine and cytosine nucleotides in the DNA, % form is the percentage of formamide in the hybridization solution, and L is the length of the hybrid in base pairs. T_m is reduced by about 1°C for each 1% of mismatching; thus, T_m , hybridization, and/or wash conditions can be adjusted to hybridize to sequences of the desired identity. For example, if sequences with >90% identity are sought, the T_m can be decreased 10°C . Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point T_m for the specific sequence and its complement at a defined ionic strength and pH. However, severely stringent

conditions can utilize a hybridization and/or wash at 1, 2, 3, or 4°C lower than the thermal melting point T_m ; moderately stringent conditions can utilize a hybridization and/or wash at 6, 7, 8, 9, or 10°C lower than the thermal melting point T_m ; low stringency conditions can utilize a hybridization and/or wash at 11, 12, 13, 14, 15, or 20°C lower than the thermal melting point T_m . Using the equation, hybridization and wash compositions, and desired T_m , those of ordinary skill will understand that variations in the stringency of hybridization and/or wash solutions are inherently described. If the desired degree of mismatching results in a T_m of less than 45°C (aqueous solution) or 32°C (formamide solution), it is preferred to increase the SSC concentration so that a higher temperature can be used. An extensive guide to the hybridization of nucleic acids is found in Tijssen, 1993. Generally, highly stringent hybridization and wash conditions are selected to be about 5°C lower than the thermal melting point T_m for the specific sequence at a defined ionic strength and pH.

15 An example of highly stringent wash conditions is 0.15 M NaCl at 72°C for about 15 minutes. An example of stringent wash conditions is a 0.2X SSC wash at 65°C for 15 minutes (see, Sambrook, *infra*, for a description of SSC buffer). Often, a high stringency wash is preceded by a low stringency wash to remove background probe signal. An example medium stringency wash for a duplex of, e.g., more than 20 100 nucleotides, is 1X SSC at 45°C for 15 minutes. An example low stringency wash for a duplex of, e.g., more than 100 nucleotides, is 4-6X SSC at 40°C for 15 minutes. For short probes (e.g., about 10 to 50 nucleotides), stringent conditions typically involve salt concentrations of less than about 1.5 M, more preferably about 0.01 to 1.0 M, Na ion concentration (or other salts) at pH 7.0 to 8.3, and the 25 temperature is typically at least about 30°C and at least about 60°C for long probes (e.g., >50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. In general, a signal to noise ratio of 2X (or higher) than that observed for an unrelated probe in the particular hybridization assay indicates detection of a specific hybridization. Nucleic acids that do not 30 hybridize to each other under stringent conditions are still substantially identical if

the proteins that they encode are substantially identical. This occurs, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code.

Very stringent conditions are selected to be equal to the T_m for a particular probe. An example of stringent conditions for hybridization of complementary nucleic acids which have more than 100 complementary residues on a filter in a Southern or Northern blot is 50% formamide, e.g., hybridization in 50% formamide, 1 M NaCl, 1% SDS at 37°C, and a wash in 0.1X SSC at 60 to 65°C. Exemplary low stringency conditions include hybridization with a buffer solution of 30 to 35% formamide, 1 M NaCl, 1% SDS (sodium dodecyl sulphate) at 37°C, and a wash in 1X to 2X SSC (20X SSC = 3.0 M NaCl/0.3 M trisodium citrate) at 50 to 55°C. Exemplary moderate stringency conditions include hybridization in 40 to 45% formamide, 1.0 M NaCl, 1% SDS at 37°C, and a wash in 0.5X to 1X SSC at 55 to 60°C.

The following are examples of sets of hybridization/wash conditions that may be used to clone orthologous nucleotide sequences that are substantially identical to reference nucleotide sequences of the present invention: a reference nucleotide sequence preferably hybridizes to the reference nucleotide sequence in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 2X SSC, 0.1% SDS at 50°C, more desirably in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 1X SSC, 0.1% SDS at 50°C, more desirably still in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 0.5X SSC, 0.1% SDS at 50°C, preferably in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 0.1X SSC, 0.1% SDS at 50°C, more preferably in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 0.1X SSC, 0.1% SDS at 65°C.

“DNA shuffling” is a method to introduce mutations or rearrangements, preferably randomly, in a DNA molecule or to generate exchanges of DNA sequences between two or more DNA molecules, preferably randomly. The DNA

molecule resulting from DNA shuffling is a shuffled DNA molecule that is a non-naturally occurring DNA molecule derived from at least one template DNA molecule. The shuffled DNA preferably encodes a variant polypeptide modified with respect to the polypeptide encoded by the template DNA, and may have an altered biological activity with respect to the polypeptide encoded by the template DNA.

“Recombinant DNA molecule” is a combination of DNA sequences that are joined together using recombinant DNA technology and procedures used to join together DNA sequences as described, for example, in Sambrook et al., 1989.

The word “plant” refers to any plant, particularly to seed plant, and “plant cell” is a structural and physiological unit of the plant, which comprises a cell wall but may also refer to a protoplast. The plant cell may be in form of an isolated single cell or a cultured cell, or as a part of higher organized unit such as, for example, a plant tissue, or a plant organ.

“Significant increase” is an increase that is larger than the margin of error inherent in the measurement technique, preferably an increase by about 2-fold or greater.

“Significantly less” means that the decrease is larger than the margin of error inherent in the measurement technique, preferably a decrease by about 2-fold or greater.

II. DNA Sequences for Transformation

Virtually any DNA composition may be used for delivery to recipient plant cells, e.g., monocotyledonous cells, to ultimately produce fertile transgenic plants in accordance with the present invention. For example, DNA segments in the form of vectors and plasmids, or linear DNA fragments, in some instances containing only the DNA element to be expressed in the plant, and the like, may be employed. The construction of vectors which may be employed in conjunction with the present invention will be known to those of skill of the art in light of the present disclosure (see, e.g., Sambrook et al., 1989; Gelvin et al., 1990).

Vectors, plasmids, cosmids, YACs (yeast artificial chromosomes), BACs (bacterial artificial chromosomes) and DNA segments for use in transforming such

cells will, of course, generally comprise the cDNA, gene or genes which one desires to introduce into the cells. These DNA constructs can further include structures such as promoters, enhancers, polylinkers, or even regulatory genes as desired. The DNA segment or gene chosen for cellular introduction will often encode a protein which will be expressed in the resultant recombinant cells, such as will result in a screenable or selectable trait and/or which will impart an improved phenotype to the regenerated plant. However, this may not always be the case, and the present invention also encompasses transgenic plants incorporating non-expressed transgenes.

10 In certain embodiments, it is contemplated that one may wish to employ replication-competent viral vectors in monocot transformation. Such vectors include, for example, wheat dwarf virus (WDV) "shuttle" vectors, such as pW1-11 and PW1-GUS (Ugaki et al., 1991). These vectors are capable of autonomous replication in maize cells as well as *E. coli*, and as such may provide increased sensitivity for detecting DNA delivered to transgenic cells. A replicating vector may also be useful for delivery of genes flanked by DNA sequences from transposable elements such as Ac, Ds, or Mu. It has been proposed (Laufs et al., 1990) that transposition of these elements within the maize genome requires DNA replication. It is also contemplated that transposable elements would be useful for introducing DNA fragments lacking elements necessary for selection and maintenance of the plasmid vector in bacteria, e.g., antibiotic resistance genes and origins of DNA replication. It is also proposed that use of a transposable element such as Ac, Ds, or Mu would actively promote integration of the desired DNA and hence increase the frequency of stably transformed cells. The use of a transposable element such as Ac, Ds, or Mu may actively promote integration of the DNA of interest and hence increase the frequency of stably transformed cells. Transposable elements may be useful to allow separation of genes of interest from elements necessary for selection and maintenance of a plasmid vector in bacteria or selection of a transformant. By use of a transposable element, desirable and undesirable DNA sequences may be transposed apart from each other in the genome, such that through genetic

segregation in progeny, one may identify plants with either the desirable or the undesirable DNA sequences.

DNA useful for introduction into plant cells includes that which has been derived or isolated from any source, that may be subsequently characterized as to structure, size and/or function, chemically altered, and later introduced into plants. An example of DNA “derived” from a source, would be a DNA sequence that is identified as a useful fragment within a given organism, and which is then chemically synthesized in essentially pure form. An example of such DNA “isolated” from a source would be a useful DNA sequence that is excised or removed from said source by chemical means, e.g., by the use of restriction endonucleases, so that it can be further manipulated, e.g., amplified, for use in the invention, by the methodology of genetic engineering. Such DNA is commonly referred to as “recombinant DNA.”

Therefore useful DNA includes completely synthetic DNA, semi-synthetic DNA, DNA isolated from biological sources, and DNA derived from introduced RNA. Generally, the introduced DNA is not originally resident in the plant genotype which is the recipient of the DNA, but it is within the scope of the invention to isolate a gene from a given plant genotype, and to subsequently introduce multiple copies of the gene into the same genotype, e.g., to enhance production of a given gene product such as a storage protein or a protein that confers tolerance or resistance to water deficit.

The introduced DNA includes but is not limited to, DNA from plant genes, and non-plant genes such as those from bacteria, yeasts, animals or viruses. The introduced DNA can include modified genes, portions of genes, or chimeric genes, including genes from the same or different maize genotype. The term “chimeric gene” or “chimeric DNA” is defined as a gene or DNA sequence or segment comprising at least two DNA sequences or segments from species which do not combine DNA under natural conditions, or which DNA sequences or segments are positioned or linked in a manner which does not normally occur in the native genome of untransformed plant.

The introduced DNA used for transformation herein may be circular or linear, double-stranded or single-stranded. Generally, the DNA is in the form of chimeric DNA, such as plasmid DNA, that can also contain coding regions flanked by regulatory sequences which promote the expression of the recombinant DNA present in the resultant plant. For example, the DNA may itself comprise or consist of a promoter that is active in a plant which is derived from a source other than that plant, or may utilize a promoter already present in a plant genotype that is the transformation target.

Generally, the introduced DNA will be relatively small, i.e., less than about 30 kb to minimize any susceptibility to physical, chemical, or enzymatic degradation which is known to increase as the size of the DNA increases. As noted above, the number of proteins, RNA transcripts or mixtures thereof which is introduced into the plant genome is preferably preselected and defined, e.g., from one to about 5-10 such products of the introduced DNA may be formed.

Two principal methods for the control of expression are known, viz.: overexpression and underexpression. Overexpression can be achieved by insertion of one or more than one extra copy of the selected gene. It is, however, not unknown for plants or their progeny, originally transformed with one or more than one extra copy of a nucleotide sequence, to exhibit the effects of underexpression as well as overexpression. For underexpression there are two principle methods which are commonly referred to in the art as "antisense downregulation" and "sense downregulation" (sense downregulation is also referred to as "cosuppression"). Generically these processes are referred to as "gene silencing". Both of these methods lead to an inhibition of expression of the target gene.

Obtaining sufficient levels of transgene expression in the appropriate plant tissues is an important aspect in the production of genetically engineered crops. Expression of heterologous DNA sequences in a plant host is dependent upon the presence of an operably linked promoter that is functional within the plant host. Choice of the promoter sequence will determine when and where within the organism the heterologous DNA sequence is expressed.

Furthermore, it is contemplated that promoters combining elements from more than one promoter may be useful. For example, U.S. Patent No. 5,491,288 discloses combining a Cauliflower Mosaic Virus promoter with a histone promoter. Thus, the elements from the promoters disclosed herein may be combined with elements from other promoters.

Promoters which are useful for plant transgene expression include those that are inducible, viral, synthetic, constitutive (Odell et al., 1985), temporally regulated, spatially regulated, tissue-specific, and spatio-temporally regulated.

Where expression in specific tissues or organs is desired, tissue-specific promoters may be used. In contrast, where gene expression in response to a stimulus is desired, inducible promoters are the regulatory elements of choice. Where continuous expression is desired throughout the cells of a plant, constitutive promoters are utilized. Additional regulatory sequences upstream and/or downstream from the core promoter sequence may be included in expression constructs of transformation vectors to bring about varying levels of expression of heterologous nucleotide sequences in a transgenic plant.

A. Transcription Regulatory Sequences

1. Promoters

The choice of promoter will vary depending on the temporal and spatial requirements for expression, and also depending on the target species. In some cases, expression in multiple tissues is desirable. While in others, tissue-specific, e.g., leaf-specific, seed-specific, petal-specific, anther-specific, or pith-specific, expression is desirable. Although many promoters from dicotyledons have been shown to be operational in monocotyledons and *vice versa*, ideally dicotyledonous promoters are selected for expression in dicotyledons, and monocotyledonous promoters for expression in monocotyledons. However, there is no restriction to the provenance of selected promoters; it is sufficient that they are operational in driving the expression of the nucleotide sequences in the desired cell.

These promoters include, but are not limited to, constitutive, inducible, temporally regulated, developmentally regulated, spatially-regulated, chemically regulated, stress-responsive, tissue-specific, viral and synthetic promoters. Promoter

sequences are known to be strong or weak. A strong promoter provides for a high level of gene expression, whereas a weak promoter provides for a very low level of gene expression. An inducible promoter is a promoter that provides for the turning on and off of gene expression in response to an exogenously added agent, or to an environmental or developmental stimulus. A bacterial promoter such as the P_{tac} promoter can be induced to varying levels of gene expression depending on the level of isothiopropylgalactoside added to the transformed bacterial cells. An isolated promoter sequence that is a strong promoter for heterologous nucleic acid is advantageous because it provides for a sufficient level of gene expression to allow for easy detection and selection of transformed cells and provides for a high level of gene expression when desired.

Within a plant promoter region there are several domains that are necessary for full function of the promoter. The first of these domains lies immediately upstream of the structural gene and forms the “core promoter region” containing consensus sequences, normally 70 base pairs immediately upstream of the gene. The core promoter region contains the characteristic CAAT and TATA boxes plus surrounding sequences, and represents a transcription initiation sequence that defines the transcription start point for the structural gene.

The presence of the core promoter region defines a sequence as being a promoter: if the region is absent, the promoter is non-functional. Furthermore, the core promoter region is insufficient to provide full promoter activity. A series of regulatory sequences upstream of the core constitute the remainder of the promoter. The regulatory sequences determine expression level, the spatial and temporal pattern of expression and, for an important subset of promoters, expression under inductive conditions (regulation by external factors such as light, temperature, chemicals, hormones).

A range of naturally-occurring promoters are known to be operative in plants and have been used to drive the expression of heterologous (both foreign and endogenous) genes in plants: for example, the constitutive 35S cauliflower mosaic virus (CaMV) promoter, the ripening-enhanced tomato polygalacturonase promoter (Bird et al., 1988), the E8 promoter (Diekmann & Fischer, 1988) and the fruit specific

2A1 promoter (Pear et al., 1989) and many others, e.g., U2 and U5 snRNA promoters from maize, the promoter from alcohol dehydrogenase, the Z4 promoter from a gene encoding the Z4 22 kD zein protein, the Z10 promoter from a gene encoding a 10 kD zein protein, a Z27 promoter from a gene encoding a 27 kD zein protein, the A20 promoter from the gene encoding a 19 kD -zein protein, inducible promoters, such as the light inducible promoter derived from the pea rbcS gene and the actin promoter from rice, e.g., the actin 2 promoter (WO 00/70067); seed specific promoters, such as the phaseolin promoter from beans, may also be used. The nucleotide sequences of this invention can also be expressed under the regulation of promoters that are chemically regulated. This enables the nucleic acid sequence or encoded polypeptide to be synthesized only when the crop plants are treated with the inducing chemicals. Chemical induction of gene expression is detailed in EP 0 332 104 (to Ciba-Geigy) and U.S. Patent 5,614,395. A preferred promoter for chemical induction is the tobacco PR-1a promoter.

Examples of some constitutive promoters which have been described include the rice actin 1 (Wang et al., 1992; U.S. Patent No. 5,641,876), CaMV 35S (Odell et al., 1985), CaMV 19S (Lawton et al., 1987), *nos*, *Adh*, sucrose synthase; and the ubiquitin promoters.

Examples of tissue specific promoters which have been described include the lectin (Vodkin, 1983; Lindstrom et al., 1990) corn alcohol dehydrogenase 1 (Vogel et al., 1989; Dennis et al., 1984), corn light harvesting complex (Simpson, 1986; Bansal et al., 1992), corn heat shock protein (Odell et al., 1985), pea small subunit RuBP carboxylase (Poulsen et al., 1986), Ti plasmid mannopine synthase (Langridge et al., 1989), Ti plasmid nopaline synthase (Langridge et al., 1989), petunia chalcone isomerase (vanTunen et al., 1988), bean glycine rich protein 1 (Keller et al., 1989), truncated CaMV 35s (Odell et al., 1985), potato patatin (Wenzler et al., 1989), root cell (Yamamoto et al., 1990), maize zein (Reina et al., 1990; Kriz et al., 1987; Wandelt et al., 1989; Langridge et al., 1983; Reina et al., 1990), globulin-1 (Belanger et al., 1991), α -tubulin, cab (Sullivan et al., 1989), PEPCase (Hudspeth & Grula, 1989), R gene complex-associated promoters

(Chandler et al., 1989), histone, and chalcone synthase promoters (Franken et al., 1991). Tissue specific enhancers are described in Fromm et al. (1989).

Inducible promoters that have been described include the ABA- and turgor-inducible promoters, the promoter of the auxin-binding protein gene (Schwob et al., 1993), the UDP glucose flavonoid glycosyl-transferase gene promoter (Ralston et al., 1988), the MPI proteinase inhibitor promoter (Cordero et al., 1994), and the glyceraldehyde-3-phosphate dehydrogenase gene promoter (Kohler et al., 1995; Quigley et al., 1989; Martinez et al., 1989).

Several other tissue-specific regulated genes and/or promoters have been reported in plants. These include genes encoding the seed storage proteins (such as napin, cruciferin, beta-conglycinin, and phaseolin) zein or oil body proteins (such as oleosin), or genes involved in fatty acid biosynthesis (including acyl carrier protein, stearoyl-ACP desaturase. And fatty acid desaturases (fad 2-1)), and other genes expressed during embryo development (such as Bce4, see, for example, EP 255378 and Kridl et al., 1991). Particularly useful for seed-specific expression is the pea vicilin promoter (Czako et al., 1992). (See also U.S. Pat. No. 5,625,136, herein incorporated by reference.) Other useful promoters for expression in mature leaves are those that are switched on at the onset of senescence, such as the SAG promoter from Arabidopsis (Gan et al., 1995).

A class of fruit-specific promoters expressed at or during antithesis through fruit development, at least until the beginning of ripening, is discussed in U.S. 4,943,674. cDNA clones that are preferentially expressed in cotton fiber have been isolated (John et al., 1992). cDNA clones from tomato displaying differential expression during fruit development have been isolated and characterized (Mansson et al., 1985, Slater et al., 1985). The promoter for polygalacturonase gene is active in fruit ripening. The polygalacturonase gene is described in U.S. Patent No. 4,535,060, U.S. Patent No. 4,769,061, U.S. Patent No. 4,801,590, and U.S. Patent No. 5,107,065, which disclosures are incorporated herein by reference.

Other examples of tissue-specific promoters include those that direct expression in leaf cells following damage to the leaf (for example, from chewing insects), in tubers (for example, patatin gene promoter), and in fiber cells (an

example of a developmentally-regulated fiber cell protein is E6 (John et al., 1992). The E6 gene is most active in fiber, although low levels of transcripts are found in leaf, ovule and flower.

The tissue-specificity of some “tissue-specific” promoters may not be absolute and may be tested by one skilled in the art using the diphtheria toxin sequence. One can also achieve tissue-specific expression with “leaky” expression by a combination of different tissue-specific promoters (Beals et al., 1997). Other tissue-specific promoters can be isolated by one skilled in the art (see U.S. 5,589,379). Several inducible promoters (“gene switches”) have been reported. Many are described in the review by Gatz (1996) and Gatz (1997). These include tetracycline repressor system, *Lac* repressor system, copper-inducible systems, salicylate-inducible systems (such as the PR1a system), glucocorticoid- (Aoyama et al., 1997) and ecdysone-inducible systems. Also included are the benzene sulphonamide- (U.S. Patent No. 5,364,780) and alcohol-(WO 97/06269 and WO 97/06268) inducible systems and glutathione S-transferase promoters. Other studies have focused on genes inducibly regulated in response to environmental stress or stimuli such as increased salinity. Drought, pathogen and wounding. (Graham et al., 1985; Graham et al., 1985, Smith et al., 1986). Accumulation of metallocarboxypeptidase-inhibitor protein has been reported in leaves of wounded potato plants (Graham et al., 1981). Other plant genes have been reported to be induced methyl jasmonate, elicitors, heat-shock, anaerobic stress, or herbicide safeners.

Regulated expression of the chimeric transacting viral replication protein can be further regulated by other genetic strategies. For example, *Cre*-mediated gene activation as described by Odell et al. 1990. Thus, a DNA fragment containing 3' regulatory sequence bound by lox sites between the promoter and the replication protein coding sequence that blocks the expression of a chimeric replication gene from the promoter can be removed by *Cre*-mediated excision and result in the expression of the *trans*-acting replication gene. In this case, the chimeric *Cre* gene, the chimeric *trans*-acting replication gene, or both can be under the control of tissue- and developmental- specific or inducible promoters. An alternate genetic strategy is

the use of tRNA suppressor gene. For example, the regulated expression of a tRNA suppressor gene can conditionally control expression of a *trans*-acting replication protein coding sequence containing an appropriate termination codon as described by Ulmasov et al. 1997. Again, either the chimeric tRNA suppressor gene, the
5 chimeric transacting replication gene, or both can be under the control of tissue- and developmental-specific or inducible promoters.

Frequently it is desirable to have continuous or inducible expression of a DNA sequence throughout the cells of an organism in a tissue-independent manner. For example, increased resistance of a plant to infection by soil- and airborne-
10 pathogens might be accomplished by genetic manipulation of the plant's genome to comprise a continuous promoter operably linked to a heterologous pathogen-resistance gene such that pathogen-resistance proteins are continuously expressed throughout the plant's tissues.

Alternatively, it might be desirable to inhibit expression of a native DNA
15 sequence within a plant's tissues to achieve a desired phenotype. In this case, such inhibition might be accomplished with transformation of the plant to comprise a constitutive, tissue-independent promoter operably linked to an antisense nucleotide sequence, such that constitutive expression of the antisense sequence produces an RNA transcript that interferes with translation of the mRNA of the native DNA
20 sequence.

To define a minimal promoter region, a DNA segment representing the promoter region is removed from the 5' region of the gene of interest and operably linked to the coding sequence of a marker (reporter) gene by recombinant DNA techniques well known to the art. The reporter gene is operably linked downstream
25 of the promoter, so that transcripts initiating at the promoter proceed through the reporter gene. Reporter genes generally encode proteins which are easily measured, including, but not limited to, chloramphenicol acetyl transferase (CAT), beta-glucuronidase (GUS), green fluorescent protein (GFP), beta-galactosidase (beta-GAL), and luciferase.

30 The construct containing the reporter gene under the control of the promoter is then introduced into an appropriate cell type by transfection techniques well

known to the art. To assay for the reporter protein, cell lysates are prepared and appropriate assays, which are well known in the art, for the reporter protein are performed. For example, if CAT were the reporter gene of choice, the lysates from cells transfected with constructs containing CAT under the control of a promoter
5 under study are mixed with isotopically labeled chloramphenicol and acetyl-coenzyme A (acetyl-CoA). The CAT enzyme transfers the acetyl group from acetyl-CoA to the 2- or 3-position of chloramphenicol. The reaction is monitored by thin-layer chromatography, which separates acetylated chloramphenicol from unreacted material. The reaction products are then visualized by autoradiography.

10 The level of enzyme activity corresponds to the amount of enzyme that was made, which in turn reveals the level of expression from the promoter of interest. This level of expression can be compared to other promoters to determine the relative strength of the promoter under study. In order to be sure that the level of expression is determined by the promoter, rather than by the stability of the mRNA,
15 the level of the reporter mRNA can be measured directly, such as by Northern blot analysis.

Once activity is detected, mutational and/or deletional analyses may be employed to determine the minimal region and/or sequences required to initiate transcription. Thus, sequences can be deleted at the 5' end of the promoter region
20 and/or at the 3' end of the promoter region, and nucleotide substitutions introduced. These constructs are then introduced to cells and their activity determined.

In one embodiment, the promoter may be a gamma zein promoter, an oleosin ole16 promoter, a globulinI promoter, an actin I promoter, an actin cl promoter, a sucrose synthetase promoter, an INOPS promoter, an EXM5 promoter, a globulin2
25 promoter, a b-32, ADPG- pyrophosphorylase promoter, an LtpI promoter, an Ltp2 promoter, an oleosin ole17 promoter, an oleosin ole18 promoter, an actin 2 promoter, a pollen-specific protein promoter, a pollen-specific pectate lyase promoter, an anther-specific protein promoter (Huffman), an anther-specific gene RTS2 promoter, a pollen- specific gene promoter, a tapeturn-specific gene promoter,
30 tapeturn- specific gene RAB24 promoter, a anthranilate synthase alpha subunit promoter, an alpha zein promoter, an anthranilate synthase beta subunit promoter, a

dihydrodipicolinate synthase promoter, a Thil promoter, an alcohol dehydrogenase promoter, a cab binding protein promoter, an H3C4 promoter, a RUBISCO SS starch branching enzyme promoter, an ACCase promoter, an actin3 promoter, an actin7 promoter, a regulatory protein GF14-12 promoter, a ribosomal protein L9 promoter, a cellulose biosynthetic enzyme promoter, an S-adenosyl-L-homocysteine hydrolase promoter, a superoxide dismutase promoter, a C-kinase receptor promoter, a phosphoglycerate mutase promoter, a root-specific RCc3 mRNA promoter, a glucose-6 phosphate isomerase promoter, a pyrophosphate-fructose 6-phosphatetphosphotransferase promoter, an ubiquitin promoter, a beta-ketoacyl-ACP synthase promoter, a 33 kDa photosystem 11 promoter, an oxygen evolving protein promoter, a 69 kDa vacuolar ATPase subunit promoter, a metallothionein-like protein promoter, a glyceraldehyde-3 -phosphate dehydrogenase promoter, an ABA- and ripening- inducible-like protein promoter, a phenylalanine ammonia lyase promoter, an adenosine triphosphatase S-adenosyl-L-homocysteine hydrolase promoter, an a- tubulin promoter, a cab promoter, a PEPCase promoter, an R gene promoter, a lectin promoter, a light harvesting complex promoter, a heat shock protein promoter, a chalcone synthase promoter, a zein promoter, a globulin-1 promoter, an ABA promoter, an auxin-binding protein promoter, a UDP glucose flavonoid glycosyl-transferase gene promoter, an NTI promoter, an actin promoter, an opaque 2 promoter, a b70 promoter, an oleosin promoter, a CaMV 35S promoter, a CaMV 19S promoter, a histone promoter, a turgor-inducible promoter, a pea small subunit RuBP carboxylase promoter, a Ti plasmid mannopine synthase promoter, Ti plasmid nopaline synthase promoter, a petunia chalcone isomerase promoter, a bean glycine rich protein I promoter, a CaMV 35S transcript promoter, a potato patatin promoter, or a S-E9 small subunit RuBP carboxylase promoter.

2. Other Regulatory Elements

In addition to promoters, a variety of 5' and 3' transcriptional regulatory sequences are also available for use in the present invention. Transcriptional terminators are responsible for the termination of transcription and correct mRNA polyadenylation. The 3' nontranslated regulatory DNA sequence preferably includes from about 50 to about 1,000, more preferably about 100 to about 1,000, nucleotide

base pairs and contains plant transcriptional and translational termination sequences. Appropriate transcriptional terminators and those which are known to function in plants include the CaMV 35S terminator, the *tml* terminator, the nopaline synthase terminator, the pea *rbcS* E9 terminator, the terminator for the T7 transcript from the octopine synthase gene of *Agrobacterium tumefaciens*, and the 3' end of the protease inhibitor I or II genes from potato or tomato, although other 3' elements known to those of skill in the art can also be employed. Alternatively, one also could use a gamma coixin, oleosin 3 or other terminator from the genus Coix.

Preferred 3' elements include those from the nopaline synthase gene of *Agrobacterium tumefaciens* (Bevan et al., 1983), the terminator for the T7 transcript from the octopine synthase gene of *Agrobacterium tumefaciens*, and the 3' end of the protease inhibitor I or II genes from potato or tomato.

As the DNA sequence between the transcription initiation site and the start of the coding sequence, i.e., the untranslated leader sequence, can influence gene expression, one may also wish to employ a particular leader sequence. Preferred leader sequences are contemplated to include those which include sequences predicted to direct optimum expression of the attached gene, i.e., to include a preferred consensus leader sequence which may increase or maintain mRNA stability and prevent inappropriate initiation of translation. The choice of such sequences will be known to those of skill in the art in light of the present disclosure. Sequences that are derived from genes that are highly expressed in plants will be most preferred.

Other sequences that have been found to enhance gene expression in transgenic plants include intron sequences (e.g., from *Adh1*, *bronze1*, *actin1*, *actin 2* (WO 00/760067), or the sucrose synthase intron) and viral leader sequences (e.g., from TMV, MCMV and AMV). For example, a number of non-translated leader sequences derived from viruses are known to enhance expression. Specifically, leader sequences from Tobacco Mosaic Virus (TMV), Maize Chlorotic Mottle Virus (MCMV), and Alfalfa Mosaic Virus (AMV) have been shown to be effective in enhancing expression (e.g., Gallie et al., 1987; Skuzeski et al., 1990). Other leaders known in the art include but are not limited to: Picornavirus leaders, for example,

EMCV leader (Encephalomyocarditis 5 noncoding region) (Elroy-Stein et al., 1989); Potyvirus leaders, for example, TEV leader (Tobacco Etch Virus); MDMV leader (Maize Dwarf Mosaic Virus); Human immunoglobulin heavy-chain binding protein (BiP) leader, (Macejak et al., 1991); Untranslated leader from the coat protein mRNA of alfalfa mosaic virus (AMV RNA 4), (Jobling et al., 1987; Tobacco mosaic virus leader (TMV), (Gallie et al., 1989; and Maize Chlorotic Mottle Virus leader (MCMV) (Lommel et al., 1991. See also, Della-Cioppa et al., 1987.

Regulatory elements such as Adh intron 1 (Callis et al., 1987), sucrose synthase intron (Vasil et al., 1989) or TMV omega element (Gallie, et al., 1989), may further be included where desired.

Examples of enhancers include elements from the CaMV 35S promoter, octopine synthase genes (Ellis et al., 1987), the rice actin I gene, the maize alcohol dehydrogenase gene (Callis et al., 1987), the maize shrunken I gene (Vasil et al., 1989), TMV Omega element (Gallie et al., 1989) and promoters from non-plant eukaryotes (e.g. yeast; Ma et al., 1988).

Vectors for use in accordance with the present invention may be constructed to include the ocs enhancer element. This element was first identified as a 16 bp palindromic enhancer from the octopine synthase (ocs) gene of utilane (Ellis et al., 1987), and is present in at least 10 other promoters (Bouchez et al., 1989). The use of an enhancer element, such as the ocs element and particularly multiple copies of the element, will act to increase the level of transcription from adjacent promoters when applied in the context of monocot transformation.

Ultimately, the most desirable DNA segments for introduction into for example a monocot genome may be homologous genes or gene families which encode a desired trait (e.g., increased yield per acre) and which are introduced under the control of novel promoters or enhancers, etc., or perhaps even homologous or tissue specific (e.g., root-, collar/sheath-, whorl-, stalk-, earshank-, kernel- or leaf-specific) promoters or control elements. Indeed, it is envisioned that a particular use of the present invention will be the targeting of a gene in a constitutive manner or a root-specific manner. For example, insect resistant genes may be expressed specifically in the whorl and collar/sheath tissues which are targets for the first and

second broods, respectively, of ECB. Likewise, genes encoding proteins with particular activity against rootworm may be targeted directly to root tissues.

Vectors for use in tissue-specific targeting of genes in transgenic plants will typically include tissue-specific promoters and may also include other tissue-specific control elements such as enhancer sequences. Promoters which direct specific or enhanced expression in certain plant tissues will be known to those of skill in the art in light of the present disclosure. These include, for example, the *rbcS* promoter, specific for green tissue; the *ocs*, *nos* and *mas* promoters which have higher activity in roots or wounded leaf tissue; a truncated (-90 to +8) 35S promoter which directs enhanced expression in roots, an alpha-tubulin gene that directs expression in roots and promoters derived from zein storage protein genes which direct expression in endosperm. It is particularly contemplated that one may advantageously use the 16 bp *ocs* enhancer element from the octopine synthase (*ocs*) gene (Ellis et al., 1987; Bouchez et al., 1989), especially when present in multiple copies, to achieve enhanced expression in roots.

Tissue specific expression may be functionally accomplished by introducing a constitutively expressed gene (all tissues) in combination with an antisense gene that is expressed only in those tissues where the gene product is not desired. For example, a gene coding for the crystal toxin protein from *B. thuringiensis* (Bt) may be introduced such that it is expressed in all tissues using the 35S promoter from Cauliflower Mosaic Virus. Expression of an antisense transcript of the Bt gene in a maize kernel, using for example a zein promoter, would prevent accumulation of the Bt protein in seed. Hence the protein encoded by the introduced gene would be present in all tissues except the kernel.

Expression of some genes in transgenic plants will be desired only under specified conditions. For example, it is proposed that expression of certain genes that confer resistance to environmental stress factors such as drought will be desired only under actual stress conditions. It is contemplated that expression of such genes throughout a plants development may have detrimental effects. It is known that a large number of genes exist that respond to the environment. For example, expression of some genes such as *rbcS*, encoding the small subunit of ribulose

bisphosphate carboxylase, is regulated by light as mediated through phytochrome. Other genes are induced by secondary stimuli. For example, synthesis of abscisic acid (ABA) is induced by certain environmental factors, including but not limited to water stress. A number of genes have been shown to be induced by ABA (Skriver and Mundy, 1990). It is also anticipated that expression of genes conferring resistance to insect predation would be desired only under conditions of actual insect infestation. Therefore, for some desired traits inducible expression of genes in transgenic plants will be desired.

Expression of a gene in a transgenic plant will be desired only in a certain time period during the development of the plant. Developmental timing is frequently correlated with tissue specific gene expression. For example, expression of zein storage proteins is initiated in the endosperm about 15 days after pollination.

Additionally, vectors may be constructed and employed in the intracellular targeting of a specific gene product within the cells of a transgenic plant or in directing a protein to the extracellular environment. This will generally be achieved by joining a DNA sequence encoding a transit or signal peptide sequence to the coding sequence of a particular gene. The resultant transit, or signal, peptide will transport the protein to a particular intracellular, or extracellular destination, respectively, and will then be post-translationally removed. Transit or signal peptides act by facilitating the transport of proteins through intracellular membranes, e.g., vacuole, vesicle, plastid and mitochondrial membranes, whereas signal peptides direct proteins through the extracellular membrane.

A particular example of such a use concerns the direction of a herbicide resistance gene, such as the EPSPS gene, to a particular organelle such as the chloroplast rather than to the cytoplasm. This is exemplified by the use of the rbcS transit peptide which confers plastid-specific targeting of proteins. In addition, it is proposed that it may be desirable to target certain genes responsible for male sterility to the mitochondria, or to target certain genes for resistance to phytopathogenic organisms to the extracellular spaces, or to target proteins to the vacuole.

By facilitating the transport of the protein into compartments inside and outside the cell, these sequences may increase the accumulation of gene product

protecting them from proteolytic degradation. These sequences also allow for additional mRNA sequences from highly expressed genes to be attached to the coding sequence of the genes. Since mRNA being translated by ribosomes is more stable than naked mRNA, the presence of translatable mRNA in front of the gene
5 may increase the overall stability of the mRNA transcript from the gene and thereby increase synthesis of the gene product. Since transit and signal sequences are usually post- translationally removed from the initial translation product, the use of these sequences allows for the addition of extra translated sequences that may not appear on the final polypeptide. Targeting of certain proteins may be desirable in
10 order to enhance the stability of the protein (U.S. Patent No. 5,545,818).

It may be useful to target DNA itself within a cell. For example, it may be useful to target introduced DNA to the nucleus as this may increase the frequency of transformation. Within the nucleus itself it would be useful to target a gene in order to achieve site specific integration. For example, it would be useful to have an gene
15 introduced through transformation replace an existing gene in the cell.

Other elements include those that can be regulated by endogenous or exogenous agents, e.g., by zinc finger proteins, including naturally occurring zinc finger proteins or chimeric zinc finger proteins (see, e.g., U.S. Patent No. 5,789,538, WO 99/48909; WO 99/45132; WO 98/53060; WO 98/53057; WO 98/53058; WO
20 00/23464; WO 95/19431; and WO 98/54311) or myb-like transcription factors. For example, a chimeric zinc finger protein may include amino acid sequences which bind to a specific DNA sequence (the zinc finger) and amino acid sequences that activate (e.g., GAL 4 sequences) or repress the transcription of the sequences linked to the specific DNA sequence.

25 3. Preferred Nucleic Acid Molecules of the Invention

The invention relates to an isolated plant, e.g., *Arabidopsis*, *Chenopodium* and rice, nucleic acid molecule comprising a gene having an open reading frame, the expression of which is altered in response to pathogen infection, as well as the endogenous plant promoters for those genes. However, the expression of these
30 genes may also be altered in response to non-pathogens, e.g., in response to environmental stimuli. The nucleic acid molecules can be used in pathogen control

strategies, e.g., by overexpressing nucleic acid molecules which can confer tolerance to a cell, or by altering the expression of host genes which are required for pathogen infection, e.g., by “knocking out” the expression of at least one genomic copy of the gene. Plants having genetic disruptions in host genes may be less susceptible to infection, e.g., due to a decrease or absence of a host protein needed for infection, or, alternatively, hypersusceptible to infection. Plants that are hypersusceptible to infection may be useful to prepare transgenic plants as the expression of the gene(s) which was disrupted may be related to gene silencing.

Preferred sources from which the nucleic acid molecules of the invention can be obtained or isolated include, but are not limited to, corn (*Zea mays*), *Brassica* sp. (e.g., *B. napus*, *B. rapa*, *B. juncea*), particularly those *Brassica* species useful as sources of seed oil, alfalfa (*Medicago sativa*), rice (*Oryza sativa*), rye (*Secale cereale*), sorghum (*Sorghum bicolor*, *Sorghum vulgare*), millet (e.g., pearl millet (*Pennisetum glaucum*), proso millet (*Panicum miliaceum*), foxtail millet (*Setaria italica*), finger millet (*Eleusine coracana*)), sunflower (*Helianthus annuus*), safflower (*Carthamus tinctorius*), wheat (*Triticum aestivum*), soybean (*Glycine max*), tobacco (*Nicotiana tabacum*), potato (*Solanum tuberosum*), peanuts (*Arachis hypogaea*), cotton (*Gossypium barbadense*, *Gossypium hirsutum*), sweet potato (*Ipomoea batatas*), cassava (*Manihot esculenta*), coffee (*Cofea* spp.), coconut (*Cocos nucifera*), pineapple (*Ananas comosus*), citrus trees (*Citrus* spp.), cocoa (*Theobroma cacao*), tea (*Camellia sinensis*), banana (*Musa* spp.), avocado (*Persea utilane*), fig (*Ficus casica*), guava (*Psidium guajava*), mango (*Mangifera indica*), olive (*Olea europaea*), papaya (*Carica papaya*), cashew (*Anacardium occidentale*), macadamia (*Macadamia integrifolia*), almond (*Prunus amygdalus*), sugar beets (*Beta vulgaris*), sugarcane (*Saccharum* spp.), oats, duckweed (*Lemna*), barley, vegetables, ornamentals, and conifers.

Duckweed (*Lemna*, see WO 00/07210) includes members of the family *Lemnaceae*. There are known four genera and 34 species of duckweed as follows: genus *Lemna* (*L. aequinoctialis*, *L. disperma*, *L. ecuadoriensis*, *L. gibba*, *L. japonica*, *L. minor*, *L. miniscula*, *L. obscura*, *L. perpusilla*, *L. tenera*, *L. trisulca*, *L. turionifera*, *L. valdiviana*); genus *Spirodela* (*S. intermedia*, *S. polyrrhiza*, *S.*

punctata); genus *Woffia* (*Wa. Angusta*, *Wa. Arrhiza*, *Wa. Australina*, *Wa. Borealis*, *Wa. Brasiliensis*, *Wa. Columbiana*, *Wa. Elongata*, *Wa. Globosa*, *Wa. Microscopica*, *Wa. Neglecta*) and genus *Woffiella* (*W1. utila*, *W1. utilane n*, *W1. gladiata*, *W1. utila*, *W1. lingulata*, *W1. repunda*, *W1. rotunda*, and *W1. neotropica*). Any other
5 genera or species of *Lemnaceae*, if they exist, are also aspects of the present invention. *Lemna gibba*, *Lemna minor*, and *Lemna miniscula* are preferred, with *Lemna minor* and *Lemna miniscula* being most preferred. *Lemna* species can be classified using the taxonomic scheme described by Landolt, Biosystematic Investigation on the Family of Duckweeds: The family of Lemnaceae— A
10 Monograph Study. Geobotanischen Institut ETH, Stiftung Rubel, Zurich (1986)).

Vegetables from which to obtain or isolate the nucleic acid molecules of the invention include, but are not limited to, tomatoes (*Lycopersicon esculentum*), lettuce (e.g., *Lactuca sativa*), green beans (*Phaseolus vulgaris*), lima beans (*Phaseolus limensis*), peas (*Lathyrus* spp.), and members of the genus *Cucumis* such
15 as cucumber (*C. sativus*), cantaloupe (*C. cantalupensis*), and musk melon (*C. melo*). Ornamentals from which to obtain or isolate the nucleic acid molecules of the invention include, but are not limited to, azalea (*Rhododendron* spp.), hydrangea (*Macrophylla hydrangea*), hibiscus (*Hibiscus rosasanensis*), roses (*Rosa* spp.), tulips (*Tulipa* spp.), daffodils (*Narcissus* spp.), petunias (*Petunia hybrida*), carnation
20 (*Dianthus caryophyllus*), poinsettia (*Euphorbia pulcherrima*), and chrysanthemum. Conifers that may be employed in practicing the present invention include, for example, pines such as loblolly pine (*Pinus taeda*), slash pine (*Pinus elliotii*), ponderosa pine (*Pinus ponderosa*), lodgepole pine (*Pinus contorta*), and Monterey pine (*Pinus radiata*), Douglas-fir (*Pseudotsuga menziesii*); Western hemlock (*Tsuga utilane*); Sitka spruce (*Picea glauca*); redwood (*Sequoia sempervirens*); true firs
25 such as silver fir (*Abies amabilis*) and balsam fir (*Abies balsamea*); and cedars such as Western red cedar (*Thuja plicata*) and Alaska yellow-cedar (*Chamaecyparis nootkatensis*). Leguminous plants from which the nucleic acid molecules of the invention can be isolated or obtained include, but are not limited to, beans and peas.
30 Beans include guar, locust bean, fenugreek, soybean, garden beans, cowpea, mungbean, lima bean, fava bean, lentils, chickpea, and the like. Legumes include,

but are not limited to, *Arachis*, e.g., peanuts, *Vicia*, e.g., crown vetch, hairy vetch, adzuki bean, mung bean, and chickpea, *Lupinus*, e.g., lupine, trifolium, *Phaseolus*, e.g., common bean and lima bean, *Pisum*, e.g., field bean, *Melilotus*, e.g., clover, *Medicago*, e.g., alfalfa, Lotus, e.g., trefoil, lens, e.g., lentil, and false indigo.

- 5 Papaya, garlic, pea, peach, pepper, petunia, strawberry, sorghum, sweet potato, turnip, safflower, corn, pea, endive, gourd, grape, snap bean, chicory, cotton, tobacco, aubergine, beet, buckwheat, broad bean, nectarine, avocado, mango, banana, groundnut, potato,peanut, lettuce, pineapple, spinach, squash, sugarbeet, sugarcane, sweet corn, chrysanthemum.
- 10 Other preferred sources of the nucleic acid molecules of the invention include *Acacia*, aneth, artichoke, arugula, blackberry, canola, cilantro, clementines, escarole, eucalyptus, fennel, grapefruit, honey dew, jicama, kiwifruit, lemon, lime, mushroom, nut, okra, orange, parsley, persimmon, plantain, pomegranate, poplar, radiata pine, radicchio, Southern pine, sweetgum, tangerine, triticale, vine, yams,
- 15 apple, pear, quince, cherry, apricot, melon, hemp, buckwheat, grape, raspberry, chenopodium, blueberry, nectarine, peach, plum, strawberry, watermelon, eggplant, pepper, cauliflower, Brassica, e.g., broccoli, cabbage, utilan sprouts, onion, carrot, leek, beet, broad bean, celery, radish, pumpkin, endive, gourd, garlic, snapbean, spinach, squash, turnip, utilane, and zucchini.
- 20 Yet other sources of nucleic acid molecules are ornamental plants including, but not limited to, impatiens, Begonia, Pelargonium, Viola, Cyclamen, Verbena, Vinca, Tagetes, Primula, Saint Paulia, Agertum, Amaranthus, Antihirrhinum, Aquilegia, Cineraria, Clover, Cosmo, Cowpea, Dahlia, Datura, Delphinium, Gerbera, Gladiolus, Gloxinia, Hippeastrum, Mesembryanthemum, Salpiglossos, and
- 25 Zinnia, and plants such as those shown in Table 1.

Table 1

FAMILY	LATIN NAME	COMMON NAME	MAP REFERENCES RESOURCES	LINKS

FAMILY	LATIN NAME	COMMON NAME	MAP REFERENCES RESOURCES	LINKS
Cucurbitaceae	<i>Cucumis sativus</i>	Cucumber		http://www.cucurbit.org/
	<i>Cucumis melo</i>	Melon		http://genome.cornell.edu/cg
	<i>Citrullus lanatus</i>	Watermelon		
	<i>Cucurbita pepo</i>	Squash – summer		
	<i>Cucurbita maxima</i>	Squash – winter		
	<i>Cucurbita moschata</i>	Pumpkin /butternut		
Total				http://www.nal.usda.gov/pgdic/Map_proj/

FAMILY	LATIN NAME	COMMON NAME	MAP REFERENCES RESOURCES	LINKS
Solanaceae	<i>Lycopersicon esculentum</i>	Tomato	<ul style="list-style-type: none"> • 15x BAC on variety Heinz 1706 order from Clemson Genome center (www.genome.clemson.edu) • 11.6x BAC of <i>L. cheesmanii</i> (originates from J. Giovannoni) available from Clemson genome center (www.genome.clemson.edu) • EST collection from TIGR (www.tigr.org/tdb/lgi/index.html) • EST collection from Clemson Genome Center (www.genome.clemson.edu) • TAG 99:254-271, 1999 (<i>esculentum</i> x <i>pennelli</i>) • TAG 89:1007-1013, 1994 (<i>peruvianum</i>) • Plant Cell Reports 12:293-297, 1993 (RAPDs) • Genetics 132:1141-1160, 1992 (<i>potato</i> x <i>tomato</i>) • Genetics 120:1095-1105, 1988 (RFLP <i>potato</i> and <i>tomato</i>) • Genetics 115:387-393, 1986 (<i>esculentum</i> x <i>pennelli</i> isozyme and cDNAs) 	genome.cornell.edu/solgenes http://ars-genome.cornell.edu/cgi-bin/WebAce/webace?db=solgenes http://genome.cornell.edu/tgc/ http://tgrc.ucdavis.edu/
	<i>Capsicum annuum</i>	Pepper		http://neptune.netimages.com/~chile/science.html

FAMILY	LATIN NAME	COMMON NAME	MAP REFERENCES RESOURCES	LINKS
	<i>Capsicum frutescens</i>	Chile pepper		
	<i>Solanum melongena</i>	Eggplant		
	(<i>Nicotiana tabacum</i>)	(Tobacco)		
	(<i>Solanum tuberosum</i>)	(Potato)		
	(<i>Petunia x hybrida hort. Ex E. Vilm.</i>)	(Petunia)	4x BAC of <i>Petunia hybrida</i> 7984 available from Clemson genome center (www.genome.clemson.edu)	
Total				http://www.nal.usda.gov/pgdic/Map_proj/
Brassicaceae	<i>Brassica oleracea</i> L. var. <i>italica</i>	Broccoli		http://res.agr.ca/ecorc/cwmt/crucifer/traits/index.htm http://geneous.cit.cornell.edu/cabbage/abotutcab.html
	<i>Brassica oleracea</i> L. var. <i>capitata</i>	Cabbage		
	<i>Brassica rapa</i>	Chinese Cabbage		
	<i>Brassica oleracea</i> L. var. <i>botrytis</i>	Cauliflower		
	<i>Raphanus sativus</i> var. <i>niger</i>	Daikon		
	(<i>Brassica napus</i>)	(Oilseed rape)		http://ars-genome.cornell.edu/cgi-bin/WebAce/webace?db=brassicadb

FAMILY	LATIN NAME	COMMON NAME	MAP REFERENCES RESOURCES	LINKS
		Arabidopsis	12x and 6x BACs on Columbia strain available from Clemson genome center (www.genome.clemson.edu)	http://ars-genome.cornell.edu/cgi-bin/WebAce/webace?db=agr
Total				http://www.nal.usda.gov/pgdic/Map_proj/
Umbelliferae	<i>Daucus carota</i>	Carrot		
Compositae	<i>Lactuca sativa</i>	Lettuce		
	<i>Helianthus annuus</i>	(Sunflower)		
Total				
Chenopodiaceae	<i>Spinacia oleracea</i>	Spinach		
	(<i>Beta vulgaris</i>)	(Sugar Beet)		
Total				
Leguminosae	<i>Phaseolus vulgaris</i>	Bean	4.3x BAC available from Clemson genome center (www.genome.clemson.edu)	http://ars-genome.cornell.edu/cgi-bin/WebAce/webace?db=bean
	<i>Pisum sativum</i>	Pea		
	(<i>Glycine max</i>)	(Soybean)	7.5x and 7.9x BACs available from Clemson genome center (www.genome.clemson.edu)	http://ars-genome.cornell.edu/cgi-bin/WebAce/webace?db=soybase
Total			http://www.nal.usda.gov/pgdic/Map_proj/	

FAMILY	LATIN NAME	COMMON NAME	MAP REFERENCES RESOURCES	LINKS
Gramineae	<i>Zea mays</i>	Sweet Corn	Novartis BACs for Mo17 and B73 have been donated to Clemson Genome Center (www.genome.clemson.edu)	
	(<i>Zea mays</i>)	(Field Corn)		http://www.agron.missouri.edu/mnl/
Total			http://www.nal.usda.gov/pgdic/Map_proj/	
Liliaceae	<i>Allium cepa</i>	Onion		
		Leek		
		(Garlic)		
		(Asparagus)		
Total			http://www.nal.usda.gov/pgdic/Map_proj/	

Preferred forage and turf grass nucleic acid sources for the nucleic acid molecules of the invention include, but are not limited to, alfalfa, orchard grass, tall fescue, perennial ryegrass, creeping bent grass, and redtop. Yet other preferred sources include, but are not limited to, crop plants and in particular cereals (for example, corn, alfalfa, sunflower, rice, *Brassica*, canola, soybean, barley, soybean, sugarbeet, cotton, safflower, peanut, sorghum, oat, rye, rape, wheat, millet, tobacco, and the like), and even more preferably corn, rice and soybean.

According to one embodiment, the present invention is directed to a nucleic acid molecule comprising a nucleotide sequence isolated or obtained from any plant which encodes a polypeptide having at least 70% amino acid sequence identity to a polypeptide encoded by a gene comprising any one of SEQ ID NOs:1-953, 1954-1966, 2000-2129 or 2662-4737, or a gene comprising SEQ ID NOs:1001-1094, 2137-2661 or 4738-6813. Based on the *Arabidopsis*, *Chenopodium* and rice nucleic acid sequences of the present invention, orthologs may be identified or isolated from the genome of any desired organism, preferably from another plant, according to

well known techniques based on their sequence similarity to the *Arabidopsis*,
Chenopodium and rice nucleic acid sequences, e.g., hybridization, PCR or computer
generated sequence comparisons. For example, all or a portion of a particular
Arabidopsis, *Chenopodium* and rice nucleic acid sequence is used as a probe that
5 selectively hybridizes to other gene sequences present in a population of cloned
genomic DNA fragments or cDNA fragments (i.e., genomic or cDNA libraries)
from a chosen source organism. Further, suitable genomic and cDNA libraries may
be prepared from any cell or tissue of an organism. Such techniques include
hybridization screening of plated DNA libraries (either plaques or colonies; see, e.g.,
10 Sambrook et al., 1989) and amplification by PCR using oligonucleotide primers
preferably corresponding to sequence domains conserved among related polypeptide
or subsequences of the nucleotide sequences provided herein (see, e.g., Innis et al.,
1990). These methods are particularly well suited to the isolation of gene sequences
from organisms closely related to the organism from which the probe sequence is
15 derived. The application of these methods using the *Arabidopsis* sequences as
probes is well suited for the isolation of gene sequences from any source organism,
preferably other plant species. In a PCR approach, oligonucleotide primers can be
designed for use in PCR reactions to amplify corresponding DNA sequences from
cDNA or genomic DNA extracted from any plant of interest. Methods for designing
20 PCR primers and PCR cloning are generally known in the art.

In hybridization techniques, all or part of a known nucleotide sequence is
used as a probe that selectively hybridizes to other corresponding nucleotide
sequences present in a population of cloned genomic DNA fragments or cDNA
fragments (i.e., genomic or cDNA libraries) from a chosen organism. The
25 hybridization probes may be genomic DNA fragments, cDNA fragments, RNA
fragments, or other oligonucleotides, and may be labeled with a detectable group
such as ^{32}P , or any other detectable marker. Thus, for example, probes for
hybridization can be made by labeling synthetic oligonucleotides based on the
sequence of the invention. Methods for preparation of probes for hybridization and
30 for construction of cDNA and genomic libraries are generally known in the art and
are disclosed in Sambrook et al. (1989). In general, sequences that hybridize to the

sequences disclosed herein will have at least 40% to 50%, about 60% to 70% and even about 80% 85%, 90%, 95% to 98% or more identity with the disclosed sequences. That is, the sequence similarity of sequences may range, sharing at least about 40% to 50%, about 60% to 70%, and even about 80%, 85%, 90%, 95% to 98% sequence similarity.

The nucleic acid molecules of the invention can also be identified by, for example, a search of known databases for genes encoding polypeptides having a specified amino acid sequence identity or DNA having a specified nucleotide sequence identity. Methods of alignment of sequences for comparison are well known in the art and are described hereinabove.

4. Methods for Mutagenizing DNA

It is specifically contemplated by the inventors that one could mutagenize DNA having a promoter or open reading frame to, for example, potentially improve the utility of the DNA for expression of transgenes in plants. The mutagenesis can be carried out at random and the mutagenized sequences screened for activity in a trial-by-error procedure. Alternatively, particular sequences which provide the promoter with desirable expression characteristics, or a promoter with expression enhancement activity, could be identified and these or similar sequences introduced into the sequences via mutation. It is further contemplated that one could mutagenize these sequences in order to enhance their expression of transgenes in a particular species.

The means for mutagenizing a DNA segment of the current invention are well-known to those of skill in the art. As indicated, modifications may be made by random or site-specific mutagenesis procedures. The DNA may be modified by altering its structure through the addition or deletion of one or more nucleotides from the sequence which encodes the corresponding un-modified sequences.

Mutagenesis may be performed in accordance with any of the techniques known in the art, such as, and not limited to, synthesizing an oligonucleotide having one or more mutations within the sequence of a particular regulatory region. In particular, site-specific mutagenesis is a technique useful in the preparation of promoter mutants, through specific mutagenesis of the underlying DNA. The

technique further provides a ready ability to prepare and test sequence variants, for example, incorporating one or more of the foregoing considerations, by introducing one or more nucleotide sequence changes into the DNA. Site-specific mutagenesis allows the production of mutants through the use of specific oligonucleotide
5 sequences which encode the DNA sequence of the desired mutation, as well as a sufficient number of adjacent nucleotides, to provide a primer sequence of sufficient size and sequence complexity to form a stable duplex on both sides of the deletion junction being traversed. Typically, a primer of about 17 to about 75 nucleotides or more in length is preferred, with about 10 to about 25 or more residues on both sides
10 of the junction of the sequence being altered.

In general, the technique of site-specific mutagenesis is well known in the art, as exemplified by various publications. As will be appreciated, the technique typically employs a phage vector which exists in both a single stranded and double stranded form. Typical vectors useful in site-directed mutagenesis include vectors
15 such as the M13 phage. These phage are readily commercially available and their use is generally well known to those skilled in the art.

Double stranded plasmids also are routinely employed in site directed mutagenesis which eliminates the step of transferring the gene of interest from a plasmid to a phage.

20 In general, site-directed mutagenesis in accordance herewith is performed by first obtaining a single-stranded vector or melting apart of two strands of a double stranded vector which includes within its sequence a DNA sequence which encodes the promoter. An oligonucleotide primer bearing the desired mutated sequence is prepared, generally synthetically. This primer is then annealed with the single-
25 stranded vector, and subjected to DNA polymerizing enzymes such as *E. coli* polymerase I Klenow fragment, in order to complete the synthesis of the mutation-bearing strand. Thus, a heteroduplex is formed wherein one strand encodes the original non-mutated sequence and the second strand bears the desired mutation.

This heteroduplex vector is then used to transform or transfect appropriate
30 cells, such as *E. coli* cells, and cells are selected which include recombinant vectors bearing the mutated sequence arrangement. Vector DNA can then be isolated from

these cells and used for plant transformation. A genetic selection scheme was devised by Kunkel et al. (1987) to enrich for clones incorporating mutagenic oligonucleotides. Alternatively, the use of PCR with commercially available thermostable enzymes such as Taq polymerase may be used to incorporate a mutagenic oligonucleotide primer into an amplified DNA fragment that can then be cloned into an appropriate cloning or expression vector. The PCR-mediated mutagenesis procedures of Tomic et al. (1990) and Upender et al. (1995) provide two examples of such protocols. A PCR employing a thermostable ligase in addition to a thermostable polymerase also may be used to incorporate a phosphorylated mutagenic oligonucleotide into an amplified DNA fragment that may then be cloned into an appropriate cloning or expression vector. The mutagenesis procedure described by Michael (1994) provides an example of one such protocol.

The preparation of sequence variants of DNA segments using site-directed mutagenesis is provided as a means of producing potentially useful species and is not meant to be limiting as there are other ways in which sequence variants of DNA sequences may be obtained. For example, recombinant vectors encoding the desired promoter sequence may be treated with mutagenic agents, such as hydroxylamine, to obtain sequence variants.

In addition, an unmodified or modified nucleotide sequence of the present invention can be varied by shuffling the sequence of the invention. To test for a function of variant DNA sequences according to the invention, the sequence of interest is operably linked to a selectable or screenable marker gene and expression of the marker gene is tested in transient expression assays with protoplasts or in stably transformed plants. It is known to the skilled artisan that DNA sequences capable of driving expression of an associated nucleotide sequence are build in a modular way. Accordingly, expression levels from shorter DNA fragments may be different than the one from the longest fragment and may be different from each other. For example, deletion of a down-regulating upstream element will lead to an increase in the expression levels of the associated nucleotide sequence while deletion of an up-regulating element will decrease the expression levels of the associated nucleotide sequence. It is also known to the skilled artisan that deletion of

development-specific or a tissue-specific element will lead to a temporally or spatially altered expression profile of the associated nucleotide sequence.

As used herein, the term "oligonucleotide directed mutagenesis procedure" refers to template-dependent processes and vector-mediated propagation which result in an increase in the concentration of a specific nucleic acid molecule relative to its initial concentration, or in an increase in the concentration of a detectable signal, such as amplification. As used herein, the term "oligonucleotide directed mutagenesis procedure" also is intended to refer to a process that involves the template-dependent extension of a primer molecule. The term template-dependent process refers to nucleic acid synthesis of an RNA or a DNA molecule wherein the sequence of the newly synthesized strand of nucleic acid is dictated by the well-known rules of complementary base pairing (see, for example, Watson and Rarnstad, 1987). Typically, vector mediated methodologies involve the introduction of the nucleic acid fragment into a DNA or RNA vector, the clonal amplification of the vector, and the recovery of the amplified nucleic acid fragment. Examples of such methodologies are provided by U.S. Patent No. 4,237,224. A number of template dependent processes are available to amplify the target sequences of interest present in a sample, such methods being well known in the art and specifically disclosed herein below.

Where a clone comprising a promoter has been isolated in accordance with the instant invention, one may wish to delimit the essential promoter regions within the clone. One efficient, targeted means for preparing mutagenizing promoters relies upon the identification of putative regulatory elements within the promoter sequence. This can be initiated by comparison with promoter sequences known to be expressed in similar tissue-specific or developmentally unique manner. Sequences which are shared among promoters with similar expression patterns are likely candidates for the binding of transcription factors and are thus likely elements which confer expression patterns. Confirmation of these putative regulatory elements can be achieved by deletion analysis of each putative regulatory region followed by functional analysis of each deletion construct by assay of a reporter gene which is functionally attached to each construct. As such, once a starting promoter sequence

is provided, any of a number of different deletion mutants of the starting promoter could be readily prepared.

As indicated above, deletion mutants, deletion mutants of the promoter of the invention also could be randomly prepared and then assayed. With this strategy, a series of constructs are prepared, each containing a different portion of the clone (a subclone), and these constructs are then screened for activity. A suitable means for screening for activity is to attach a deleted promoter or intron construct which contains a deleted segment to a selectable or screenable marker, and to isolate only those cells expressing the marker gene. In this way, a number of different, deleted promoter constructs are identified which still retain the desired, or even enhanced, activity. The smallest segment which is required for activity is thereby identified through comparison of the selected constructs. This segment may then be used for the construction of vectors for the expression of exogenous genes.

B. Marker Genes

In order to improve the ability to identify transformants, one may desire to employ a selectable or screenable marker gene as, or in addition to, the expressible gene of interest. "Marker genes" are genes that impart a distinct phenotype to cells expressing the marker gene and thus allow such transformed cells to be distinguished from cells that do not have the marker. Such genes may encode either a selectable or screenable marker, depending on whether the marker confers a trait which one can 'select' for by chemical means, i.e., through the use of a selective agent (e.g., a herbicide, antibiotic, or the like), or whether it is simply a trait that one can identify through observation or testing, i.e., by 'screening' (e.g., the R-locus trait, the green fluorescent protein (GFP)). Of course, many examples of suitable marker genes are known to the art and can be employed in the practice of the invention.

Included within the terms selectable or screenable marker genes are also genes which encode a "secretable marker" whose secretion can be detected as a means of identifying or selecting for transformed cells. Examples include markers which encode a secretable antigen that can be identified by antibody interaction, or even secretable enzymes which can be detected by their catalytic activity.

Secretable proteins fall into a number of classes, including small, diffusible proteins detectable, e.g., by ELISA; small active enzymes detectable in extracellular solution (e.g., alpha-amylase, beta-lactamase, phosphinothricin acetyltransferase); and proteins that are inserted or trapped in the cell wall (e.g., proteins that include a leader sequence such as that found in the expression unit of extensin or tobacco PR-S).

With regard to selectable secretable markers, the use of a gene that encodes a protein that becomes sequestered in the cell wall, and which protein includes a unique epitope is considered to be particularly advantageous. Such a secreted antigen marker would ideally employ an epitope sequence that would provide low background in plant tissue, a promoter-leader sequence that would impart efficient expression and targeting across the plasma membrane, and would produce protein that is bound in the cell wall and yet accessible to antibodies. A normally secreted wall protein modified to include a unique epitope would satisfy all such requirements.

One example of a protein suitable for modification in this manner is extensin, or hydroxyproline rich glycoprotein (HPRG). For example, the maize HPRG (Steifel et al., 1990) molecule is well characterized in terms of molecular biology, expression and protein structure. However, any one of a variety of utilane and/or glycine-rich wall proteins (Keller et al., 1989) could be modified by the addition of an antigenic site to create a screenable marker.

One exemplary embodiment of a secretable screenable marker concerns the use of a maize sequence encoding the wall protein HPRG, modified to include a 15 residue epitope from the pro-region of murine interleukin, however, virtually any detectable epitope may be employed in such embodiments, as selected from the extremely wide variety of antigen-antibody combinations known to those of skill in the art. The unique extracellular epitope can then be straightforwardly detected using antibody labeling in conjunction with chromogenic or fluorescent adjuncts.

Elements of the present disclosure may be exemplified in detail through the use of the bar and/or GUS genes, and also through the use of various other markers. Of course, in light of this disclosure, numerous other possible selectable and/or

screenable marker genes will be apparent to those of skill in the art in addition to the one set forth hereinbelow. Therefore, it will be understood that the following discussion is exemplary rather than exhaustive. In light of the techniques disclosed herein and the general recombinant techniques which are known in the art, the present invention renders possible the introduction of any gene, including marker genes, into a recipient cell to generate a transformed plant.

1. Selectable Markers

Possible selectable markers for use in connection with the present invention include, but are not limited to, a *neo* gene which codes for kanamycin resistance and can be selected for using kanamycin, G418, paromomycin, and the like; a *bar* gene which codes for bialaphos or phosphinothricin resistance; a gene which encodes an altered EPSP synthase protein (Hinchee et al., 1988) thus conferring glyphosate resistance; a nitrilase gene such as *bxn* from *Klebsiella ozaenae* which confers resistance to bromoxynil (Stalker et al., 1988); a mutant acetolactate synthase gene (ALS) which confers resistance to imidazolinone, sulfonyleurea or other ALS-inhibiting chemicals (European Patent Application 154,204, 1985); a methotrexate-resistant DHFR gene (Thillet et al., 1988); a dalapon dehalogenase gene that confers resistance to the herbicide dalapon; a mutated anthranilate synthase gene that confers resistance to 5-methyl tryptophan. Preferred selectable marker genes encode phosphinothricin acetyltransferase; glyphosate resistant EPSPS, aminoglycoside phosphotransferase; hygromycin phosphotransferase, or neomycin phosphotransferase. Where a mutant EPSP synthase gene is employed, additional benefit may be realized through the incorporation of a suitable chloroplast transit peptide, CTP (European Patent Application 0,218,571, 1987).

An illustrative embodiment of a selectable marker gene capable of being used in systems to select transformants is the genes that encode the enzyme phosphinothricin acetyltransferase, such as the *bar* gene from *Streptomyces hygroscopicus* or the *pat* gene from *Streptomyces viridochromogenes*. The enzyme phosphinothricin acetyl transferase (PAT) inactivates the active ingredient in the herbicide bialaphos, phosphinothricin (PPT). PPT inhibits glutamine synthetase, (Murakami et al., 1986; Twell et al., 1989) causing rapid accumulation of ammonia

and cell death. The success in using this selective system in conjunction with monocots was particularly surprising because of the major difficulties which have been reported in transformation of cereals.

Where one desires to employ a bialaphos resistance gene in the practice of the invention, a particularly useful gene for this purpose is the *bar* or *pat* genes obtainable from species of *Streptomyces* (e.g., ATCC No. 21,705). The cloning of the *bar* gene has been described (Murakami et al., 1986; Thompson et al., 1987) as has the use of the *bar* gene in the context of plants other than monocots (De Block et al., 1987; De Block et al., 1989).

Selection markers resulting in positive selection, such as a phosphomannose isomerase gene, as described in patent application WO 93/05163, may also be used. Alternative genes to be used for positive selection are described in WO 94/20627 and encode xyloisomerases and phosphomanno-isomerases such as mannose-6-phosphate isomerase and mannose-1-phosphate isomerase; phosphomanno mutase; mannose epimerases such as those which convert carbohydrates to mannose or mannose to carbohydrates such as glucose or galactose; phosphatases such as mannose or xylose phosphatase, mannose-6-phosphatase and mannose-1-phosphatase, and permeases which are involved in the transport of mannose, or a derivative, or a precursor thereof into the cell. Transformed cells are identified without damaging or killing the non-transformed cells in the population and without co-introduction of antibiotic or herbicide resistance genes. As described in WO 93/05163, in addition to the fact that the need for antibiotic or herbicide resistance genes is eliminated, it has been shown that the positive selection method is often far more efficient than traditional negative selection.

2. Screenable Markers

Screenable markers that may be employed include, but are not limited to, a beta-glucuronidase (GUS) or *uidA* gene which encodes an enzyme for which various chromogenic substrates are known; an R-locus gene, which encodes a product that regulates the production of anthocyanin pigments (red color) in plant tissues (Dellaporta et al., 1988); a beta-lactamase gene (Sutcliffe, 1978), which encodes an

enzyme for which various chromogenic substrates are known (e.g., PADAC, a chromogenic cephalosporin); a *xylE* gene (Zukowsky et al., 1983) which encodes a catechol dioxygenase that can convert chromogenic catechols; an α -amylase gene (Ikuta et al., 1990); a tyrosinase gene (Katz et al., 1983) which encodes an enzyme
5 capable of oxidizing tyrosine to DOPA and dopaquinone which in turn condenses to form the easily detectable compound melanin; a β -galactosidase gene, which encodes an enzyme for which there are chromogenic substrates; a luciferase (*lux*) gene (Ow et al., 1986), which allows for bioluminescence detection; or even an aequorin gene (Prasher et al., 1985), which may be employed in calcium-sensitive
10 bioluminescence detection, or a green fluorescent protein gene (Niedz et al., 1995).

Genes from the maize R gene complex are contemplated to be particularly useful as screenable markers. The R gene complex in maize encodes a protein that acts to regulate the production of anthocyanin pigments in most seed and plant tissue. A gene from the R gene complex was applied to maize transformation,
15 because the expression of this gene in transformed cells does not harm the cells. Thus, an R gene introduced into such cells will cause the expression of a red pigment and, if stably incorporated, can be visually scored as a red sector. If a maize line is carries dominant ultila for genes encoding the enzymatic intermediates in the anthocyanin biosynthetic pathway (C2, A1, A2, Bz1 and Bz2)
20 (Roth et al., 1990), but carries a recessive allele at the R locus, transformation of any cell from that line with R will result in red pigment formation. Exemplary lines include Wisconsin 22 which contains the rg-Stadler allele and TR112, a K55 derivative which is r-g, b, P1. Alternatively any genotype of maize can be utilized if the C1 and R alleles are introduced together.

25 It is further proposed that R gene regulatory regions may be employed in chimeric constructs in order to provide mechanisms for controlling the expression of chimeric genes. More diversity of phenotypic expression is known at the R locus than at any other locus (Coe et al., 1988). It is contemplated that regulatory regions obtained from regions 5' to the structural R gene would be valuable in directing the
30 expression of genes, e.g., insect resistance, drought resistance, herbicide tolerance or other protein coding regions. For the purposes of the present invention, it is

believed that any of the various R gene family members may be successfully employed (e.g., P, S, Lc, etc.). However, the most preferred will generally be Sn (particularly Sn:bol3). Sn is a dominant member of the R gene complex and is functionally similar to the R and B loci in that Sn controls the tissue specific deposition of anthocyanin pigments in certain seedling and plant cells, therefore, its phenotype is similar to R.

A further screenable marker contemplated for use in the present invention is firefly luciferase, encoded by the *lux* gene. The presence of the *lux* gene in transformed cells may be detected using, for example, X-ray film, scintillation counting, fluorescent spectrophotometry, low-light video cameras, photon counting cameras or multiwell luminometry. It is also envisioned that this system may be developed for populational screening for bioluminescence, such as on tissue culture plates, or even for whole plant screening. Where use of a screenable marker gene such as *lux* or GFP is desired, benefit may be realized by creating a gene fusion between the screenable marker gene and a selectable marker gene, for example, a GFP-NPTII gene fusion. This could allow, for example, selection of transformed cells followed by screening of transgenic plants or seeds.

C. Exogenous Genes for Modification of Plant Phenotypes

Genes of interest are reflective of the commercial markets and interests of those involved in the development of the crop. Crops and markets of interest changes, and as developing nations open up world markets, new crops and technologies will also emerge. In addition, as the understanding of agronomic traits and characteristics such as yield and heterosis increase, the choice of genes for transformation will change accordingly. General categories of genes of interest include, for example, those genes involved in information, such as zinc fingers, those involved in communication, such as kinases, and those involved in housekeeping, such as heat shock proteins. More specific categories of transgenes, for example, include genes encoding important traits for agronomics, insect resistance, disease resistance, herbicide resistance, sterility, grain characteristics, and commercial products. Genes of interest include, generally, those involved in starch, oil, carbohydrate, or nutrient metabolism, as well as those affecting kernel size,

sucrose loading, zinc finger proteins, see, e.g., U.S. Patent No. 5,789,538, WO 99/48909; WO 99/45132; WO 98/53060; WO 98/53057; WO 98/53058; WO 00/23464; WO 95/19431; and WO 98/54311, and the like.

One skilled in the art recognizes that the expression level and regulation of a transgene in a plant can vary significantly from line to line. Thus, one has to test several lines to find one with the desired expression level and regulation. Once a line is identified with the desired regulation specificity of a chimeric Cre transgene, it can be crossed with lines carrying different inactive replicons or inactive transgene for activation.

Other sequences which may be linked to the gene of interest which encodes a polypeptide are those which can target to a specific organelle, e.g., to the mitochondria, nucleus, or plastid, within the plant cell. Targeting can be achieved by providing the polypeptide with an appropriate targeting peptide sequence, such as a secretory signal peptide (for secretion or cell wall or membrane targeting, a plastid transit peptide, a chloroplast transit peptide, e.g., the chlorophyll a/b binding protein, a mitochondrial target peptide, a vacuole targeting peptide, or a nuclear targeting peptide, and the like. For example, the small subunit of ribulose biphosphate carboxylase transit peptide, the EPSPS transit peptide or the dihydrodipicolinic acid synthase transit peptide may be used. For examples of plastid organelle targeting sequences (see WO 00/12732). Plastids are a class of plant organelles derived from proplastids and include chloroplasts, leucoplasts, aravloplast, and chromoplasts. The plastids are major sites of biosynthesis in plants. In addition to photosynthesis in the chloroplast, plastids are also sites of lipid biosynthesis, nitrate reduction to ammonium, and starch storage. And while plastids contain their own circular genome, most of the proteins localized to the plastids are encoded by the nuclear genome and are imported into the organelle from the cytoplasm.

Transgenes used with the present invention will often be genes that direct the expression of a particular protein or polypeptide product, but they may also be non-expressible DNA segments, e.g., transposons such as Ds that do not direct their own transposition. As used herein, an "expressible gene" is any gene that is capable of being transcribed into RNA (e.g., mRNA, antisense RNA, etc.) or translated into a

protein, expressed as a trait of interest, or the like, etc., and is not limited to selectable, screenable or non-selectable marker genes. The invention also contemplates that, where both an expressible gene that is not necessarily a marker gene is employed in combination with a marker gene, one may employ the separate
5 genes on either the same or different DNA segments for transformation. In the latter case, the different vectors are delivered concurrently to recipient cells to maximize cotransformation.

The choice of the particular DNA segments to be delivered to the recipient cells will often depend on the purpose of the transformation. One of the major
10 purposes of transformation of crop plants is to add some commercially desirable, agronomically important traits to the plant. Such traits include, but are not limited to, herbicide resistance or tolerance; insect resistance or tolerance; disease resistance or tolerance (viral, bacterial, fungal, nematode); stress tolerance and/or resistance, as exemplified by resistance or tolerance to drought, heat, chilling, freezing, excessive
15 moisture, salt stress; oxidative stress; increased yields; food content and makeup; physical appearance; male sterility; drydown; standability; prolificacy; starch properties; oil quantity and quality; and the like. One may desire to incorporate one or more genes conferring any such desirable trait or traits, such as, for example, a gene or genes encoding pathogen resistance.

In certain embodiments, the present invention contemplates the transformation of a recipient cell with more than one advantageous transgene. Two or more transgenes can be supplied in a single transformation event using either distinct transgene-encoding vectors, or using a single vector incorporating two or more gene coding sequences. For example, plasmids bearing the *bar* and *aroA*
20 expression units in either convergent, divergent, or colinear orientation, are considered to be particularly useful. Further preferred combinations are those of an insect resistance gene, such as a *Bt* gene, along with a protease inhibitor gene such as *pinII*, or the use of *bar* in combination with either of the above genes. Of course, any two or more transgenes of any description, such as those conferring herbicide,
25 insect, disease (viral, bacterial, fungal, nematode) or drought resistance, male
30

sterility, drydown, standability, prolificacy, starch properties, oil quantity and quality, or those increasing yield or nutritional quality may be employed as desired.

1. Herbicide Resistance

The genes encoding phosphinothricin acetyltransferase (*bar* and *pat*),
5 glyphosate tolerant EPSP synthase genes, the glyphosate degradative enzyme gene
gox encoding glyphosate oxidoreductase, *deh* (encoding a dehalogenase enzyme that
inactivates dalapon), herbicide resistant (e.g., sulfonylurea and imidazolinone)
acetolactate synthase, and *bxn* genes (encoding a nitrilase enzyme that degrades
bromoxynil) are good examples of herbicide resistant genes for use in
10 transformation. The *bar* and *pat* genes code for an enzyme, phosphinothricin
acetyltransferase (PAT), which inactivates the herbicide phosphinothricin and
prevents this compound from inhibiting glutamine synthetase enzymes. The enzyme
5-enolpyruvylshikimate 3-phosphate synthase (EPSP Synthase), is normally
inhibited by the herbicide N-(phosphonomethyl)glycine (glyphosate). However,
15 genes are known that encode glyphosate-resistant EPSP Synthase enzymes.

These genes are particularly contemplated for use in monocot
transformation. The *deh* gene encodes the enzyme dalapon dehalogenase and
confers resistance to the herbicide dalapon. The *bxn* gene codes for a specific
nitrilase enzyme that converts bromoxynil to a non-herbicidal degradation product.

20 2. Insect Resistance

An important aspect of the present invention concerns the introduction of
insect resistance-conferring genes into plants. Potential insect resistance genes
which can be introduced include *Bacillus thuringiensis* crystal toxin genes or *Bt*
genes (Watrud et al., 1985). *Bt* genes may provide resistance to lepidopteran or
25 coleopteran pests such as European Corn Borer (ECB) and corn rootworm (CRW).
Preferred *Bt* toxin genes for use in such embodiments include the CryIA(b) and
CryIA(c) genes. Endotoxin genes from other species of *B. thuringiensis* which
affect insect growth or development may also be employed in this regard.

The poor expression of *Bt* toxin genes in plants is a well-documented
30 phenomenon, and the use of different promoters, fusion proteins, and leader
sequences has not led to significant increases in *Bt* protein expression (Vaeck et al.,

1989; Barton et al., 1987). It is therefore contemplated that the most advantageous *Bt* genes for use in the transformation protocols disclosed herein will be those in which the coding sequence has been modified to effect increased expression in plants, and more particularly, those in which maize preferred codons have been used. Examples of such modified *Bt* toxin genes include the variant *Bt* CryIA(b) gene termed Iab6 (Perlak et al., 1991) and the synthetic CryIA(c) genes termed 1800a and 1800b.

Protease inhibitors may also provide insect resistance (Johnson et al., 1989), and will thus have utility in plant transformation. The use of a protease inhibitor II gene, *pinII*, from tomato or potato is envisioned to be particularly useful. Even more advantageous is the use of a *pinII* gene in combination with a *Bt* toxin gene, the combined effect of which has been discovered by the present inventors to produce synergistic insecticidal activity. Other genes which encode inhibitors of the insects' digestive system, or those that encode enzymes or co-factors that facilitate the production of inhibitors, may also be useful. This group may be exemplified by oryzacystatin and amylase inhibitors, such as those from wheat and barley.

Also, genes encoding lectins may confer additional or alternative insecticide properties. Lectins (originally termed phytohemagglutinins) are multivalent carbohydrate-binding proteins which have the ability to agglutinate red blood cells from a range of species. Lectins have been identified recently as insecticidal agents with activity against weevils, ECB and rootworm (Murdock et al., 1990; Czapla and Lang, 1990). Lectin genes contemplated to be useful include, for example, barley and wheat germ agglutinin (WGA) and rice lectins (Gatehouse et al., 1984), with WGA being preferred.

Genes controlling the production of large or small polypeptides active against insects when introduced into the insect pests, such as, e.g., lytic peptides, peptide hormones and toxins and venoms, form another aspect of the invention. For example, it is contemplated that the expression of juvenile hormone esterase, directed towards specific insect pests, may also result in insecticidal activity, or perhaps cause cessation of metamorphosis (Hammock et al., 1990).

Transgenic plants expressing genes which encode enzymes that affect the integrity of the insect cuticle form yet another aspect of the invention. Such genes include those encoding, e.g., chitinase, proteases, lipases and also genes for the production of nikkomycin, a compound that inhibits chitin synthesis, the
5 introduction of any of which is contemplated to produce insect resistant maize plants. Genes that code for activities that affect insect molting, such those affecting the production of ecdysteroid UDP-glucosyl transferase, also fall within the scope of the useful transgenes of the present invention.

Genes that code for enzymes that facilitate the production of compounds that
10 reduce the nutritional quality of the host plant to insect pests are also encompassed by the present invention. It may be possible, for instance, to confer insecticidal activity on a plant by altering its sterol composition. Sterols are obtained by insects from their diet and are used for hormone synthesis and membrane stability. Therefore alterations in plant sterol composition by expression of novel genes, e.g.,
15 those that directly promote the production of undesirable sterols or those that convert desirable sterols into undesirable forms, could have a negative effect on insect growth and/or development and hence endow the plant with insecticidal activity. Lipxygenases are naturally occurring plant enzymes that have been shown to exhibit anti-nutritional effects on insects and to reduce the nutritional quality of
20 their diet. Therefore, further embodiments of the invention concern transgenic plants with enhanced lipxygenase activity which may be resistant to insect feeding.

The present invention also provides methods and compositions by which to achieve qualitative or quantitative changes in plant secondary metabolites. One example concerns transforming plants to produce DIMBOA which, it is
25 contemplated, will confer resistance to European corn borer, rootworm and several other maize insect pests. Candidate genes that are particularly considered for use in this regard include those genes at the *bx* locus known to be involved in the synthetic DIMBOA pathway (Dunn et al., 1981). The introduction of genes that can regulate the production of maysin, and genes involved in the production of dhurrin in
30 sorghum, is also contemplated to be of use in facilitating resistance to earworm and rootworm, respectively.

Tripsacum dactyloides is a species of grass that is resistant to certain insects, including corn root worm. It is anticipated that genes encoding proteins that are toxic to insects or are involved in the biosynthesis of compounds toxic to insects will be isolated from *Tripsacum* and that these novel genes will be useful in

5 conferring resistance to insects. It is known that the basis of insect resistance in *Tripsacum* is genetic, because said resistance has been transferred to *Zea mays* via sexual crosses (Branson and Guss, 1972).

Further genes encoding proteins characterized as having potential insecticidal activity may also be used as transgenes in accordance herewith. Such

10 genes include, for example, the cowpea trypsin inhibitor (CpTI; Hilder et al., 1987) which may be used as a rootworm deterrent; genes encoding avermectin (Campbell, 1989; Ikeda et al., 1987) which may prove particularly useful as a corn rootworm deterrent; ribosome inactivating protein genes; and even genes that regulate plant structures. Transgenic maize including anti-insect antibody genes and genes that

15 code for enzymes that can covert a non-toxic insecticide (pro-insecticide) applied to the outside of the plant into an insecticide inside the plant are also contemplated.

3. Environment or Stress Resistance

Improvement of a plant's ability to tolerate various environmental stresses such as, but not limited to, drought, excess moisture, chilling, freezing, high

20 temperature, salt, and oxidative stress, can also be effected through expression of heterologous, or overexpression of homologous genes. Benefits may be realized in terms of increased resistance to freezing temperatures through the introduction of an "antifreeze" protein such as that of the Winter Flounder (Cutler et al., 1989) or synthetic gene derivatives thereof. Improved chilling tolerance may also be

25 conferred through increased expression of glycerol-3-phosphate acetyltransferase in chloroplasts (Murata et al., 1992; Wolter et al., 1992). Resistance to oxidative stress (often exacerbated by conditions such as chilling temperatures in combination with high light intensities) can be conferred by expression of superoxide dismutase (Gupta et al., 1993), and may be improved by glutathione reductase (Bowler et al.,

30 1992). Such strategies may allow for tolerance to freezing in newly emerged fields

as well as extending later maturity higher yielding varieties to earlier relative maturity zones.

Expression of novel genes that favorably effect plant water content, total water potential, osmotic potential, and turgor can enhance the ability of the plant to tolerate drought. As used herein, the terms “drought resistance” and “drought tolerance” are used to refer to a plants increased resistance or tolerance to stress induced by a reduction in water availability, as compared to normal circumstances, and the ability of the plant to function and survive in lower-water environments, and perform in a relatively superior manner. In this aspect of the invention it is proposed, for example, that the expression of a gene encoding the biosynthesis of osmotically-active solutes can impart protection against drought. Within this class of genes are DNAs encoding mannitol dehydrogenase (Lee and Saier, 1982) and trehalose-6-phosphate synthase (Kaasen et al., 1992). Through the subsequent action of native phosphatases in the cell or by the introduction and coexpression of a specific phosphatase, these introduced genes will result in the accumulation of either mannitol or trehalose, respectively, both of which have been well documented as protective compounds able to mitigate the effects of stress. Mannitol accumulation in transgenic tobacco has been verified and preliminary results indicate that plants expressing high levels of this metabolite are able to tolerate an applied osmotic stress (Tarczynski et al., cited supra (1992), 1993).

Similarly, the efficacy of other metabolites in protecting either enzyme function (e.g. alanopine or propionic acid) or membrane integrity (e.g., alanopine) has been documented (Loomis et al., 1989), and therefore expression of gene encoding the biosynthesis of these compounds can confer drought resistance in a manner similar to or complimentary to mannitol. Other examples of naturally occurring metabolites that are osmotically active and/or provide some direct protective effect during drought and/or desiccation include sugars and sugar derivatives such as fructose, erythritol (Coxson et al., 1992), sorbitol, dulcitol (Karsten et al., 1992), glucosylglycerol (Reed et al., 1984; Erdmann et al., 1992), sucrose, stachyose (Koster and Leopold, 1988; Blackman et al., 1992), ononitol and pinitol (Vernon and Bohnert, 1992), and raffinose (Bernal-Lugo and Leopold, 1992).

Other osmotically active solutes which are not sugars include, but are not limited to, proline and glycine-betaine (Wyn-Jones and Storey, 1981). Continued canopy growth and increased reproductive fitness during times of stress can be augmented by introduction and expression of genes such as those controlling the osmotically active compounds discussed above and other such compounds, as represented in one exemplary embodiment by the enzyme myoinositol 0-methyltransferase.

It is contemplated that the expression of specific proteins may also increase drought tolerance. Three classes of Late Embryogenic Proteins have been assigned based on structural similarities (see Dure et al., 1989). All three classes of these proteins have been demonstrated in maturing (i.e., desiccating) seeds. Within these 3 types of proteins, the Type-II (dehydrin-type) have generally been implicated in drought and/or desiccation tolerance in vegetative plant parts (i.e. Mundy and Chua, 1988; Piatkowski et al., 1990; Yamaguchi-Shinozaki et al., 1992). Recently, expression of a Type-III LEA (HVA-1) in tobacco was found to influence plant height, maturity and drought tolerance (Fitzpatrick, 1993). Expression of structural genes from all three groups may therefore confer drought tolerance. Other types of proteins induced during water stress include thiol proteases, aldolases and transmembrane transporters (Guerrero et al., 1990), which may confer various protective and/or repair-type functions during drought stress. The expression of a gene that effects lipid biosynthesis and hence membrane composition can also be useful in conferring drought resistance on the plant.

Many genes that improve drought resistance have complementary modes of action. Thus, combinations of these genes might have additive and/or synergistic effects in improving drought resistance in plants. Many of these genes also improve freezing tolerance (or resistance); the physical stresses incurred during freezing and drought are similar in nature and may be mitigated in similar fashion. Benefit may be conferred via constitutive expression of these genes, but the preferred means of expressing these novel genes may be through the use of a turgor-induced promoter (such as the promoters for the turgor-induced genes described in Guerrero et al. 1990 and Shagan et al., 1993). Spatial and temporal expression patterns of these genes may enable maize to better withstand stress.

Expression of genes that are involved with specific morphological traits that allow for increased water extractions from drying soil would be of benefit. For example, introduction and expression of genes that alter root characteristics may enhance water uptake. Expression of genes that enhance reproductive fitness during times of stress would be of significant value. For example, expression of DNAs that improve the synchrony of pollen shed and receptiveness of the female flower parts, i.e., silks, would be of benefit. In addition, expression of genes that minimize kernel abortion during times of stress would increase the amount of grain to be harvested and hence be of value. Regulation of cytokinin levels in monocots, such as maize, by introduction and expression of an isopentenyl transferase gene with appropriate regulatory sequences can improve monocot stress resistance and yield (Gan et al., Science, 270:1986 (1995)).

Given the overall role of water in determining yield, it is contemplated that enabling plants to utilize water more efficiently, through the introduction and expression of novel genes, will improve overall performance even when soil water availability is not limiting. By introducing genes that improve the ability of plants to maximize water usage across a full range of stresses relating to water availability, yield stability or consistency of yield performance may be realized.

4. Disease Resistance

It is proposed that increased resistance to diseases may be realized through introduction of genes into plants period. It is possible to produce resistance to diseases caused by viruses, bacteria, fungi, root pathogens, insects and nematodes. It is also contemplated that control of mycotoxin producing organisms may be realized through expression of introduced genes.

Resistance to viruses may be produced through expression of novel genes. For example, it has been demonstrated that expression of a viral coat protein in a transgenic plant can impart resistance to infection of the plant by that virus and perhaps other closely related viruses (Cuozzo et al., 1988, Hemenway et al., 1988, Abel et al., 1986). It is contemplated that expression of antisense genes targeted at essential viral functions may impart resistance to said virus. For example, an antisense gene targeted at the gene responsible for replication of viral nucleic acid

may inhibit said replication and lead to resistance to the virus. It is believed that interference with other viral functions through the use of antisense genes may also increase resistance to viruses. Further it is proposed that it may be possible to achieve resistance to viruses through other approaches, including, but not limited to the use of satellite viruses.

It is proposed that increased resistance to diseases caused by bacteria and fungi may be realized through introduction of novel genes. It is contemplated that genes encoding so-called "peptide antibiotics," pathogenesis related (PR) proteins, toxin resistance, and proteins affecting host-pathogen interactions such as morphological characteristics will be useful. Peptide antibiotics are polypeptide sequences which are inhibitory to growth of bacteria and other microorganisms. For example, the classes of peptides referred to as cecropins and magainins inhibit growth of many species of bacteria and fungi. It is proposed that expression of PR proteins in plants may be useful in conferring resistance to bacterial disease. These genes are induced following pathogen attack on a host plant and have been divided into at least five classes of proteins (Bol et al., 1990). Included amongst the PR proteins are beta-1,3-glucanases, chitinases, and osmotin and other proteins that are believed to function in plant resistance to disease organisms. Other genes have been identified that have antifungal properties, e.g., UDA (stinging nettle lectin) and hevein (Broakgert et al., 1989; Barkai-Golan et al., 1978). It is known that certain plant diseases are caused by the production of phytotoxins. Resistance to these diseases could be achieved through expression of a novel gene that encodes an enzyme capable of degrading or otherwise inactivating the phytotoxin. Expression novel genes that alter the interactions between the host plant and pathogen may be useful in reducing the ability the disease organism to invade the tissues of the host plant, e.g., an increase in the waxiness of the leaf cuticle or other morphological characteristics.

Plant parasitic nematodes are a cause of disease in many plants. It is proposed that it would be possible to make the plant resistant to these organisms through the expression of novel genes. It is anticipated that control of nematode infestations would be accomplished by altering the ability of the nematode to

recognize or attach to a host plant and/or enabling the plant to produce nematicidal compounds, including but not limited to proteins.

5. Mycotoxin Reduction/Elimination

Production of mycotoxins, including aflatoxin and fumonisin, by fungi associated with plants is a significant factor in rendering the grain not useful. These fungal organisms do not cause disease symptoms and/or interfere with the growth of the plant, but they produce chemicals (mycotoxins) that are toxic to animals. Inhibition of the growth of these fungi would reduce the synthesis of these toxic substances and, therefore, reduce grain losses due to mycotoxin contamination. Novel genes may be introduced into plants that would inhibit synthesis of the mycotoxin without interfering with fungal growth. Expression of a novel gene which encodes an enzyme capable of rendering the mycotoxin nontoxic would be useful in order to achieve reduced mycotoxin contamination of grain. The result of any of the above mechanisms would be a reduced presence of mycotoxins on grain.

15 6. Grain Composition or Quality

Genes may be introduced into plants, particularly commercially important cereals such as maize, wheat or rice, to improve the grain for which the cereal is primarily grown. A wide range of novel transgenic plants produced in this manner may be envisioned depending on the particular end use of the grain.

20 For example, the largest use of maize grain is for feed or food. Introduction of genes that alter the composition of the grain may greatly enhance the feed or food value. The primary components of maize grain are starch, protein, and oil. Each of these primary components of maize grain may be improved by altering its level or composition. Several examples may be mentioned for illustrative purposes but in no way provide an exhaustive list of possibilities.

25 The protein of many cereal grains is suboptimal for feed and food purposes especially when fed to pigs, poultry, and humans. The protein is deficient in several amino acids that are essential in the diet of these species, requiring the addition of supplements to the grain. Limiting essential amino acids may include lysine, methionine, tryptophan, threonine, valine, arginine, and histidine. Some amino acids become limiting only after the grain is supplemented with other inputs for feed

formulations. For example, when the grain is supplemented with soybean meal to meet lysine requirements, methionine becomes limiting. The levels of these essential amino acids in seeds and grain may be elevated by mechanisms which include, but are not limited to, the introduction of genes to increase the biosynthesis of the amino acids, decrease the degradation of the amino acids, increase the storage of the amino acids in proteins, or increase transport of the amino acids to the seeds or grain.

One mechanism for increasing the biosynthesis of the amino acids is to introduce genes that deregulate the amino acid biosynthetic pathways such that the plant can no longer adequately control the levels that are produced. This may be done by deregulating or bypassing steps in the amino acid biosynthetic pathway which are normally regulated by levels of the amino acid end product of the pathway. Examples include the introduction of genes that encode deregulated versions of the enzymes aspartokinase or dihydrodipicolinic acid (DHDP)-synthase for increasing lysine and threonine production, and anthranilate synthase for increasing tryptophan production. Reduction of the catabolism of the amino acids may be accomplished by introduction of DNA sequences that reduce or eliminate the expression of genes encoding enzymes that catalyse steps in the catabolic pathways such as the enzyme lysine-ketoglutarate reductase.

The protein composition of the grain may be altered to improve the balance of amino acids in a variety of ways including elevating expression of native proteins, decreasing expression of those with poor composition, changing the composition of native proteins, or introducing genes encoding entirely new proteins possessing superior composition. DNA may be introduced that decreases the expression of members of the zein family of storage proteins. This DNA may encode ribozymes or antisense sequences directed to impairing expression of zein proteins or expression of regulators of zein expression such as the opaque-2 gene product. The protein composition of the grain may be modified through the phenomenon of cosuppression, i.e., inhibition of expression of an endogenous gene through the expression of an identical structural gene or gene fragment introduced through transformation (Goring et al., 1991). Additionally, the introduced DNA may encode

enzymes which degrade seines. The decreases in zein expression that are achieved may be accompanied by increases in proteins with more desirable amino acid composition or increases in other major seed constituents such as starch.

Alternatively, a chimeric gene may be introduced that comprises a coding sequence
5 for a native protein of adequate amino acid composition such as for one of the globulin proteins or 10 kD zein of maize and a promoter or other regulatory sequence designed to elevate expression of said protein. The coding sequence of said gene may include additional or replacement codons for essential amino acids. Further, a coding sequence obtained from another species, or, a partially or
10 completely synthetic sequence encoding a completely unique peptide sequence designed to enhance the amino acid composition of the seed may be employed.

The introduction of genes that alter the oil content of the grain may be of value. Increases in oil content may result in increases in metabolizable energy content and density of the seeds for uses in feed and food. The introduced genes
15 may encode enzymes that remove or reduce rate-limitations or regulated steps in fatty acid or lipid biosynthesis. Such genes may include, but are not limited to, those that encode acetyl-CoA carboxylase, ACP-acyltransferase, beta-ketoacyl-ACP synthase, plus other well known fatty acid biosynthetic activities. Other possibilities are genes that encode proteins that do not possess enzymatic activity such as acyl
20 carrier protein. Additional examples include 2-acetyltransferase, oleosin pyruvate dehydrogenase complex, acetyl CoA synthetase, ATP citrate lyase, ADP-glucose pyrophosphorylase and genes of the carnitine-CoA- acetyl-CoA shuttles. It is anticipated that expression of genes related to oil biosynthesis will be targeted to the plastid, using a plastid transit peptide sequence and preferably expressed in the seed
25 embryo. Genes may be introduced that alter the balance of fatty acids present in the oil providing a more healthful or nutritive feedstuff. The introduced DNA may also encode sequences that block expression of enzymes involved in fatty acid biosynthesis, altering the proportions of fatty acids present in the grain such as described below.

Genes may be introduced that enhance the nutritive value of the starch component of the grain, for example by increasing the degree of branching, resulting in improved utilization of the starch in cows by delaying its metabolism.

Besides affecting the major constituents of the grain, genes may be introduced that affect a variety of other nutritive, processing, or other quality aspects of the grain as used for feed or food. For example, pigmentation of the grain may be increased or decreased. Enhancement and stability of yellow pigmentation is desirable in some animal feeds and may be achieved by introduction of genes that result in enhanced production of xanthophylls and carotenes by eliminating rate-limiting steps in their production. Such genes may encode altered forms of the enzymes phytoene synthase, phytoene desaturase, or lycopene synthase. Alternatively, unpigmented white corn is desirable for production of many food products and may be produced by the introduction of DNA which blocks or eliminates steps in pigment production pathways.

Feed or food comprising some cereal grains possesses insufficient quantities of vitamins and must be supplemented to provide adequate nutritive value. Introduction of genes that enhance vitamin biosynthesis in seeds may be envisioned including, for example, vitamins A, E, B₁₂, choline, and the like. For example, maize grain also does not possess sufficient mineral content for optimal nutritive value. Genes that affect the accumulation or availability of compounds containing phosphorus, sulfur, calcium, manganese, zinc, and iron among others would be valuable. An example may be the introduction of a gene that reduced phytic acid production or encoded the enzyme phytase which enhances phytic acid breakdown. These genes would increase levels of available phosphate in the diet, reducing the need for supplementation with mineral phosphate.

Numerous other examples of improvement of cereals for feed and food purposes might be described. The improvements may not even necessarily involve the grain, but may, for example, improve the value of the grain for silage. Introduction of DNA to accomplish this might include sequences that alter lignin production such as those that result in the “brown midrib” phenotype associated with superior feed value for cattle.

In addition to direct improvements in feed or food value, genes may also be introduced which improve the processing of grain and improve the value of the products resulting from the processing. The primary method of processing certain grains such as maize is via wetmilling. Maize may be improved though the
5 expression of novel genes that increase the efficiency and reduce the cost of processing such as by decreasing steeping time.

Improving the value of wetmilling products may include altering the quantity or quality of starch, oil, corn gluten meal, or the components of corn gluten feed. Elevation of starch may be achieved through the identification and elimination of
10 rate limiting steps in starch biosynthesis or by decreasing levels of the other components of the grain resulting in proportional increases in starch. An example of the former may be the introduction of genes encoding ADP-glucose pyrophosphorylase enzymes with altered regulatory activity or which are expressed at higher level. Examples of the latter may include selective inhibitors of, for
15 example, protein or oil biosynthesis expressed during later stages of kernel development.

The properties of starch may be beneficially altered by changing the ratio of amylose to amylopectin, the size of the starch molecules, or their branching pattern. Through these changes a broad range of properties may be modified which include,
20 but are not limited to, changes in gelatinization temperature, heat of gelatinization, clarity of films and pastes, Theological properties, and the like. To accomplish these changes in properties, genes that encode granule-bound or soluble starch synthase activity or branching enzyme activity may be introduced alone or combination. DNA such as antisense constructs may also be used to decrease levels
25 of endogenous activity of these enzymes. The introduced genes or constructs may possess regulatory sequences that time their expression to specific intervals in starch biosynthesis and starch granule development. Furthermore, it may be advisable to introduce and express genes that result in the *in vivo* derivatization, or other modification, of the glucose moieties of the starch molecule. The covalent
30 attachment of any molecule may be envisioned, limited only by the existence of enzymes that catalyze the derivatizations and the accessibility of appropriate

substrates in the starch granule. Examples of important derivations may include the addition of functional groups such as amines, carboxyls, or phosphate groups which provide sites for subsequent *in vitro* derivatizations or affect starch properties through the introduction of ionic charges. Examples of other modifications may include direct changes of the glucose units such as loss of hydroxyl groups or their oxidation to aldehyde or carboxyl groups.

Oil is another product of wetmilling of corn and other grains, the value of which may be improved by introduction and expression of genes. The quantity of oil that can be extracted by wetmilling may be elevated by approaches as described for feed and food above. Oil properties may also be altered to improve its performance in the production and use of cooking oil, shortenings, lubricants or other oil-derived products or improvement of its health attributes when used in the food-related applications. Novel fatty acids may also be synthesized which upon extraction can serve as starting materials for chemical syntheses. The changes in oil properties may be achieved by altering the type, level, or lipid arrangement of the fatty acids present in the oil. This in turn may be accomplished by the addition of genes that encode enzymes that catalyze the synthesis of novel fatty acids and the lipids possessing them or by increasing levels of native fatty acids while possibly reducing levels of precursors. Alternatively DNA sequences may be introduced which slow or block steps in fatty acid biosynthesis resulting in the increase in precursor fatty acid intermediates. Genes that might be added include desaturases, epoxidases, hydratases, dehydratases, and other enzymes that catalyze reactions involving fatty acid intermediates. Representative examples of catalytic steps that might be blocked include the desaturations from stearic to oleic acid and oleic to linolenic acid resulting in the respective accumulations of stearic and oleic acids.

Improvements in the other major cereal wetmilling products, gluten meal and gluten feed, may also be achieved by the introduction of genes to obtain novel plants. Representative possibilities include but are not limited to those described above for improvement of food and feed value.

In addition it may further be considered that the plant be used for the production or manufacturing of useful biological compounds that were either not

produced at all, or not produced at the same level, in the plant previously. The novel plants producing these compounds are made possible by the introduction and expression of genes by transformation methods. The possibilities include, but are not limited to, any biological compound which is presently produced by any organism such as proteins, nucleic acids, primary and intermediary metabolites, carbohydrate polymers, etc. The compounds may be produced by the plant, extracted upon harvest and/or processing, and used for any presently recognized useful purpose such as pharmaceuticals, fragrances, industrial enzymes to name a few.

Further possibilities to exemplify the range of grain traits or properties potentially encoded by introduced genes in transgenic plants include grain with less breakage susceptibility for export purposes or larger grit size when processed by dry milling through introduction of genes that enhance gamma-zein synthesis, popcorn with improved popping quality and expansion volume through genes that increase pericarp thickness, corn with whiter grain for food uses through introduction of genes that effectively block expression of enzymes involved in pigment production pathways, and improved quality of alcoholic beverages or sweet corn through introduction of genes which affect flavor such as the shrunken gene (encoding sucrose synthase) for sweet corn.

7. Plant Agronomic Characteristics

Two of the factors determining where plants can be grown are the average daily temperature during the growing season and the length of time between frosts. Within the areas where it is possible to grow a particular plant, there are varying limitations on the maximal time it is allowed to grow to maturity and be harvested.

The plant to be grown in a particular area is selected for its ability to mature and dry down to harvestable moisture content within the required period of time with maximum possible yield. Therefore, plant of varying maturities are developed for different growing locations. Apart from the need to dry down sufficiently to permit harvest is the desirability of having maximal drying take place in the field to minimize the amount of energy required for additional drying post-harvest. Also the more readily the grain can dry down, the more time there is available for growth and

kernel fill. Genes that influence maturity and/or dry down can be identified and introduced into plant lines using transformation techniques to create new varieties adapted to different growing locations or the same growing location but having improved yield to moisture ratio at harvest. Expression of genes that are involved in regulation of plant development may be especially useful, e.g., the liguleless and rough sheath genes that have been identified in plants.

Genes may be introduced into plants that would improve standability and other plant growth characteristics. For example, expression of novel genes which confer stronger stalks, improved root systems, or prevent or reduce ear droppage would be of great value to the corn farmer. Introduction and expression of genes that increase the total amount of photoassimilate available by, for example, increasing light distribution and/or interception would be advantageous. In addition the expression of genes that increase the efficiency of photosynthesis and/or the leaf canopy would further increase gains in productivity. Such approaches would allow for increased plant populations in the field.

Delay of late season vegetative senescence would increase the flow of assimilate into the grain and thus increase yield. Overexpression of genes within plants that are associated with “stay green” or the expression of any gene that delays senescence would achieve be advantageous. For example, a non-yellowing mutant has been identified in *Festuca pratensis* (Davies et al., 1990). Expression of this gene as well as others may prevent premature breakdown of chlorophyll and thus maintain canopy function.

8. Nutrient Utilization

The ability to utilize available nutrients and minerals may be a limiting factor in growth of many plants. It is proposed that it would be possible to alter nutrient uptake, tolerate pH extremes, mobilization through the plant, storage pools, and availability for metabolic activities by the introduction of novel genes. These modifications would allow a plant to more efficiently utilize available nutrients. It is contemplated that an increase in the activity of, for example, an enzyme that is normally present in the plant and involved in nutrient utilization would increase the availability of a nutrient. An example of such an enzyme would be phytase. It is

also contemplated that expression of a novel gene may make a nutrient source available that was previously not accessible, e.g., an enzyme that releases a component of nutrient value from a more complex molecule, perhaps a macromolecule.

5 9. Male Sterility

Male sterility is useful in the production of hybrid seed. It is proposed that male sterility may be produced through expression of novel genes. For example, it has been shown that expression of genes that encode proteins that interfere with development of the male inflorescence and/or gametophyte result in male sterility.

10 Chimeric ribonuclease genes that express in the anthers of transgenic tobacco and oilseed rape have been demonstrated to lead to male sterility (Mariani et al, 1990).

For example, a number of mutations were discovered in maize that confer cytoplasmic male sterility. One mutation in particular, referred to as T cytoplasm, also correlates with sensitivity to Southern corn leaf blight. A DNA sequence, designated TURF-13 (Levings, 1990), was identified that correlates with T cytoplasm. It would be possible through the introduction of TURF-13 via transformation to separate male sterility from disease sensitivity. As it is necessary to be able to restore male fertility for breeding purposes and for grain production, it is proposed that genes encoding restoration of male fertility may also be introduced.

20 10. Negative Selectable Markers

Introduction of genes encoding traits that can be selected against may be useful for eliminating undesirable linked genes. When two or more genes are introduced together by cotransformation, the genes will be linked together on the host chromosome. For example, a gene encoding a *Bt* gene that confers insect resistance on the plant may be introduced into a plant together with a *bar* gene that is useful as a selectable marker and confers resistance to the herbicide Ignite® on the plant. However, it may not be desirable to have an insect resistant plant that is also resistant to the herbicide Ignite®. It is proposed that one could also introduce an antisense *bar* gene that is expressed in those tissues where one does not want expression of the *bar* gene, e.g., in whole plant parts. Hence, although the *bar* gene is expressed and is useful as a selectable marker, it is not useful to confer herbicide

resistance on the whole plant. The *bar* antisense gene is a negative selectable marker.

Negative selection is necessary in order to screen a population of transformants for rare homologous recombinants generated through gene targeting.

- 5 For example, a homologous recombinant may be identified through the inactivation of a gene that was previously expressed in that cell. The antisense gene to neomycin phosphotransferase II (*nptII*) has been investigated as a negative selectable marker in tobacco (*Nicotiana tabacum*) and *Arabidopsis thaliana* (Xiang and Guerra, 1993). In this example both sense and antisense *nptII* genes are introduced into a plant
- 10 through transformation and the resultant plants are sensitive to the antibiotic kanamycin. An introduced gene that integrates into the host cell chromosome at the site of the antisense *nptII* gene, and inactivates the antisense gene, will make the plant resistant to kanamycin and other aminoglycoside antibiotics. Therefore, rare site specific recombinants may be identified by screening for antibiotic resistance.
- 15 Similarly, any gene, native to the plant or introduced through transformation, that when inactivated confers resistance to a compound, may be useful as a negative selectable marker.

- It is contemplated that negative selectable markers may also be useful in other ways. One application is to construct transgenic lines in which one could
- 20 select for transposition to unlinked sites. In the process of tagging it is most common for the transposable element to move to a genetically linked site on the same chromosome. A selectable marker for recovery of rare plants in which transposition has occurred to an unlinked locus would be useful. For example, the enzyme cytosine deaminase may be useful for this purpose (Stouggard, 1993). In
- 25 the presence of this enzyme the compound 5-fluorocytosine is converted to 5-fluoruracil which is toxic to plant and animal cells. If a transposable element is linked to the gene for the enzyme cytosine deaminase, one may select for transposition to unlinked sites by selecting for transposition events in which the resultant plant is now resistant to 5-fluorocytosine. The parental plants and plants
- 30 containing transpositions to linked sites will remain sensitive to 5-fluorocytosine. Resistance to 5-fluorocytosine is due to loss of the cytosine deaminase gene through

genetic segregation of the transposable element and the cytosine deaminase gene. Other genes that encode proteins that render the plant sensitive to a certain compound will also be useful in this context. For example, T-DNA gene 2 from *Agrobacterium tumefaciens* encodes a protein that catalyzes the conversion of alpha-naphthalene acetamide (NAM) to alpha-naphthalene acetic acid (NAA) renders plant cells sensitive to high concentrations of NAM (Depicker et al., 1988).

It is also contemplated that negative selectable markers may be useful in the construction of transposon tagging lines. For example, by marking an autonomous transposable element such as Ac, Master Mu, or En/Spn with a negative selectable marker, one could select for transformants in which the autonomous element is not stably integrated into the genome. This would be desirable, for example, when transient expression of the autonomous element is desired to activate in *trans* the transposition of a defective transposable element, such as Ds, but stable integration of the autonomous element is not desired. The presence of the autonomous element may not be desired in order to stabilize the defective element, i.e., prevent it from further transposing. However, it is proposed that if stable integration of an autonomous transposable element is desired in a plant the presence of a negative selectable marker may make it possible to eliminate the autonomous element during the breeding process.

11. Non-Protein-Expressing Sequences

a. RNA-Expressing

DNA may be introduced into plants for the purpose of expressing RNA transcripts that function to affect plant phenotype yet are not translated into protein. Two examples are antisense RNA and RNA with ribozyme activity. Both may serve possible functions in reducing or eliminating expression of native or introduced plant genes.

Genes may be constructed or isolated, which when transcribed, produce antisense RNA that is complementary to all or part(s) of a targeted messenger RNA(s). The antisense RNA reduces production of the polypeptide product of the messenger RNA. The polypeptide product may be any protein encoded by the plant genome. The aforementioned genes will be referred to as antisense genes. An

antisense gene may thus be introduced into a plant by transformation methods to produce a novel transgenic plant with reduced expression of a selected protein of interest. For example, the protein may be an enzyme that catalyzes a reaction in the plant. Reduction of the enzyme activity may reduce or eliminate products of the reaction which include any enzymatically synthesized compound in the plant such as fatty acids, amino acids, carbohydrates, nucleic acids and the like. Alternatively, the protein may be a storage protein, such as a zein, or a structural protein, the decreased expression of which may lead to changes in seed amino acid composition or plant morphological changes respectively. The possibilities cited above are provided only by way of example and do not represent the full range of applications.

Genes may also be constructed or isolated, which when transcribed produce RNA enzymes, or ribozymes, which can act as endoribonucleases and catalyze the cleavage of RNA molecules with selected sequences. The cleavage of selected messenger RNA's can result in the reduced production of their encoded polypeptide products. These genes may be used to prepare novel transgenic plants which possess them. The transgenic plants may possess reduced levels of polypeptides including but not limited to the polypeptides cited above that may be affected by antisense RNA.

It is also possible that genes may be introduced to produce novel transgenic plants which have reduced expression of a native gene product by a mechanism of cosuppression. It has been demonstrated in tobacco, tomato, and petunia (Goring et al, 1991; Smith et al., 1990; Napoli et al., 1990; van der Krol et al., 1990) that expression of the sense transcript of a native gene will reduce or eliminate expression of the native gene in a manner similar to that observed for antisense genes. The introduced gene may encode all or part of the targeted native protein but its translation may not be required for reduction of levels of that native protein.

b. Non-RNA-Expressing

For example, DNA elements including those of transposable elements such as Ds, Ac, or Mu, may be inserted into a gene and cause mutations. These DNA elements may be inserted in order to inactivate (or activate) a gene and thereby "tag" a particular trait. In this instance the transposable element does not cause instability

of the tagged mutation, because the utility of the element does not depend on its ability to move in the genome. Once a desired trait is tagged, the introduced DNA sequence may be used to clone the corresponding gene, e.g., using the introduced DNA sequence as a PCR primer together with PCR gene cloning techniques (Shapiro, 1983; Dellaporta et al., 1988). Once identified, the entire gene(s) for the particular trait, including control or regulatory regions where desired may be isolated, cloned and manipulated as desired. The utility of DNA elements introduced into an organism for purposes of gene tagging is independent of the DNA sequence and does not depend on any biological activity of the DNA sequence, i.e., transcription into RNA or translation into protein. The sole function of the DNA element is to disrupt the DNA sequence of a gene.

It is contemplated that unexpressed DNA sequences, including novel synthetic sequences could be introduced into cells as proprietary "labels" of those cells and plants and seeds thereof. It would not be necessary for a label DNA element to disrupt the function of a gene endogenous to the host organism, as the sole function of this DNA would be to identify the origin of the organism. For example, one could introduce a unique DNA sequence into a plant and this DNA element would identify all cells, plants, and progeny of these cells as having arisen from that labeled source. It is proposed that inclusion of label DNAs would enable one to distinguish proprietary germplasm or germplasm derived from such, from unlabelled germplasm.

Another possible element which may be introduced is a matrix attachment region element (MAR), such as the chicken lysozyme A element (Stief et al., 1989), which can be positioned around an expressible gene of interest to effect an increase in overall expression of the gene and diminish position dependant effects upon incorporation into the plant genome (Stief et al., 1989; Phi-Van et al., 1990).

III. Transformed (Transgenic) Plants of the Invention and Methods of Preparation

Plant species may be transformed with the DNA construct of the present invention by the DNA-mediated transformation of plant cell protoplasts and

subsequent regeneration of the plant from the transformed protoplasts in accordance with procedures well known in the art.

Any plant tissue capable of subsequent clonal propagation, whether by organogenesis or embryogenesis, may be transformed with a vector of the present invention. The term “organogenesis,” as used herein, means a process by which shoots and roots are developed sequentially from meristematic centers; the term “embryogenesis,” as used herein, means a process by which shoots and roots develop together in a concerted fashion (not sequentially), whether from somatic cells or gametes. The particular tissue chosen will vary depending on the clonal propagation systems available for, and best suited to, the particular species being transformed. Exemplary tissue targets include leaf disks, pollen, embryos, cotyledons, hypocotyls, megagametophytes, callus tissue, existing meristematic tissue (e.g., apical meristems, axillary buds, and root meristems), and induced meristem tissue (e.g., cotyledon meristem and utilane meristem).

Plants of the present invention may take a variety of forms. The plants may be chimeras of transformed cells and non-transformed cells; the plants may be clonal transformants (e.g., all cells transformed to contain the expression cassette); the plants may comprise grafts of transformed and untransformed tissues (e.g., a transformed root stock grafted to an untransformed scion in citrus species). The transformed plants may be propagated by a variety of means, such as by clonal propagation or classical breeding techniques. For example, first generation (or T1) transformed plants may be selfed to give homozygous second generation (or T2) transformed plants, and the T2 plants further propagated through classical breeding techniques. A dominant selectable marker (such as npt II) can be associated with the expression cassette to assist in breeding.

Thus, the present invention provides a transformed (transgenic) plant cell, *in planta* or *ex planta*, including a transformed plastid or other organelle, e.g., nucleus, mitochondria or chloroplast. The present invention may be used for transformation of any plant species, including, but not limited to, cells from corn (*Zea mays*), *Brassica* sp. (e.g., *B. napus*, *B. rapa*, *B. juncea*), particularly those *Brassica* species useful as sources of seed oil, alfalfa (*Medicago sativa*), rice (*Oryza sativa*), rye

(*Secale cereale*), sorghum (*Sorghum bicolor*, *Sorghum vulgare*), millet (e.g., pearl millet (*Pennisetum glaucum*), proso millet (*Panicum miliaceum*), foxtail millet (*Setaria italica*), finger millet (*Eleusine coracana*)), sunflower (*Helianthus annuus*), safflower (*Carthamus tinctorius*), wheat (*Triticum aestivum*), soybean (*Glycine max*), tobacco (*Nicotiana tabacum*), potato (*Solanum tuberosum*), peanuts (*Arachis hypogaea*), cotton (*Gossypium barbadense*, *Gossypium hirsutum*), sweet potato (*Ipomoea batatas*), cassava (*Manihot esculenta*), coffee (*Coffea* spp.), coconut (*Cocos nucifera*), pineapple (*Ananas comosus*), citrus trees (*Citrus* spp.), cocoa (*Theobroma cacao*), tea (*Camellia sinensis*), banana (*Musa* spp.), avocado (*Persea* 5 *utilis*), fig (*Ficus carica*), guava (*Psidium guajava*), mango (*Mangifera indica*), olive (*Olea europaea*), papaya (*Carica papaya*), cashew (*Anacardium occidentale*), macadamia (*Macadamia integrifolia*), almond (*Prunus amygdalus*), sugar beets (*Beta vulgaris*), sugarcane (*Saccharum* spp.), oats, duckweed (*Lemna*), barley, vegetables, ornamentals, and conifers.

15 Duckweed (*Lemna*, see WO 00/07210) includes members of the family *Lemnaceae*. There are known four genera and 34 species of duckweed as follows: genus *Lemna* (*L. aequinoctialis*, *L. disperma*, *L. ecuadoriensis*, *L. gibba*, *L. japonica*, *L. minor*, *L. miniscula*, *L. obscura*, *L. perpusilla*, *L. tenera*, *L. trisulca*, *L. turionifera*, *L. valdiviana*); genus *Spirodela* (*S. intermedia*, *S. polyrrhiza*, *S. punctata*); genus *Woffia* (*Wa. Angusta*, *Wa. Arrhiza*, *Wa. Australina*, *Wa. Borealis*, 20 *Wa. Brasiliensis*, *Wa. Columbiana*, *Wa. Elongata*, *Wa. Globosa*, *Wa. Microscopica*, *Wa. Neglecta*) and genus *Wolffia* (*W1. utilis*, *W1. utilanen*, *W1. gladiata*, *W1. utilis*, *W1. lingulata*, *W1. repunda*, *W1. rotunda*, and *W1. neotropica*). Any other genera or species of *Lemnaceae*, if they exist, are also aspects of the present 25 invention. *Lemna gibba*, *Lemna minor*, and *Lemna miniscula* are preferred, with *Lemna minor* and *Lemna miniscula* being most preferred. *Lemna* species can be classified using the taxonomic scheme described by Landolt, Biosystematic Investigation on the Family of Duckweeds: The family of Lemnaceae— A Monograph Study. Geobotanischen Institut ETH, Stiftung Rubel, Zurich (1986)).

30 Vegetables within the scope of the invention include tomatoes (*Lycopersicon esculentum*), lettuce (e.g., *Lactuca sativa*), green beans (*Phaseolus vulgaris*), lima

beans (*Phaseolus limensis*), peas (*Lathyrus* spp.), and members of the genus *Cucumis* such as cucumber (*C. sativus*), cantaloupe (*C. cantalupensis*), and musk melon (*C. melo*). Ornamentals include azalea (*Rhododendron* spp.), hydrangea (*Macrophylla hydrangea*), hibiscus (*Hibiscus rosasanensis*), roses (*Rosa* spp.), tulips (*Tulipa* spp.), daffodils (*Narcissus* spp.), petunias (*Petunia hybrida*), carnation (*Dianthus caryophyllus*), poinsettia (*Euphorbia pulcherrima*), and chrysanthemum. Conifers that may be employed in practicing the present invention include, for example, pines such as loblolly pine (*Pinus taeda*), slash pine (*Pinus elliotii*), ponderosa pine (*Pinus ponderosa*), lodgepole pine (*Pinus contorta*), and Monterey pine (*Pinus radiata*), Douglas-fir (*Pseudotsuga menziesii*); Western hemlock (*Tsuga ultilane*); Sitka spruce (*Picea glauca*); redwood (*Sequoia sempervirens*); true firs such as silver fir (*Abies amabilis*) and balsam fir (*Abies balsamea*); and cedars such as Western red cedar (*Thuja plicata*) and Alaska yellow-cedar (*Chamaecyparis nootkatensis*). Leguminous plants include beans and peas. Beans include guar, locust bean, fenugreek, soybean, garden beans, cowpea, mungbean, lima bean, fava bean, lentils, chickpea, etc. Legumes include, but are not limited to, *Arachis*, e.g., peanuts, *Vicia*, e.g., crown vetch, hairy vetch, adzuki bean, mung bean, and chickpea, *Lupinus*, e.g., lupine, trifolium, *Phaseolus*, e.g., common bean and lima bean, *Pisum*, e.g., field bean, *Melilotus*, e.g., clover, *Medicago*, e.g., alfalfa, Lotus, e.g., trefoil, lens, e.g., lentil, and false indigo. Preferred forage and turf grass for use in the methods of the invention include alfalfa, orchard grass, tall fescue, perennial ryegrass, creeping bent grass, and redtop.

Papaya, garlic, pea, peach, pepper, petunia, strawberry, sorghum, sweet potato, turnip, safflower, corn, pea, endive, gourd, grape, snap bean, chicory, cotton, tobacco, aubergine, beet, buckwheat, broad bean, nectarine, avocado, mango, banana, groundnut, potato, peanut, lettuce, pineapple, spinach, squash, sugarbeet, sugarcane, sweet corn, chrysanthemum.

Other plants within the scope of the invention include *Acacia*, aneth, artichoke, arugula, blackberry, canola, cilantro, clementines, escarole, eucalyptus, fennel, grapefruit, honey dew, jicama, kiwifruit, lemon, lime, mushroom, nut, okra, orange, parsley, persimmon, plantain, pomegranate, poplar, radiata pine, radicchio,

Southern pine, sweetgum, tangerine, triticale, vine, yams, apple, pear, quince, cherry, apricot, melon, hemp, buckwheat, grape, raspberry, chenopodium, blueberry, nectarine, peach, plum, strawberry, watermelon, eggplant, pepper, cauliflower, Brassica, e.g., broccoli, cabbage, utilian sprouts, onion, carrot, leek, beet, broad
5 bean, celery, radish, pumpkin, endive, gourd, garlic, snapbean, spinach, squash, turnip, utilane, and zucchini.

Ornamental plants within the scope of the invention include impatiens, Begonia, Pelargonium, Viola, Cyclamen, Verbena, Vinca, Tagetes, Primula, Saint
Paulia, Agertum, Amaranthus, Antihirrhinum, Aquilegia, Cineraria, Clover, Cosmo,
10 Cowpea, Dahlia, Datura, Delphinium, Gerbera, Gladiolus, Gloxinia, Hippeastrum, Mesembryanthemum, Salpiglossos, and Zinnia. Other plants within the scope of the invention are shown in Table 1 (above).

Preferably, transgenic plants of the present invention are crop plants and in particular cereals (for example, corn, alfalfa, sunflower, rice, *Brassica*, canola,
15 soybean, barley, soybean, sugarbeet, cotton, safflower, peanut, sorghum, wheat, millet, tobacco, etc.), and even more preferably corn, rice and soybean.

Transformation of plants can be undertaken with a single DNA molecule or multiple DNA molecules (i.e., co-transformation), and both these techniques are suitable for use with the expression cassettes of the present invention. Numerous
20 transformation vectors are available for plant transformation, and the expression cassettes of this invention can be used in conjunction with any such vectors. The selection of vector will depend upon the preferred transformation technique and the target species for transformation.

A variety of techniques are available and known to those skilled in the art for
25 introduction of constructs into a plant cell host. These techniques generally include transformation with DNA employing *A. tumefaciens* or *A. rhizogenes* as the transforming agent, liposomes, PEG precipitation, electroporation, DNA injection, direct DNA uptake, microprojectile bombardment, particle acceleration, and the like (See, for example, EP 295959 and EP 138341) (see below). However, cells other
30 than plant cells may be transformed with the expression cassettes of the invention. The general descriptions of plant expression vectors and reporter genes, and

Agrobacterium and *Agrobacterium*-mediated gene transfer, can be found in Gruber et al. (1993).

Expression vectors containing genomic or synthetic fragments can be introduced into protoplasts or into intact tissues or isolated cells. Preferably expression vectors are introduced into intact tissue. General methods of culturing plant tissues are provided for example by Maki et al., (1993); and by Phillips et al. (1988). Preferably, expression vectors are introduced into maize or other plant tissues using a direct gene transfer method such as microprojectile-mediated delivery, DNA injection, electroporation and the like. More preferably expression vectors are introduced into plant tissues using the microprojectile media delivery with the biolistic device. See, for example, Tomes et al. (1995). The vectors of the invention can not only be used for expression of structural genes but may also be used in exon-trap cloning, or promoter trap procedures to detect differential gene expression in varieties of tissues, (Lindsey et al., 1993; Auch & Reth et al.).

It is particularly preferred to use the binary type vectors of Ti and Ri plasmids of *Agrobacterium spp.* Ti-derived vectors transform a wide variety of higher plants, including monocotyledonous and dicotyledonous plants, such as soybean, cotton, rape, tobacco, and rice (Pacciotti et al., 1985; Byrne et al., 1987; Sukhapinda et al., 1987; Park et al., 1985; Hiei et al., 1994). The use of T-DNA to transform plant cells has received extensive study and is amply described (EP 120516; Hoekema, 1985; Knauf, et al., 1983; and An et al., 1985). For introduction into plants, the chimeric genes of the invention can be inserted into binary vectors as described in the examples.

Other transformation methods are available to those skilled in the art, such as direct uptake of foreign DNA constructs (see EP 295959), techniques of electroporation (Fromm et al., 1986) or high velocity ballistic bombardment with metal particles coated with the nucleic acid constructs (Kline et al., 1987, and U.S. Patent No. 4,945,050). Once transformed, the cells can be regenerated by those skilled in the art. Of particular relevance are the recently described methods to transform foreign genes into commercially important crops, such as rapeseed (De Block et al., 1989), sunflower (Everett et al., 1987), soybean (McCabe et al., 1988;

Hinchee et al., 1988; Chee et al., 1989; Christou et al., 1989; EP 301749), rice (Hiei et al., 1994), and corn (Gordon Kamm et al., 1990; Fromm et al., 1990).

Those skilled in the art will appreciate that the choice of method might depend on the type of plant, i.e., monocotyledonous or dicotyledonous, targeted for transformation. Suitable methods of transforming plant cells include, but are not limited to, microinjection (Crossway et al., 1986), electroporation (Riggs et al., 1986), *Agrobacterium*-mediated transformation (Hinchee et al., 1988), direct gene transfer (Paszkowski et al., 1984), and ballistic particle acceleration using devices available from Agracetus, Inc., Madison, Wis. And BioRad, Hercules, Calif. (see, for example, Sanford et al., U.S. Pat. No. 4,945,050; and McCabe et al., 1988). Also see, Weissinger et al., 1988; Sanford et al., 1987 (onion); Christou et al., 1988 (soybean); McCabe et al., 1988 (soybean); Datta et al., 1990 (rice); Klein et al., 1988 (maize); Klein et al., 1988 (maize); Klein et al., 1988 (maize); Fromm et al., 1990 (maize); and Gordon-Kamm et al., 1990 (maize); Svab et al., 1990 (tobacco chloroplast); Koziel et al., 1993 (maize); Shimamoto et al., 1989 (rice); Christou et al., 1991 (rice); European Patent Application EP 0 332 581 (orchardgrass and other Pooideae); Vasil et al., 1993 (wheat); Weeks et al., 1993 (wheat). In one embodiment, the protoplast transformation method for maize is employed (European Patent Application EP 0 292 435, U. S. Pat. No. 5,350,689).

In another embodiment, a nucleotide sequence of the present invention is directly transformed into the plastid genome. Plastid transformation technology is extensively described in U.S. Patent Nos. 5,451,513, 5,545,817, and 5,545,818, in PCT application no. WO 95/16783, and in McBride et al., 1994. The basic technique for chloroplast transformation involves introducing regions of cloned plastid DNA flanking a selectable marker together with the gene of interest into a suitable target tissue, e.g., using biolistics or protoplast transformation (e.g., calcium chloride or PEG mediated transformation). The 1 to 1.5 kb flanking regions, termed targeting sequences, facilitate orthologous recombination with the plastid genome and thus allow the replacement or modification of specific regions of the plastome. Initially, point mutations in the chloroplast 16S rRNA and rps12 genes conferring resistance to spectinomycin and/or streptomycin are utilized as selectable markers

for transformation (Svab et al., 1990; Staub et al., 1992). This resulted in stable homoplasmic transformants at a frequency of approximately one per 100 bombardments of target leaves. The presence of cloning sites between these markers allowed creation of a plastid targeting vector for introduction of foreign genes (Staub et al., 1993). Substantial increases in transformation frequency are obtained by replacement of the recessive rRNA or r-protein antibiotic resistance genes with a dominant selectable marker, the bacterial *aadA* gene encoding the spectinomycin-detoxifying enzyme aminoglycoside-3'-adenyltransferase (Svab et al., 1993). Other selectable markers useful for plastid transformation are known in the art and encompassed within the scope of the invention. Typically, approximately 15-20 cell division cycles following transformation are required to reach a homoplastidic state. Plastid expression, in which genes are inserted by orthologous recombination into all of the several thousand copies of the circular plastid genome present in each plant cell, takes advantage of the enormous copy number advantage over nuclear-expressed genes to permit expression levels that can readily exceed 10% of the total soluble plant protein. In a preferred embodiment, a nucleotide sequence of the present invention is inserted into a plastid targeting vector and transformed into the plastid genome of a desired plant host. Plants homoplasmic for plastid genomes containing a nucleotide sequence of the present invention are obtained, and are preferentially capable of high expression of the nucleotide sequence.

Agrobacterium tumefaciens cells containing a vector comprising an expression cassette of the present invention, wherein the vector comprises a Ti plasmid, are useful in methods of making transformed plants. Plant cells are infected with an *Agrobacterium tumefaciens* as described above to produce a transformed plant cell, and then a plant is regenerated from the transformed plant cell. Numerous *Agrobacterium* vector systems useful in carrying out the present invention are known.

For example, vectors are available for transformation using *Agrobacterium tumefaciens*. These typically carry at least one T-DNA border sequence and include vectors such as pBIN19 (Bevan, 1984). In one preferred embodiment, the

expression cassettes of the present invention may be inserted into either of the binary vectors pCIB200 and pCIB2001 for use with *Agrobacterium*. These vector cassettes for *Agrobacterium*-mediated transformation wear constructed in the following manner. PTJS75kan was created by NarI digestion of pTJS75 (Schmidhauser & Helinski, 1985) allowing excision of the tetracycline-resistance gene, followed by insertion of an AccI fragment from pUC4K carrying an NPTII (Messing & Vierra, 1982; Bevan et al., 1983; McBride et al., 1990). XhoI linkers were ligated to the EcoRV fragment of pCIB7 which contains the left and right T-DNA borders, a plant selectable nos/nptII chimeric gene and the pUC polylinker (Rothstein et al., 1987), and the XhoI- digested fragment was cloned into Sall-digested pTJS75kan to create pCIB200 (see also EP 0 332 104, example 19). PCIB200 contains the following unique polylinker restriction sites: EcoRI, SstI, KpnI, BglII, XbaI, and Sall. The plasmid pCIB2001 is a derivative of pCIB200 which was created by the insertion into the polylinker of additional restriction sites. Unique restriction sites in the polylinker of pCIB2001 are EcoRI, SstI, KpnI, BglII, XbaI, Sall, MluI, BclI, AvrII, ApaI, HpaI, and StuI. PCIB2001, in addition to containing these unique restriction sites also has plant and bacterial kanamycin selection, left and right T-DNA borders for *Agrobacterium*-mediated transformation, the RK2-derived trfA function for mobilization between *E. coli* and other hosts, and the OriT and OriV functions also from RK2. The pCIB2001 polylinker is suitable for the cloning of plant expression cassettes containing their own regulatory signals.

An additional vector useful for *Agrobacterium*-mediated transformation is the binary vector pCIB 10, which contains a gene encoding kanamycin resistance for selection in plants, T-DNA right and left border sequences and incorporates sequences from the wide host- range plasmid pRK252 allowing it to replicate in both *E. coli* and *Agrobacterium*. Its construction is described by Rothstein et al., 1987. Various derivatives of pCIB10 have been constructed which incorporate the gene for hygromycin B phosphotransferase described by Gritz et al., 1983. These derivatives enable selection of transgenic plant cells on hygromycin only (pCIB743), or hygromycin and kanamycin (pCIB715, pCIB717).

Methods using either a form of direct gene transfer or *Agrobacterium*-mediated transfer usually, but not necessarily, are undertaken with a selectable marker which may provide resistance to an antibiotic (e.g., kanamycin, hygromycin or methotrexate) or a herbicide (e.g., phosphinothricin). The choice of selectable
5 marker for plant transformation is not, however, critical to the invention.

For certain plant species, different antibiotic or herbicide selection markers may be preferred. Selection markers used routinely in transformation include the nptII gene which confers resistance to kanamycin and related antibiotics (Messing & Vierra, 1982; Bevan et al., 1983), the bar gene which confers resistance to the
10 herbicide phosphinothricin (White et al., 1990, Spencer et al., 1990), the hph gene which confers resistance to the antibiotic hygromycin (Blochinger & Diggelmann), and the dhfr gene, which confers resistance to methotrexate (Bourouis et al., 1983).

One such vector useful for direct gene transfer techniques in combination with selection by the herbicide Basta (or phosphinothricin) is pCIB3064. This
15 vector is based on the plasmid pCIB246, which comprises the CaMV 35S promoter in operational fusion to the *E. coli* GUS gene and the CaMV 35S transcriptional terminator and is described in the PCT published application WO 93/07278, herein incorporated by reference. One gene useful for conferring resistance to phosphinothricin is the bar gene from *Streptomyces viridochromogenes* (Thompson
20 et al., 1987). This vector is suitable for the cloning of plant expression cassettes containing their own regulatory signals.

An additional transformation vector is pSOG35 which utilizes the *E. coli* gene dihydrofolate reductase (DHFR) as a selectable marker conferring resistance to methotrexate. PCR was used to amplify the 35S promoter (about 800 bp), intron 6
25 from the maize Adh1 gene (about 550 bp) and 18 bp of the GUS untranslated leader sequence from pSOG10. A 250 bp fragment encoding the *E. coli* dihydrofolate reductase type II gene was also amplified by PCR and these two PCR fragments were assembled with a SacI-PstI fragment from pBI221 (Clontech) which comprised the pUC19 vector backbone and the nopaline synthase terminator. Assembly of
30 these fragments generated pSOG19 which contains the 35S promoter in fusion with the intron 6 sequence, the GUS leader, the DHFR gene and the nopaline synthase

terminator. Replacement of the GUS leader in pSOG19 with the leader sequence from Maize Chlorotic Mottle Virus check (MCMV) generated the vector pSOG35. pSOG19 and pSOG35 carry the pUC-derived gene for ampicillin resistance and have HindIII, SphI, PstI and EcoRI sites available for the cloning of foreign sequences.

IV. Production and Characterization of Stably Transformed Plants

Transgenic plant cells are then placed in an appropriate selective medium for selection of transgenic cells which are then grown to callus. Shoots are grown from callus and plantlets generated from the shoot by growing in rooting medium. The various constructs normally will be joined to a marker for selection in plant cells. Conveniently, the marker may be resistance to a biocide (particularly an antibiotic, such as kanamycin, G418, bleomycin, hygromycin, chloramphenicol, herbicide, or the like). The particular marker used will allow for selection of transformed cells as compared to cells lacking the DNA which has been introduced. Components of DNA constructs including transcription cassettes of this invention may be prepared from sequences which are native (endogenous) or foreign (exogenous) to the host. By "foreign" it is meant that the sequence is not found in the wild-type host into which the construct is introduced. Heterologous constructs will contain at least one region which is not native to the gene from which the transcription-initiation-region is derived.

To confirm the presence of the transgenes in transgenic cells and plants, a variety of assays may be performed. Such assays include, for example, "molecular biological" assays well known to those of skill in the art, such as Southern and Northern blotting, *in situ* hybridization and nucleic acid-based amplification methods such as PCR or RT-PCR; "biochemical" assays, such as detecting the presence of a protein product, e.g., by immunological means (ELISAs and Western blots) or by enzymatic function; plant part assays, such as leaf or root assays; and also, by analyzing the phenotype of the whole regenerated plant, e.g., for disease or pest resistance.

DNA may be isolated from cell lines or any plant parts to determine the presence of the preselected nucleic acid segment through the use of techniques well

known to those skilled in the art. Note that intact sequences will not always be present, presumably due to rearrangement or deletion of sequences in the cell.

The presence of nucleic acid elements introduced through the methods of this invention may be determined by polymerase chain reaction (PCR). Using this technique discrete fragments of nucleic acid are amplified and detected by gel electrophoresis. This type of analysis permits one to determine whether a preselected nucleic acid segment is present in a stable transformant, but does not prove integration of the introduced preselected nucleic acid segment into the host cell genome. In addition, it is not possible using PCR techniques to determine whether transformants have exogenous genes introduced into different sites in the genome, i.e., whether transformants are of independent origin. It is contemplated that using PCR techniques it would be possible to clone fragments of the host genomic DNA adjacent to an introduced preselected DNA segment.

Positive proof of DNA integration into the host genome and the independent identities of transformants may be determined using the technique of Southern hybridization. Using this technique specific DNA sequences that were introduced into the host genome and flanking host DNA sequences can be identified. Hence the Southern hybridization pattern of a given transformant serves as an identifying characteristic of that transformant. In addition it is possible through Southern hybridization to demonstrate the presence of introduced preselected DNA segments in high molecular weight DNA, i.e., confirm that the introduced preselected DNA segment has been integrated into the host cell genome. The technique of Southern hybridization provides information that is obtained using PCR, e.g., the presence of a preselected DNA segment, but also demonstrates integration into the genome and characterizes each individual transformant.

It is contemplated that using the techniques of dot or slot blot hybridization which are modifications of Southern hybridization techniques one could obtain the same information that is derived from PCR, e.g., the presence of a preselected DNA segment.

Both PCR and Southern hybridization techniques can be used to demonstrate transmission of a preselected DNA segment to progeny. In most instances the

characteristic Southern hybridization pattern for a given transformant will segregate in progeny as one or more Mendelian genes (Spencer et al., 1992); Laursen et al., 1994) indicating stable inheritance of the gene. The nonchimeric nature of the callus and the parental transformants (R_0) was suggested by germline transmission and the identical Southern blot hybridization patterns and intensities of the transforming DNA in callus, R_0 plants and R_1 progeny that segregated for the transformed gene.

Whereas DNA analysis techniques may be conducted using DNA isolated from any part of a plant, RNA may only be expressed in particular cells or tissue types and hence it will be necessary to prepare RNA for analysis from these tissues. PCR techniques may also be used for detection and quantitation of RNA produced from introduced preselected DNA segments. In this application of PCR it is first necessary to reverse transcribe RNA into DNA, using enzymes such as reverse transcriptase, and then through the use of conventional PCR techniques amplify the DNA. In most instances PCR techniques, while useful, will not demonstrate integrity of the RNA product. Further information about the nature of the RNA product may be obtained by Northern blotting. This technique will demonstrate the presence of an RNA species and give information about the integrity of that RNA. The presence or absence of an RNA species can also be determined using dot or slot blot Northern hybridizations. These techniques are modifications of Northern blotting and will only demonstrate the presence or absence of an RNA species.

While Southern blotting and PCR may be used to detect the preselected DNA segment in question, they do not provide information as to whether the preselected DNA segment is being expressed. Expression may be evaluated by specifically identifying the protein products of the introduced preselected DNA segments or evaluating the phenotypic changes brought about by their expression.

Assays for the production and identification of specific proteins may make use of physical-chemical, structural, functional, or other properties of the proteins. Unique physical-chemical or structural properties allow the proteins to be separated and identified by electrophoretic procedures, such as native or denaturing gel electrophoresis or isoelectric focusing, or by chromatographic techniques such as

ion exchange or gel exclusion chromatography. The unique structures of individual proteins offer opportunities for use of specific antibodies to detect their presence in formats such as an ELISA assay. Combinations of approaches may be employed with even greater specificity such as Western blotting in which antibodies are used to locate individual gene products that have been separated by electrophoretic techniques. Additional techniques may be employed to absolutely confirm the identity of the product of interest such as evaluation by amino acid sequencing following purification. Although these are among the most commonly employed, other procedures may be additionally used.

Assay procedures may also be used to identify the expression of proteins by their functionality, especially the ability of enzymes to catalyze specific chemical reactions involving specific substrates and products. These reactions may be followed by providing and quantifying the loss of substrates or the generation of products of the reactions by physical or chemical procedures. Examples are as varied as the enzyme to be analyzed.

Very frequently the expression of a gene product is determined by evaluating the phenotypic results of its expression. These assays also may take many forms including but not limited to analyzing changes in the chemical composition, morphology, or physiological properties of the plant. Morphological changes may include greater stature or thicker stalks. Most often changes in response of plants or plant parts to imposed treatments are evaluated under carefully controlled conditions termed bioassays.

V. Uses of Transgenic Plants

Once an expression cassette of the invention has been transformed into a particular plant species, it may be propagated in that species or moved into other varieties of the same species, particularly including commercial varieties, using traditional breeding techniques. Particularly preferred plants of the invention include the agronomically important crops listed above. The genetic properties engineered into the transgenic seeds and plants described above are passed on by sexual reproduction and can thus be maintained and propagated in progeny plants. The present invention also relates to a transgenic plant cell, tissue, organ, seed or plant

part obtained from the transgenic plant. Also included within the invention are transgenic descendants of the plant as well as transgenic plant cells, tissues, organs, seeds and plant parts obtained from the descendants.

Preferably, the expression cassette in the transgenic plant is sexually transmitted. In one preferred embodiment, the coding sequence is sexually transmitted through a complete normal sexual cycle of the R0 plant to the R1 generation. Additionally preferred, the expression cassette is expressed in the cells, tissues, seeds or plant of a transgenic plant in an amount that is different than the amount in the cells, tissues, seeds or plant of a plant which only differs in that the expression cassette is absent.

The transgenic plants produced herein are thus expected to be useful for a variety of commercial and research purposes. Transgenic plants can be created for use in traditional agriculture to possess traits beneficial to the grower (e.g., agronomic traits such as resistance to water deficit, pest resistance, herbicide resistance or increased yield), beneficial to the consumer of the grain harvested from the plant (e.g., improved nutritive content in human food or animal feed; increased vitamin, amino acid, and antioxidant content; the production of antibodies (passive immunization) and nutraceuticals), or beneficial to the food processor (e.g., improved processing traits). In such uses, the plants are generally grown for the use of their grain in human or animal foods. Additionally, the use of root-specific promoters in transgenic plants can provide beneficial traits that are localized in the consumable (by animals and humans) roots of plants such as carrots, parsnips, and beets. However, other parts of the plants, including stalks, husks, vegetative parts, and the like, may also have utility, including use as part of animal silage or for ornamental purposes. Often, chemical constituents (e.g., oils or starches) of maize and other crops are extracted for foods or industrial use and transgenic plants may be created which have enhanced or modified levels of such components.

Transgenic plants may also find use in the commercial manufacture of proteins or other molecules, where the molecule of interest is extracted or purified from plant parts, seeds, and the like. Cells or tissue from the plants may also be cultured, grown *in vitro*, or fermented to manufacture such molecules.

The transgenic plants may also be used in commercial breeding programs, or may be crossed or bred to plants of related crop species. Improvements encoded by the expression cassette may be transferred, e.g., from maize cells to cells of other species, e.g., by protoplast fusion.

5 The transgenic plants may have many uses in research or breeding, including creation of new mutant plants through insertional mutagenesis, in order to identify beneficial mutants that might later be created by traditional mutation and selection. An example would be the introduction of a recombinant DNA sequence encoding a transposable element that may be used for generating genetic variation. The
10 methods of the invention may also be used to create plants having unique “signature sequences” or other marker sequences which can be used to identify proprietary lines or varieties.

 Thus, the transgenic plants and seeds according to the invention can be used in plant breeding which aims at the development of plants with improved properties
15 conferred by the expression cassette, such as tolerance of drought, disease, or other stresses. The various breeding steps are characterized by well-defined human intervention such as selecting the lines to be crossed, directing pollination of the parental lines, or selecting appropriate descendant plants. Depending on the desired properties different breeding measures are taken. The relevant techniques are well
20 known in the art and include but are not limited to hybridization, inbreeding, backcross breeding, utilane breeding, variety blend, interspecific hybridization, aneuploid techniques, etc. Hybridization techniques also include the sterilization of plants to yield male or female sterile plants by mechanical, chemical or biochemical means. Cross pollination of a male sterile plant with pollen of a different line
25 assures that the genome of the male sterile but female fertile plant will uniformly obtain properties of both parental lines. Thus, the transgenic seeds and plants according to the invention can be used for the breeding of improved plant lines which for example increase the effectiveness of conventional methods such as herbicide or pesticide treatment or allow to dispense with said methods due to their
30 modified genetic properties. Alternatively new crops with improved stress tolerance can be obtained which, due to their optimized genetic “equipment”, yield harvested

product of better quality than products which were not able to tolerate comparable adverse developmental conditions.

VI. A Computer Readable Medium

5 The invention also provides a computer readable medium having stored thereon a data structure containing nucleic acid sequences having at least 70% sequence identity to a nucleic acid sequence selected from those listed in SEQ ID Nos: 1-953, 1001-1095, 1954-1966, 2000-2129, 2137-2661, 2662-4737 and 4738-6813, as well as complementary, ortholog, and variant sequences thereof. Storage and use of nucleic acid sequences on a computer readable medium is well known in
10 the art. (See for example U.S. Patent Nos. 6,023,659; 5,867,402; 5,795,716) Examples of such medium include, but are not limited to, magnetic tape, optical disk, CD-ROM, random access memory, volatile memory, non-volatile memory and bubble memory. Accordingly, the nucleic acid sequences contained on the computer readable medium may be compared through use of a module that receives the
15 sequence information and compares it to other sequence information. Examples of other sequences to which the nucleic acid sequences of the invention may be compared include those maintained by the National Center for Biotechnology Information (NCBI)(<http://www.ncbi.nlm.nih.gov/>) and the Swiss Protein Data Bank. A computer is an example of such a module that can read and compare
20 nucleic acid sequence information. Accordingly, the invention also provides the method of comparing a nucleic acid sequence of the invention to another sequence. For example, a sequence of the invention may be submitted to the NCBI for a Blast search as described herein where the sequence is compared to sequence information contained within the NCBI database and a comparison is returned. The invention
25 also provides nucleic acid sequence information in a computer readable medium that allows the encoded polypeptide to be optimized for a desired property. Examples of such properties include, but are not limited to, increased or decreased: thermal stability, chemical stability, hydrophylicity, hydrophobicity, and the like. Methods for the use of computers to model polypeptides and polynucleotides having altered
30 activities are well known in the art and have been reviewed. (Lesyng et al., 1993; Surles et al., 1994; Koehl et al., 1996; Rossi et al., 2001).

Mix well

Incubate at 42°C for 1 hour

Step 4. Second strand synthesis:

Place reactions on ice, quick spin

- 5 DEPC-water- 91 μ l
5X 2nd strand cDNA buffer- 30 μ l
mM dNTP mix (250 mM final) - 3 μ l
E. coli DNA ligase (10 U/ μ l)-1 μ l
E. coli DNA polymerase 1-10 U/ μ l- 4 μ l
10 RnaseH 2U/ μ l -1 μ l
T4 DNA polymerase 5 U/ μ l-2 μ l
0.5 M EDTA (0.5 M final)--10 μ l
Total 162 μ l
Mix/spin down/incubate 16°C for 2 hours

15 Step 5. Completing the reaction:

Incubate at 16°C for 5 minutes

Purification of double stranded cDNA

- 20 1. Centrifuge PLG (Phase Lock Gel, Eppendorf 5 Prime, Inc., PI-188233) at
14,000X, transfer 162 μ l of cDNA to PLG
2. Add 162 μ l of Phenol:Chloroform:Isoamyl alcohol (pH 8.0), centrifuge 2
minutes
3. Transfer the supernatant to a fresh 1.5 ml tube, add
Glycogen (5 mg/ml) 2
25 0.5 M NH₄OAC (0.75xVol) 120
ETOH (2.5xVol, -20 C) 400
4. Mix well and centrifuge at 14,000X for 20 minutes
5. Remove supernatant, add 0.5 ml 80% EtOH (-20°C)
6. Centrifuge for 5 minutes, air dry or by speed vac for 5-10 minutes
30 7. Add 44 μ l DEPC H₂O

Analyze of quantity and size distribution of cDNA

Run a gel using 1 µl of the double-stranded synthesis product

Synthesis of biotinylated cRNA

5 (use Enzo BioArray High Yield RNA Transcript Labeling Kit Cat#900182)

Purified cDNA 22 µl

10X Hy buffer 4 µl

10X biotin ribonucleotides 4 µl

10X DTT 4 µl

10 10X Rnase inhibitor mix 4 µl

20X T7 RNA polymerase 2 µl

Total 40 µl

Centrifuge 5 seconds, and incubate for 4 hours at 37°C

Gently mix every 30-45 minutes

15

Purification and quantification of cRNA

(use Qiagen Rneasy Mini kit Cat# 74103)

Determine concentration and dilute to 1 µg/µl concentration

20 Fragmentation of cRNA

cRNA (1 µg/µl) 15 µl

5X Fragmentation Buffer* 6 µl

DEPC H₂O 9 µl

30 µl

25

*5x Fragmentation Buffer

1M Tris (pH8.1) 4.0 ml

MgOAc 0.64 g

KOAc 0.98 g

30 DEPC H₂O

Total 20 ml

Filter Sterilize

Array wash and staining

Stringent Wash Buffer**

5 Non-Stringent Wash Buffer***

SAPE Stain****

Antibody Stain*****

Wash on fluidics station using the appropriate antibody amplification protocol

10 **Stringent Buffer: 12X MES 83.3 ml, 5 M NaCl 5.2 ml, 10% Tween 1.0 ml,
H₂O 910 ml,
Filter Sterilize

***Non-Stringent Buffer: 20X SSPE 300 ml, 10% Tween 1.0 ml, H₂O 698 ml,
Filter Sterilize, Antifoam 1.0.

15 ****SAPE stain: 2X Stain Buffer 600 µl, BSA 48 µl, SAPE 12µl, H₂O 540 µl.

*****Antibody Stain: 2X Stain Buffer 300 µl, H₂O 266.4 µl, BSA 24 ul, Goat IgG 6
µl, Biotinylated Ab 3.6 µl

Image analysis and data mining

1. Two text files are included in the analysis:

- 20 a. One with Absolute analysis: giving the status of each gene, either absent or
present in the samples
b. The other with Comparison analysis: comparing gene expression levels
between two samples

25 **Example 2**

Analysis of the RPS2 Mediated Interaction in *Arabidopsis*

The identification and cloning of resistance genes is extremely important for
the treatment of crops. For example, bacterial blight disease caused by
Xanthomonas spp. infects virtually all crop plants and leads to extensive crop losses
30 worldwide. Therefore, it is of interest to identify diverse and abundant plant

resistance genes for use as future crop treatments for pathogen resistance, e.g., to identify particular pathogen resistance (*R*) genes in a plant.

Differential gene expression analysis was used to identify pathogen resistance (*R*) genes in a plant. This method takes advantage of the HR-associated disease resistance. One model plant-pathogen interaction is that of *Arabidopsis thaliana* and *Pseudomonas syringae* pv *tomato*. There are four possible genetic interactions of a *P. syringae* infection of *Arabidopsis* when analyzing HR-associated disease resistance (Table 2). However, there are only two possible outcomes: a compatible outcome occurs when there is disease, and an incompatible outcome occurs when there is no disease. An incompatible outcome, or disease resistance, occurs only when the plant possesses the resistance gene, e.g., *RPS2*, and the pathogen possesses the corresponding *avr* gene, e.g., *avrRpt2*. *RPS2* belongs to the NBS-LRR class of *R* genes, which can confer resistance to a wide variety of phytopathogens. It has been suggested that AvrRpt2 is delivered to the plant via the bacteria's type III secretion system and recognized by a surveillance system involving RPS2 inside the plant cell. The plant response during an incompatible interaction includes a change in ion flux across the plasma membrane, generation of reactive oxygen species, induction of defense genes, induction of HR, fortification of the cell wall, accumulation of salicylic acid, and anti-microbial compounds.

Table 2

Number	Plant	Pathogen	Outcome	
1	<i>RPS2</i>	no <i>avr</i>	Disease	Compatible
2	<i>RPS2</i>	<i>avrRpt2</i>	No disease	Incompatible
3	<i>rps2</i>	no <i>avr</i>	Disease	Compatible
4	<i>rps2</i>	<i>avrRpt2</i>	Disease	Compatible

Methods

Differential Expression

Analysis of differential gene expression is a classic and very powerful tool in experimental biology not only to study large trends in gene regulation but also small

1 differences among similar responses. Historically, methods for analysis only
2 allowed the comparison of a very few genes in each experiment. However, with
3 new methods to identify and quantitate differential mRNA profiles, such as long
4 distance differential display PCR, cDNA microarrays, and gene chips, one can much
5 more quickly and comprehensively identify and analyze differentially expressed
6 genes.

7 By analyzing and comparing the expression profile of genes in the above 4-
8 way matrix, a number of types of genes can be identified that are involved in the
9 resistance pathway. Resistance genes would be highly expressed or strongly
10 downregulated in outcome number 2 in the four way matrix and less oppositely
11 expressed in outcome numbers 1, 3, and 4. Genes that are highly expressed or
12 strongly downregulated in outcome numbers 1 and 2 and oppositely expressed or not
13 expressed above baseline in outcome numbers 3 and 4 are of interest as being
14 associated with the reaction of a plant having resistance genes to a bacterial
15 infection, regardless of the *avr* genotype of the bacterium. Such a comparison is
16 very useful in identifying strong candidates for different roles in plant/pathogen
17 interactions, as are numerous other kinds of outcomes in the four-way
18 plant/pathogen interaction analysis of gene expression. Such genes include those
19 involved in recognition of pathogen (unrelated to virulence status); genes involved
20 in recognition of pathogen having a virulence or avirulence gene (regardless of the
21 status of the corresponding plant); genes related to the status of the plant, regardless
22 of the status of the pathogen; and genes that do not change expression during plant-
23 pathogen interaction.

24 Use of a Gene Chip to Study Gene Regulation in *Arabidopsis* in Response to 25 Exposure to Pathogen

26 Initially isogenic strains of *Arabidopsis thaliana* ecotype Col-0 were used,
27 one having the wild type *RPS2* gene that confers resistance, and one having the *rps2*
28 mutant that confers susceptibility to attack by *Pseudomonas syringae* pathovar
29 *tomato* (Pst). Subsequently, comparisons between ecotypes, mutant *Arabidopsis*,
30 and infection with different pathogens were made. After infection, the RNA was
31 isolated and a probe produced using the Affymetrix GeneChip™ protocol. A gene

array representing approximately 8,100 *Arabidopsis thaliana* genes was used to carry out global gene expression profiling in response to exposure to a particular pathogen.

Initially, the analysis involved comparing all four of the interactions to a water control (plants “infected” with water). In the initial analysis, the mRNA levels of approximately 1,600 genes were significantly affected (> 2.5-fold change in expression) by exposure to the bacterial pathogen. This suggested a dramatic change in the molecular biology of the cell and a more detailed analysis was performed.

10 Results

A. Comparison Of Compatible To Incompatible Infections

Two different types of interactions between *Arabidopsis* and *Pseudomonas syringae* were analyzed. In one type of experiment, a gene for gene interaction conditioned by the plant resistance (*R*) gene *RPS2* and the bacterial avirulence gene *avrRpt2* at a relatively early stage was analyzed. When the pathogen has an *avr* gene and the plant has the corresponding *R* gene, the plant is resistant to the pathogen and the interaction is called incompatible. When the plant-pathogen system lacks either or both genes, the plant is susceptible to the pathogen and the interaction is called compatible. A hypersensitive response (HR, localized rapid cell death of the plant) is one aspect of resistance.

Isogenic strains of *Arabidopsis thaliana* ecotype Col-0 were used, one having the wild type *RPS2* gene that confers resistance, and one having the mutant *rps2* mutant that confers susceptibility to attack by *Pseudomonas syringae* pathovar *tomato* (Pst) carrying *avrRpt2*. Two strains of *Pseudomonas syringae* were used, one having the *avr* gene *avrRpt2* and the other having no *avr*. The *avr* gene is carried on a plasmid.

A gene array having 8,700 probe sets representing approximately 8,100 *Arabidopsis thaliana* genes was used to carry out global gene expression profiling of each of the infection outcomes. The pairings were as follows:

1. RPS2 WT plant; *P. syringae* (no *avr*)
2. RPS2 WT plant; *P. syringae/avrRpt2*

3. rps2-101C mutant plant; *P. syringae* (no *avr*)
4. rps2-101C mutant plant; *P. syringae/avrRpt2*

Additionally, two controls were used:

5. RPS2 WT plant; water control
- 5 6. Rps2-101C mutant plant; water control

Data were processed such that genes having a difference in mRNA levels that was greater than 2.5-fold increased or reduced, compared with controls were selected. The fold change for each gene was log-scaled and normalized.

1. Data analysis: identification of expression clusters

10 Data analysis was carried out by comparing expression of each gene in interactions 1-4 (Table 2), plotting that expression level, and identifying the genes of interest, i.e., those that show more than a 2.5X change in expression (about 1,600 genes). Classification of patterns, or expression clusters were as follows:

- 15 a) Genes strongly induced (> 2.5X change in expression level) only in the resistant (incompatible) response;
- b) Genes responding weakly only in the resistance response, but strongly induced in the compatible response;
- c) Genes that show a high level of expression in all outcomes;
- d) Genes that show a high level of repression in all outcomes;
- 20 e) Genes that show a very high level of repression only when the bacterial *avr* is expressed; and
- f) Genes that show a very different level of expression in the presence of the plant resistance compared to the level in the absence of the plant resistance (the mutant *rps2*).

25 Genes that fall within groups 1a and 1b, i.e., those that are differentially expressed only when an incompatible interaction occurs, include genes directly involved in resistance to pathogens. These genes show a peak (either up or down) only during plant-pathogen interaction 2. The differential expression can be of two types: upregulated (increased expression of this gene is potentially important in the incompatible interaction) or downregulated (decreased expression of this gene is potentially important in the incompatible interaction).

30

2. Heat shock proteins and transcription factors

All major heat shock proteins (HSPs) were identified to be upregulated only during the incompatible interaction. Heat shock factors (HSFs) are transcription factors which control the transcription of the HSP genes. Eight HSF genes are known in *Arabidopsis*. HSF4 and HSF21 were identified as being upregulated when the plant was infected with *P. syringae*. HSF4 showed strong induction that was restricted to resistance, and HSF4 was the only HSF specifically upregulated during the incompatible interaction. The data suggests that the upregulation of HSPs is downstream of upregulation of HSF4.

To analyze whether the response was a more general one, or specific to a given ecotype, expression of HSF4 was analysed in two different *Arabidopsis* ecotypes, *A. thaliana*, ecotypes Col-0 and Ws. HSF4 was also upregulated in the response of Ws ecotype to infection and, specifically, was upregulated during an incompatible response. HSF21 is thus a preferred protein for resistance applications, and HSF4, a protein which is expressed in all plants, is especially preferred for engineering resistance.

A transgene containing the ACT2 promoter and the HSF4 open reading frame was introduced to *Arabidopsis* and transgenic HSF4 *Arabidopsis* lines generated to overexpress and underexpress HSF4. The expression of HSF4 during pathogen infection may cause lower general resistance to *P. syringae*.

Conditional overexpression lines were also generated using the estradiol-inducible promoter system. Infiltration of 20 μ M estradiol into the intercellular space of the leaves of transgenic plants induced expression of HSF4 mRNA for a short time (down by 4 hours). Addition of 20 estradiol to the hydroponic medium yielded sustained HSF4 mRNA accumulation.

B. Genes Involved in *Arabidopsis* Responses to Pathogens

A number of mutations in *Arabidopsis thaliana* that disrupt expression of pathogen-induced genes and cause enhanced disease susceptibility have been identified. Pathogen-induced genes whose expression is altered in these enhanced disease susceptibility mutants are likely to play important roles in conferring disease resistance.

To identify such genes, wild type and various mutant plants were infected with strain *Psm* ES4326 at a dose of 10,000 colony forming units per square centimeter of leaf tissue. Control plants were mock-infected. After thirty hours, tissue samples were collected and used to prepare RNA. Three sets of experiments were carried out. Each set of experiments included three independent replicate experiments. RNA from replicate experiments was pooled to reduce errors arising from the effects of variations in environmental conditions. Each RNA sample was used to prepare a fluorescently-labelled probe which was applied to an Affymetrix GeneChip™, allowing the expression level of each gene represented on the GeneChip™ to be determined for each sample. The plant genotypes included in each experiment were as follows:

Experiment #1

Wild-type (ecotype Columbia)
nahG
pad4-1
eds5-1
eds4
pad2-1
npr1-1
npr1-3

Experiment #2

Wild-type (ecotype Columbia)
coil
ein2
pad1
FN1-3
eds3
eds8

Experiment #3

Wild-type (ecotype Columbia)
pad4-1
nahG
sid2
eds5-3
FN1-9
FN3-2

1. Data analysis

Expression values that were less than 5 were set to five. This ensures that no values are 0 or negative. Such values interfere with subsequent analysis steps. To obtain a list of pathogen-induced genes, the ratios of infected wild-type to mock infected wild type were calculated for each experiment. Then genes were selected in which expression levels were infected wild-type/mock wild-type > 2.5 , and infected wild-type > 50 for at least 2 of 3 experiments. The ratio of 2.5 was chosen because the false positive rate for the GeneChip™ is essentially 0 at this level of stringency, and the absolute value of 50 was chosen to eliminate expression values below the detection limit of the GeneChip™. The result of this analysis was a list of 745 probe sets representing genes that are induced by infection in wild-type plants (note that some genes are represented by more than one probe set, so the number of different genes is somewhat fewer) (see Table 3 below). Hence, the expression of genes comprising SEQ ID NOs:2-6, 8-13, 16, 18, 22-23, 25, 28-29, 31-32, 35-37, 39-43, 45-47, 49-50, 52, 54-55, 57-58, 60-66, 70-72, 74, 76-77, 79, 81, 83, 85, 87-90, 92, 94, 97, 100-107, 111-115, 117-125, 127-135, 138-140, 142-153, 156-158, 160, 162-165, 168-170, 173-181, 183-184, 186-188, 190-198, 200-201, 203-211, 214-215, 218-224, 227-232, 234-249, 251-262, 264, 266-268, 270, 272-275, 277-281, 283, 286-294, 297-298, 302, 304-306, 308-326, 328-339, 341, 344-345, 347, 350-351, 353-358, 361-371, 373-377, 379-386, 388-390, 392, 394-400, 402-406, 408-410, 412-417, 419-427, 429-433, 435-443, 445-452, 454-457, 459-460, 462-464, 466-470, 473-475, 478-479, 481-482, 484-187, 489-494, 496-498, 500-501, 503-506, 508, 510, 512-515, 517-523, 526, 528-529, 531-538, 540, 544-548, 550-558, 560, 563-568, 570, 572-577, 579-580, 582-585, 588-594, 596, 598-600, 602-603, 605-606, 608-612, 614-617, 619-624, 626-630, 632-639, 642, 644, 646-651, 653-657, 659-665, 667-671, 673-678, 681-689, 691-693, 695-713, 715-717, 719, 721-727, 729-733, 736-738, 740, 742, 744, 746, 748-752, 755-756, 758-760, 762-769, 771, 774, 776-781, 783-788, 790-796, 798-799, 802, 804-808, 810-815, 817-831, 833-848, 850-855, 857-869, 871-880, 882-900, 903-907, 909, 911-915, 918-920, 922-

925, 927, 929, 931-938, 940, 943-945, 947, and 950-953 is increased after infection of wild-type *Arabidopsis* with *Pseudomonas syringae*.

To identify pathogen-induced genes whose expression is affected by the mutations, genes for which the ratio of infected mutant/infected wild-type was < 0.5 or > 2 for at least one mutant were selected from the list of 745 pathogen-inducible probe sets. The limits of 5 and 2 were chosen because changes of at least 2-fold are likely to be significant for impact on disease resistance, and because the false positive rate for the GeneChip™ at 2-fold is 0.2%. This selection yielded a list of 530 probe sets corresponding to genes, the expression of which is induced by *Pseudomonas* infection in wild-type plants and perturbed in at least one mutant plant (see Tables 4a and 4b below). Thus, the expression of genes comprising SEQ ID NOs:2, 4-6, 11-13, 18, 22-23, 28, 31, 36, 39-43, 45, 47, 49-50, 52, 54-55, 57-58, 60-61, 63-66, 71-72, 74, 77, 81, 83, 85, 87-89, 92, 97, 100-107, 111-112, 114-115, 117-120, 122, 125, 127-128, 134, 138-140, 143-144, 148-151, 153, 156-157, 160, 165, 168-170, 173-174, 176-180, 183, 187-188, 191, 193-194, 197-198, 200, 203-210, 214, 219-224, 227, 230-232, 235-237, 239-240, 243-246, 248-249, 251-254, 256-258, 261, 264, 266-268, 270, 272-275, 277-278, 280, 283, 286-287, 290-293, 297, 302, 305-306, 308-310, 312-316, 321-326, 328-331, 333, 336-339, 341, 345, 351, 353, 355-358, 361-363, 365-366, 368-371, 373, 375, 377, 379-381, 384-385, 388-390, 392, 394-400, 402-406, 410, 412, 415-416, 419-420, 422-425, 429-433, 435-439, 441-443, 445-452, 454, 459-460, 463, 466, 468-470, 473, 481-482, 485-486, 489, 491-494, 497-498, 500-501, 503, 505-506, 508, 510, 513-515, 517, 520-521, 523, 528-529, 531, 533-538, 540, 545-548, 550-551, 553-554, 556-558, 560, 566-567, 575, 580, 582-584, 588-593, 596, 598-600, 602-603, 605-606, 608-610, 612, 614, 616, 620-622, 627-629, 633-634, 636-639, 644, 646, 648-651, 654-657, 659, 661-663, 667, 669, 673-674, 677, 682, 684-687, 689, 691-693, 697, 699, 701, 703-708, 713, 717, 719, 721-727, 730-733, 736, 740, 744, 746, 749-752, 755-756, 758-760, 762-764, 766-769, 774, 776-778, 780-781, 786, 788, 791-796, 799, 802, 804-808, 810-812, 815, 818-821, 823-825, 827-829, 831, 833-836, 838-843, 845, 847-848, 852-853, 855, 858, 860-869, 871-874, 876, 878-880, 884-887, 889, 892-894, 896-900, 904-907, 911-915, 918-920, 922-924, 931, 933, 938, 943-945, 947, and

950-952 is increased after infection of wild-type *Arabidopsis*, and altered after infection of at least one mutant *Arabidopsis*, with *Pseudomonas syringae*.

2. Data interpretation

Genes that encode regulatory proteins such as transcription factors, protein
5 kinases, calcium binding proteins and the like, are likely to play important roles in disease resistance, as they are likely to affect the expression of multiple defense effector genes. The list of 530 probe sets include 81 that correspond to genes encoding regulatory factors. These are likely to be useful for engineering plants to respond more quickly to pathogen attack by activating expression of defense
10 responses (see Table 5 below). Thus, the expression of genes comprising SEQ ID NOs:39, 52, 60, 63, 81, 83, 106, 107, 115, 117, 118, 168, 174, 176, 179, 204, 207, 208, 220, 221, 248, 258, 268, 275, 280, 309, 323, 326, 329, 351, 419, 422, 429, 430, 432, 459, 460, 468, 469, 473, 500, 505, 506, 508, 529, 531, 533, 535, 538, 545, 553, 602, 606, 608, 610, 614, 616, 634, 654, 655, 684, 686, 687, 691, 717, 751, 752, 766,
15 777, 815, 831, 834, 835, 839, 841, 847, 876, 884, 906, 920, and 924 is increased after infection of wild-type *Arabidopsis*, and altered after infection of at least one mutant *Arabidopsis*, with *Pseudomonas syringae*.

The mutations *nahG*, *pad4-1*, *eds5-1*, *eds4*, *pad2-1*, *npr1-1*, *npr1-3*, *pad1*, *FN1-3*, *eds3*, *eds8*, *sid2*, *eds5-3*, *FN1-3* and *FN3-2* cause enhanced susceptibility to
20 *Pseudomonas syringae*. Consequently, pathogen-inducible genes whose expression is reduced by one of these mutations are likely to be important for resistance to *Pseudomonas syringae* and possibly other bacterial pathogens. These 333 probe sets are shown in Table 6 (below). Therefore, the expression of genes comprising SEQ ID NOs:12-13, 18, 23, 36, 39-40, 43, 45, 50, 52, 57-58, 60-61, 64, 71-72, 81,
25 87-89, 97, 100, 102-105, 107, 111-112, 115, 119-120, 122, 125, 127-128, 140, 144, 148-150, 153, 165, 168-169, 176-177, 179, 183, 188, 191, 193-194, 197-198, 203-206, 208-209, 214, 219-222, 227, 230, 232, 237, 244-246, 248-249, 251-253, 258, 261, 264, 266, 268, 273-275, 283, 287, 290, 293, 297, 302, 305-306, 308, 312-315, 321-322, 324, 326, 330, 333, 338, 341, 345, 353, 356-358, 362-363, 366, 369, 371,
30 375, 377, 380, 384-385, 389, 392, 394-395, 398-399, 402-404, 406, 410, 415, 419, 422, 425, 429-430, 433, 435-439, 443, 445-452, 454, 463, 466, 468-470, 473, 486,

489, 491-492, 494, 498, 500-501, 503, 508, 513-514, 517, 529, 533-538, 548, 550, 553-554, 4556-558, 566, 575, 580, 582-583, 590-591, 593, 600, 602, 609-610, 612, 614, 620-622, 627-629, 637-638, 644, 649, 654-657, 659, 663, 667, 669, 673-674, 677, 684-685, 689, 691-693, 699, 703-705, 708, 719, 721, 724-726, 730-732, 744, 746, 749-750, 752, 755-756, 758, 760, 762-764, 767, 769, 774, 780-781, 786, 788, 791-792, 794-796, 799, 804-808, 810-812, 815, 818-819, 823, 828-829, 833, 840-841, 843, 847, 852-853, 858, 860, 862-865, 867-868, 872-874, 876, 885-887, 889, 892-894, 896-900, 904-905, 907, 911-914, 918-920, 922-924, 931, 933, 938, 947, 950, and 952 is increased after infection of wild-type *Arabidopsis*, and altered after infection of at least one mutant *Arabidopsis* having a mutation that results in enhanced susceptibility to *Pseudomonas* (*nahG*, *pad 4-1*, *eds 5-1*, *eds4*, *pad2-1*, *np4 1-1*, *npr 1-3*, *pad1*, *FN1-3*, *eds3*, *eds8*, *sid2*, *eds5-3*, *NF1-3* and *FN3-2*).

The mutations *coil* and *ein2* block jasmonate and ethylene signaling, respectively. Jasmonate and ethylene-dependent disease resistance responses are known to be important for resistance to the fungal pathogens *Alternaria brassicicola* and *Botrytis cinerea*, and may also be important for resistance to other necrotrophic fungal pathogens. *Alternaria* and *Botrytis* are distantly related, yet plant resistance to these fungi is controlled similarly, suggesting that jasmonate- and ethylene-dependent responses function to limit growth of a wide range of fungal pathogens. Consequently, pathogen-induced genes whose expression is reduced in *coil* and *ein2* mutants are likely to be important for resistance to these necrotrophic fungal pathogens. These 296 probe sets are shown in Table 7 (see below). Hence, the expression of genes comprising SEQ ID NOs:2, 4, 6, 11-13, 18, 22-23, 31, 41-43, 49-50, 54, 57-58, 61, 64-66, 71-72, 74, 77, 85, 87, 89, 92, 97, 101, 103, 106-107, 112, 114, 117-119, 125, 128, 134, 138, 143, 149, 151, 156-157, 165, 169-170, 174, 176-180, 187-188, 191, 193, 206, 208, 219-220, 222, 224, 231, 236, 239, 243-245, 251-254, 256-257, 267, 272, 287, 290, 292, 297, 302, 312-313, 315-316, 321-322, 324-325, 328, 330, 345, 351, 353, 355-357, 362-363, 366, 368-371, 373, 375, 379, 381, 384, 388-390, 392, 395-400, 405, 410, 415-416, 419, 422, 424, 431-432, 435-436, 438-439, 447, 459-460, 470, 473, 481-482, 489, 491, 493-494, 500-501, 505-506, 513-514, 517, 520-521, 523, 528-529, 531, 535, 537-538, 540, 545-548, 551,

553-554, 557-558, 566, 575, 580, 582, 584, 589, 591, 593, 596, 598-599, 603, 605, 608-609, 612, 628, 633-634, 636-637, 639, 646, 648, 650-651, 656, 661, 663, 667, 674, 685-687, 689, 691, 693, 697, 699, 701, 705, 707, 713, 723-724, 726, 736, 740, 749, 751-752, 756, 758-759, 764, 766-768, 774, 776, 778, 780, 792-796, 799, 802, 806, 810-812, 818, 820-821, 825, 827-829, 833-836, 838-839, 841-843, 848, 855, 860-861, 866, 868-869, 871, 873-874, 876, 878-880, 889, 892, 898-900, 904-905, 907, 915, 918, 922, 924, 933, 943-945, 947, and 951 is increased after infection of wild-type *Arabidopsis*, and altered after infection of at least one mutant *Arabidopsis* having a mutation in a gene whose expression is important for resistance to necrotrophic fungi (a mutation that blocks or interferes with jasmonate and ethylene signaling such as *col1* and *ein2*). Accordingly, these genes are useful to improve the resistance of plants to fungal infection.

The mutations *nahG*, *pad4-1*, *sid2*, *eds5-1*, *eds5-3*, and *eds4* are known to interfere with salicylic acid dependent signaling. Such signaling is known to be important for resistance to the bacterial pathogen *Pseudomonas syringae*, the oomycete pathogen *Peronospora parasitica*, the viral pathogen tobacco mosaic virus, as well as various other plant pathogens. Consequently, pathogen-induced genes whose expression is reduced by one of the mutations that block salicylate signaling are likely to be important for disease resistance, and useful for engineering improved disease resistance. These 288 probesets are shown in Table 8 (see below). Therefore, the expression of genes comprising SEQ ID NOs: 12-13, 18, 23, 36, 39-40, 43, 45, 50, 52, 57-58, 60-61, 64, 71-72, 81, 87-88, 100, 102-105, 107, 111-112, 115, 119-120, 122, 125, 127-128, 140, 148-150, 153, 168-169, 176-177, 188, 191, 193-194, 197-198, 203-206, 209, 219-222, 227, 232, 237, 244-246, 248-249, 251-253, 258, 261, 264, 266, 268, 273-275, 283, 287, 290, 293, 297, 302, 305-306, 308, 312-315, 324, 326, 330, 333, 341, 345, 353, 356, 358, 366, 371, 375, 377, 380, 385, 389, 392, 394, 398, 402-404, 406, 410, 415, 419, 425, 429-430, 433, 435-438, 443, 445-447, 449-452, 454, 463, 466, 468-470, 473, 486, 489, 492, 494, 498, 500-501, 503, 508, 513-514, 517, 533-538, 548, 550, 553-554, 57-558, 566, 575, 582-583, 590-591, 593, 600, 602, 609-610, 612, 620-622, 627-629, 637-638, 644, 649, 654-657, 659, 667, 669, 673, 677, 684, 689, 692-693, 703-705, 719, 721, 724-726, 730-

732, 744, 746, 749-750, 752, 755-756, 760, 762-764, 767, 769, 774, 780-781, 786,
788, 791-792, 795-796, 805-808, 810-812, 815, 818-819, 823, 828, 833, 840-841,
843, 852-853, 858, 860, 862-865, 867-868, 872-874, 876, 887, 889, 893-894, 896-
898, 900, 905, 907, 911-914, 918-920, 922-923, 931, 933, 938, 947, 950, and 952
5 which is increased after infection of wild-type *Arabidopsis* and altered after
infection of at least one mutant *Arabidopsis* having a mutation in a gene that
interferes with salicylic acid dependent signaling (*nahG*, *pad4-1*, *sid2*, *eds5-1*, *eds5-3*
and *eds4*). Thus, these genes are particularly useful to improve the resistance of
plants to infection by more than one pathogen including bacteria, oomycetes and
10 viruses, such as TMV.

Example 3

Further Analysis of the Pathogen Response and Comparison of the Response in Different Ecotypes

Materials and Methods

Arabidopsis ecotypes (or accessions) (the wild-types of all the *Arabidopsis*
ecotypes used here have wild-type alleles of *RPS2* and *RPM1*).

Col, Columbia-0

Ler, Landsberg *erecta*

20 Ws, Wassilewskija

***Arabidopsis* mutants and transgenics**

Col *rps2-101C*, a loss-of-function mutant of the resistance gene *RPS2* in
Col background.

NahG, transgene for salicylic acid hydroxylase (inactivating salicylic
25 acid). Col background.

ndr1-1, null mutant allele of *NDRI* (non-race specific disease resistance).

The mutation strongly affects *RPS2*-mediated resistance and
partially affects *RPM1*-mediated resistance. Col background.

Bacterial strains

30 Pst, *Pseudomonas syringae* pv. *tomato* DC3000 (virulent strain of
Arabidopsis)

Psm, *P. syringae* pv. *maculicola* ES4326 (another virulent strain of *Arabidopsis*)

Psp, *P. syringae* pv. *phaseolicola* NPS3121 (very weak pathogen of *Arabidopsis*)

5 Avirulence (*avr*) genes of *P. syringae*

avrRpt2: corresponding to the *Arabidopsis* resistance (*R*) gene *RPS2*

avrB: corresponding to the *Arabidopsis* resistance (*R*) gene *RPM1*

Experimental Protocols

A. Gene for gene resistance (6 hours after treatment)

10	<u>plant</u>	<u>treatment</u>
	Col WT	H ₂ O
	Col WT	Pst
	Col WT	Pst/ <i>avrRpt2</i>
	Col <i>rps2-101C</i>	H ₂ O
15	Col <i>rps2-101C</i>	Pst
	Col <i>rps2-101C</i>	Pst/ <i>avrRpt2</i>
	Ws WT	H ₂ O
	Ws WT	Pst
	Ws WT	Pst/ <i>avrRpt2</i>

20 B. Differences in the response to bacterial pathogens among ecotypes (3, 6, and 9 hours after treatment)

	<u>Plant</u>	<u>treatment</u>
	Col	H ₂ O
	Col	Pst
25	Col	Pst/ <i>avrRpt2</i>
	Ler	H ₂ O
	Ler	Pst
	Ler	Pst/ <i>avrRpt2</i>
	Ws	H ₂ O
30	Ws	Pst
	Ws	Pst/ <i>avrRpt2</i>

Note that overall results for Cvi were very similar to Ler.

C. Genetic factors that affect the plant response to incompatible interactions (3, 6, and 9 hours after treatment)

	<u>plant</u>	<u>treatment</u>
5	Col	H ₂ O
	Col	Pst
	Col	Pst/avrRpt2
	Col	Pst/avrB
	Col	Psm
10	Col	Psm/avrRpt2
	Col	Psp (not 9 hours)
	Col	Psp/avrRpt2 (not 9 hours)
	Col NahG	Pst
	Col NahG	Pst/avrRpt2
15	Col NahG	Pst/avrB
	Col ndr1-1	Pst
	Col ndr1-1	Pst/avrRpt2
	Col ndr1-1	Pst/avrB

Results

20 Four hundred sixty-five genes were specifically/preferentially induced in the incompatible interaction (WT and Pst/avrRpt2), and 616 genes were specifically/preferentially repressed in the incompatible interaction. Examples of these genes are provided in Tables 10 and 13. Gene expression patterns in the incompatible interaction in Col and Ws were significantly different, indicating that

25 the genetic diversity among ecotypes can affect gene regulation during the incompatible interaction significantly. In comparison, a relatively small number of genes (314 genes for induction, 167 genes for repression) were affected at this time point during the compatible interactions (but not preferential to the incompatible interactions). A comparison of the results in three genetically different compatible

30 interactions (WT and Pst, rps2 and Pst, rps2 and avrRpt2) revealed that 25 genes were repressed in an avrRpt2-dependent manner (see Table 9). Thus, the expression

of genes comprising SEQ ID NOs:1, 15, 19, 20, 24, 26, 27, 34, 38, 51, 56, 59, 67-69, 99, 116, 155, 159, 182, 212, 284, 372, 444, and 789 is downregulated (repressed) in an *avrRpt2*-dependent manner in *Arabidopsis*. These genes are good candidates to be involved in *avrRpt2* virulence functions (in *rps2* plants).

5 Genes that were induced in *rps2* plants after infection irrespective of *avrRpt2* indicate a function of RPS2 other than an interaction with *avrRpt2*. Thus, global gene expression profiling can identify large and minor trends in gene regulation and is useful in gene discovery.

10 One general phenomenon when plants are resistant to a pathogen is the early response of pathogen-responsive (induced or repressed) genes compared to plants that are susceptible to infection. This has been proposed based on observing expression of a very limited number of genes, but it has not been proven as a global trend. To examine the results from early incompatible interactions and late compatible interactions, 4 week old Col-0 plants with well expanded leaves were
15 infected with a high dose ($OD_{600} = 0.02$) or low dose ($OD_{600} = 0.002$) of *P. syringae* and samples collected at 6 or 30 hours, respectively. The two expression patterns were similar. The correlation values between the late compatible and incompatible interaction at either 6 hours, 9 hours or the average of 3-9 hour time points was 0.71, 0.72 and 0.75, respectively.

20 The majority of genes that did not respond within 9 hours after infection of a virulent strain but that responded in 30 hours (Pst or Psm, for *Pseudomonas syringae* pv. tomato DC3000 and *Pseudomonas syringae* pv. *maculicola* ES4326, respectively; the plant is susceptible to these strains) responded within 6 hours after infection of an avirulent strain (Pst/*avrRpt2*; Pst carrying the avirulence gene
25 *avrRpt2*; the plant is resistant to this strain). This strongly suggests that early response of the pathogen-responsive genes is crucial for the plant to be resistant.

A comparison of the differences in the expression patterns of the 2 primary ecotypes of *Arabidopsis*' response to infection provides a further way to identify which genes have a more universal role (unchanged expression pattern) and which
30 may be very specific to a particular plant ecotype involved in a very specific gene-for-gene interaction. For example, responses that are common between two

ecotypes may be important for resistance. Genes that show the same pattern in both ecotypes may be part of more universal, or commonly-used, mechanisms involved in plant-pathogen interactions. Responses that are different may indicate that the two ecotypes use different combinations of responses to achieve resistance. This implies that a variety of genes can participate in plant-pathogen interactions. Nevertheless, ecotype-specific responses are expected to have counterparts in other plant species.

The differences in resistance response between ecotypes can be used for improving resistance in plants. In responses that are different between ecotypes, using the methods and compounds of the invention, such a response can be added to (induced or repressed) the response seen in the ecotype which does not normally use that response. This will likely give the plant a more robust or a wider range of resistance.

Table shows a comparison of gene expression in 4 ecotypes, i.e., Col-0, Ws-2, Cvi and Ler in response to infection. Table 10A shows the expression data for 9 probe sets corresponding to genes that are specifically induced at 3 hours after incompatible infection of four different ecotypes of *Arabidopsis* with *P. syringae* pv. tomato DC3000. Table 10B shows expression data for 18 probe sets corresponding to genes that are induced by 6 hours but not at 3 hours after incompatible infection of four different ecotypes of *Arabidopsis* with three different bacterial strains, i.e., *P. syringae* pv. tomato DC3000. Table 10C illustrates the expression data for 6 probe sets corresponding to genes that are activated by *P. syringae* at 6 hours post-infection. Most of the genes are compatible interaction-specific or -preferential.

Four week old plants with fully expanded leaves were infected and samples collected at 3 or 6 hours post-infection ($OD_{600} = 0.02$). Some common patterns were observed. At 3 hours after infection of an avirulent strain, Pst/avrRpt2, the overall qualitative gene expression patterns were very similar for all the ecotypes tested. Common responses to Pst/avrRpt2 could be important for gene-for-gene resistance and so may be useful to identify targets for reverse genetics. Quantitative and qualitative differences in the response were noted, indicating that there are qualitative and/or quantitative differences in the signal transduction mechanisms

that regulate the response among the ecotypes. Such signal transduction mechanism differences are attributed to genetic differences among the ecotypes.

In particular, early inducible genes (3 hours) in the incompatible interaction were identified (70 genes are common in all the ecotypes, and 360 genes if selected for induced in at least one ecotype). One group of the early genes (38 genes in Col) were repressed to the control level by 6 hours. These genes did not respond in the compatible interaction at 3 hours and were repressed below the control level in the compatible interaction by 6 hours. This suggests that shutting down these genes in the incompatible interaction by 6 hours could be caused by defense response inhibiting factor(s) delivered by bacteria. Another group of the early genes were expressed even higher at 6 hours in the incompatible interaction. One hundred eighty-eight genes showed significant induction or repression at 3 hours in the compatible interaction in at least one of the ecotypes. Of these, 3 induced genes and 3 repressed genes were induced or repressed in all three ecotypes.

At 3 hours in the incompatible interaction, a major difference among the ecotypes was quantitative; overall expression patterns were very similar, but overall fold change amplitudes were clearly in the order of Ws>Col>Ler. Thus, in this type of analysis it is not appropriate to analyze datasets by comparing the genes from different datasets that are selected by a certain cut-off value (e.g., 2.5-fold difference). This fold change difference was mainly caused by differences in the basal expression of these genes. In fact, a strong negative correlation in each gene was found between the relative basal expression level in Ws (relative to the other ecotypes; Pearson correlation -0.78) and response in the incompatible interaction (especially at 3 hours) and a moderate positive correlation between the relative basal expression level in Ler and response in the incompatible interaction (Person correlation 0.38) (almost no correlation for the relative basal expression level in Col; Person correlation 0.10). These observations indicate that Ws has the tightest regulation of these incompatible interaction-responsive genes, and Ler has the loosest. Another interesting observation is that the relative susceptibility to a virulent strain (Pst) was in the order of Ws>Col>Ler. Although it is unknown whether these two phenomena are controlled by same gene(s), it is conceivable that

leaky expression of early response genes (in Ler) confers relative resistance to a virulent strain. At 6 hours in the incompatible interaction, the gene expression pattern for Col was significantly different from the other ecotypes.

Moreover, different ecotypes may use a different but overlapping set of responses to achieve resistance against the same pathogen. Gene expression profiling can thus reveal ecotype differences. Therefore, it is possible to isolate the genes responsible for these differences in regulatory mechanisms using ecotype differences in gene expression as a phenotype, by a map-based cloning approach.

For example, a majority of the incompatible response-inducible genes have lower basal levels in ecotype Ws and higher basal levels in ecotype Ler. Among the numerous genes, a few genes that display large differences in the basal level in two ecotypes are chosen. The large differences in expression level constitute easy-to-score phenotypic markers. Ws and Ler are crossed to obtain F2 populations. The larger the F2 population is, the better resolution in the map position can be obtained. For each of the F2 plants, expression levels of the chosen phenotypic marker genes are measured and physical markers that distinguish these ecotype genomes are scored. The map position of the responsible gene is determined by analyzing the linkage between the phenotype and the physical markers. If more than a single gene is responsible for the ecotype difference and each of the genes has a quantitative effect on the phenotype, quantitative trait locus (QTL) analysis can be used for mapping. Instead of using F2 populations, the use of recombinant inbred lines (RILs) between the ecotypes of interest may facilitate the analysis, especially using RILs that are already mapped for recombination points. Once the gene(s) responsible for the phenotype is mapped, a combination of increasing the map resolution, sequencing the chromosomal region identified by mapping in both ecotypes, and gene transfer from one ecotype to the other leads to isolation of the gene.

If the phenotype of interest in gene expression depends on bacterial infection, such as expression of ecotype Col-specific inducible genes at 6 hours after infection of Pst/avrRpt2, expression of the corresponding phenotypic marker genes

(e.g., genes that show good difference in induction between Col and Ler) can be measured at an appropriate time after bacterial infection.

Differences in gene expression patterns between two virulent strain backgrounds (Pst and Psm) are relatively small. Gene expression patterns for Pst/avrRpt2 and Pst/avrB were quite similar at 3 hours, but the difference increased at 6 hours. Psp (no avr) shows similar expression pattern to incompatible bacteria although the amplitude of fold difference was smaller in general. This suggests that Psp, which does not induce the HR in the plant, is still recognized by the plant and induce major part of the defense response seen during the incompatible interaction. It also suggests that plants monitor the effect of the defense response and that if it seems effective (bacteria do not grow like Psp), the plant does not go for a full-blown defense response.

Preferred Genes

Preferred early inducible genes were selected as induced > 2.5 fold (except for 2 fold for Psp at 6 hours) in all of the following datasets: Pst/avrRpt2 at 3 hours in Col, Ws, and Ler; Pst/avrRpt2 at 3 hours, Psm/avrRpt2 at 3 hours, Psp at 6 hours, and Pst/avrB at 3 hours, relative to the water control, as well as estradiol-inducible (avrRpm1 at 0, 45, and 120 minutes and avrRpt2 at 0, 45, and 120 minutes, where the fold change was relative to the appropriate resistance gene mutant carrying the same transgenes. Among these genes, the genes were ranked according to genes that are not induced by SA or BTH and not induced in late time points with Psm.

Regulatory genes were given higher rankings (see Table 11). Hence, the expression of genes comprising SEQ ID NOs:17, 70, 76, 81, 84, 109, 123, 144, 160, 230, 265, 268, 269, 271, 323, 333, 385, 427, 428, 430, 457, 505, 569, 597, 602, 606, 616, 708, 730, 741, 812, 862, and 942 is induced early after infection of different *Arabidopsis* ecotypes with *Pseudomonas syringae* pv tomato DC3000, *P. maculicola* ES4326 and *P. phaseolica* NPS3121 (at 3 or 6 hours) or is estradiol inducible (at 45 or 120 minutes).

Preferred early repressible genes were selected as repressed > 2.5 fold (except for > 2 fold for Psp at 6 hours) in all of the following datasets: Pst/avrRpt2 at 3 hours, Psm/avrRpt2 at 3 hours, Psp at 6 hours, and Pst/avrB at 3 hours) and

Pst/avrRpt2 at 3 hours in Col (the fold change was relative to the appropriate water controls). Among them, the genes were ranked in order of expression (highest to lower levels of expression) (see Table 12). Thus, the expression for genes comprising SEQ ID NOs:30, 73, 282, 541, 640, 679, 761, 870, 917, and 930 is repressed early after infection of *Arabidopsis* with *Pseudomonas syringae* pv tomato DC3000, *P. maculicola* ES4326 and *P. phaseolica* NPS3121.

Other genes are induced/repressed during incompatible interactions at 3 and/or 6 hours after inoculation of bacteria. Preferred genes in this group were selected as induced/repressed > 2.5 fold in the incompatible interaction compared to water inoculated control and 2 > fold compared to the corresponding compatible interaction at 3 and/or 6 hours after inoculation with Pst/avrRpt2 and Pst/avrB, and Psm/avrRpt2 and Pst/avrRpt2, in all four ecotypes (see Tables 13a and 13b). Hence, the expression of genes comprising SEQ ID NOs:21, 44, 46, 60, 86, 91, 93, 106, 110, 119, 122, 130, 131, 161, 166, 167, 168, 171, 176, 200, 203, 213, 225, 227, 248, 261, 262, 266, 274, 285, 300, 301, 302, 320, 326, 341, 345, 348, 349, 360, 366, 378, 615, 618, 406, 409, 422, 425, 441, 443, 446, 449, 454, 461, 475, 476, 485, 500, 511, 512, 527, 533, 543, 545, 549, 550, 552, 567, 575, 590, 608, 611, 625, 643, 656, 659, 666, 668, 671, 680, 690, 704, 706, 711, 721, 728, 738, 757, 791, 807, 811, 813, 827, 857, 864, 868, 875, 881, 893, 901, 905, 908, 912, 939, 941, 951, and 952 is induced in an incompatible interaction at 3 and/or 6 hours after infection of four *Arabidopsis* ecotypes with *Pseudomonas syringae* pv tomato DC3000, *P. maculicola* ES4326 and *P. phaseolica* NPS3121, while the expression of genes comprising SEQ ID NOs:7, 33, 82, 136, 141, 154, 185, 189, 199, 202, 434, 471, 483, 499, 516, 530, 578, 586, 631, 658, 694, 714, 718, 734, 770, 772, 816, and 916 is decreased in an incompatible interaction at 3 and/or 6 hours after infection of four *Arabidopsis* ecotypes with *Pseudomonas syringae* pv tomato DC3000, *P. maculicola* ES4326 and *P. phaseolica* NPS3121.

Garlic T-DNA insertion lines corresponding to these genes are searched by BLAST. Global expression profiling after infection with one of two different pathogens (*P. syringae* and *Alternaria brassicicola*) may be employed as a

phenotyping method. Transgenic plants for overexpression, underexpression, and conditional overexpression of selected genes are also prepared.

Example 4

Promoters of Genes Responsive to Pathogen Infection

In many cases the major outcomes of plant-pathogen interactions are largely determined by how plants react in an early stage. Therefore, it is useful to isolate promoters that rapidly react to pathogen attack for use in expressing proteins that provide tolerance or resistance to pathogen attack.

- Genes were selected according to the conditions described below based on the results of a GeneChip™ analysis. These genes were particularly selected for a high level of induction in the *avrRpt2-RPS2* interaction and for a very low mRNA level in the absence of pathogen attack among four *Arabidopsis* ecotypes tested (Col, Ws, Ler, and Cvi). The genes were also analyzed to determine if their expression was similar in other combinations of incompatible interactions (three different bacterial strain backgrounds: *P. syringae* pv. tomato DC3000, *P. syringae* pv. *maculicola* ES4326, and *P. syringae* pv. *phaseolicola* NP3121; three different avirulence genes: *avrRpt2*, *avrB*, and *avrRpm1*; and direct expression of avirulence genes in plants using an estradiol-inducible system). For each gene, the 1.2-kb sequence upstream of the initiation codon is provided in SEQ ID NOs: 1047-1095.

Preferred Highly Inducible Promoters

- Promoters were selected that had low basal expression level (i.e., uninduced level) in all the ecotypes (Col, Ler, Ws, and Cvi) and high inducibility in Col. Five such promoters of genes represented by the probe sets in Table 14 were identified: the promoters of germin precursor-like oxalate oxidase gene, extra-large G protein gene, PR-1, EREBP5 gene, and a C2H2-type zinc finger protein gene were chosen. The promoters for the germin-precursor like oxalate oxidase gene and PR-1 gene are relatively slow response promoters (no induction 3 hours after infection), but have high induction by 6 hours. The extralarge G protein gene is an intermediate in terms of response time, but maintains high expression over time. The other two are useful as early transient response promoters (good induction by 3 hours, but shut down by

6 hours) in the incompatible interaction (wild type plant infected with Pst/avrRpt2). Promoter sequences comprising SEQ ID NOs:1046-1095 and 1047-1055 correspond to genes comprising one of SEQ ID Nos: 17, 21, 80, 81, 109, 156, 174, 176, 221, 227, 296, 302, 303, 306, 333, 340, 360, 500, 505, 524, 575, 601, 602, 614, 628, 687, 733, 782, 811, 835, 862, 900, 905, 912, and 109, 306, 524, 600, 875, 912, 913, 941 and 942, respectively. Promoter-LUC reporter fusions are prepared and tested in a transient expression system using biolistic co-bombardment of avrRpt2 gene.

Promoters Responsive to Particular Pathogens

Proteins that are useful for protecting plants from pathogen attack may have deleterious effects on plant growth if expressed constitutively. Consequently, it is desirable to have promoter sequences that control gene expression in such a way that expression is absent or very low in the absence of pathogens, and high in the presence of pathogens.

Wild-type *Arabidopsis* plants (ecotype Columbia) were either mock-infected or infected with the bacterial pathogen *Pseudomonas syringae* pv. *maculiola* strain ES4326 (2×10^4 cfu per square centimeter of leaf). After 30 hours, samples were collected, and RNA was purified. This procedure was repeated three times independently, and the RNAs from corresponding samples were pooled, in order to reduce the impact of variation due to uncontrolled variables. The two pools of RNA representing mock-infected and infected plants were then used for gene expression profiling using an *Arabidopsis* GeneChip®. This entire procedure was repeated three times, yielding three sets of GeneChip® data representing a total of nine independent experiments.

To identify promoter sequences that are likely to be useful for driving expression of transgenes in plants in response to pathogen attack, genes were selected whose expression level was less than 40 in all of the mock-infected samples and whose expression level was greater than 400 in all of the infected samples. The value of 40 was chosen arbitrarily as a low expression level and the value of 400 was chosen arbitrarily as a reasonably high expression level. Thirty-seven genes met these criteria and promoter sequences could be identified for 36 of them. Table 15 indicates the identifying probe set number for these 36 genes, the corresponding

Arabidopsis gene, the mean expression level of each gene in mock-infected plants, the mean expression level of each gene in infected plants, and the fold induction in expression of each gene after infection. For 11 genes, expression in mock-infected plants was undetectable, so it was not possible to calculate fold induction.

5 Therefore, the expression of genes comprising SEQ ID NOs:104-106, 119, 123, 129, 131, 151-152, 183, 191, 198, 200, 227, 249, 274, 302, 358, 415, 481, 547, 566, 582, 628, 633, 639, 656, 673, 793, 818, 827, 864, 874, 880, and 904-905 is induced in *Pseudomonas syringae* pv. *maculiola*-infected *Arabidopsis*.

10 It is possible that promoters that strongly activate gene expression in response to infection by a bacterial pathogen might be different from promoters that strongly activate gene expression in response to infection by a fungal pathogen. To test this possibility, a second GeneChip® experiment was conducted, in which wild-type *Arabidopsis* plants (ecotype Columbia) were mock-infected or infected with the fungus *Botrytis cinerea*. Samples were collected at 0, 12, 36, 60, and 84 hours after infection, RNA was purified and used for expression profiling using an *Arabidopsis* GeneChip®. To identify useful promoters, genes were selected whose expression level was less than 40 in mock-infected samples from all time points and whose expression level was greater than 400 in infected plants at 84 hours after infection. Twenty-three genes met these criteria, and promoter sequences could be identified 15 for 21 of them. These genes are described in Table 16, with their identifying probe set number, the corresponding *Arabidopsis* gene, the mean expression level of each gene in mock-infected plants, and the expression level of each gene in infected plants at various times after infection. Among these 23 genes, 11 genes were previously identified in the search for genes whose expression was strongly induced 20 by *Pseudomonas syringae* infection. These 11 genes correspond to identifying codes 12989, 13015, 13100, 13215, 13565, 14609, 16649, 16914, 19284, 19991, and 20356. Hence, the expression of genes comprising SEQ ID NOs:18, 71, 119, 123, 129, 151, 191, 244, 245, 302, 545, 547, 562, 566, 637, 653, 747, 756, 774, 793, 842, 864, and 905 is induced in *Botrytis cinerea*-infected *Arabidopsis*.

25 30 The promoter sequences for the 25 genes that were only identified in the *P. syringae* data set are shown in SEQ ID NOs:1001-1025. The promoter sequences

for the 10 genes that were only identified in the *B. cinerea* data set are listed in SEQ ID NOs:1026-1035) The promoter sequences of the 11 genes that were identified in both data sets are listed in SEQ ID NOs:1036-1046. The 11 promoter sequences that were identified in both data sets are most likely to be useful for driving

5 expression of transgenes in response to attacks by various pathogens, as these promoters are activated in response to attack by either *Pseudomonas syringae* or *Botrytis cinerea*, two very different pathogens. The other promoters may also be useful for driving expression of transgenes that are efficiently expressed in response to infection by certain types of pathogens.

10 Further, orthologs of the *Arabidopsis* promoters are also useful to drive expression of transgenes. To identify the orthologous promoter, a BLAST search for orthologous genes was conducted. To identify the ortholog, the alignments from the BLAST search are used to determine the range of nucleotides showing

15 homology to the *Arabidopsis* gene. The coding sequences shown at the beginning of each search result that contain regions corresponding to the nucleotides showing homology are likely orthologous genes. Orthologous promoter sequences may be isolated by any method known to the art, e.g., cloning of genomic DNA 5' to the ATG in orthologous genes identified in a computer assisted database search or hybridization of a probe comprising any one of SEQ ID NOs:1001-1046 to genomic

20 plant DNA.

Example 6

Genes the Expression of Which Are Altered by Viral Infection

To identify host genes that are commonly up or down regulated during local

25 RNA or DNA virus infection, gene expression profiling was employed. The host genes may include host factors that are induced by viral infection, e.g., activated host defense genes, suppressed by viral infection, e.g., suppressed host defense genes, genes involved in symptom development, as well as genes regulated by virus inducible promoters. Once the genes are identified, the function of each is then

30 determined. Reverse genetics is then employed to examine the effect of mutations on these genes during virus infection.

Experimental Procedure

Arabidopsis thaliana (Columbia-0 (Col-0)) were grown in a Conviron growth chamber to 4 weeks of age. The growth conditions were 22°C, 12 hour day length and 75% relative humidity. At least four rosette leaves of twenty plants were inoculated with one of five viruses or a mock control (120 plants total). The viruses were turnip vein clearing virus (TVCV), a tobamovirus, an oil seed rape mosaic virus (ORMV), a tobamovirus, tobacco rattle tobravirus (TRV), a tobravirus, cucumber mosaic virus strain Y (CMV-Y), a cucumovirus, and turnip mosaic virus (TuMV), a potyvirus. Each virus was diluted to approximately 0.5 to 1.0 µg/ml in 10 mM potassium phosphate buffer pH 7.2 (or 20 mM Tris-HCl pH 8.0 for the TuMV). The phosphate buffer was used as the mock infection control for the experiments. Inoculated Col-0 leaves were first dusted with carborundum then 10 µl of virus solution or phosphate buffer were pipetted onto the leaf surface. The virus solution or phosphate buffer alone were then rubbed into the leaf surface using a gloved finger, and the leaf surfaces were washed with distilled water at about 10 minutes post inoculation.

Inoculated leaf tissue was removed from each plant at 1, 2, 4 and 5 days post inoculation (dpi), weighed, snap frozen in liquid nitrogen and stored at -80°C. Total RNA was extracted from leaf tissue by the *RNAwiz* method (Ambion, Inc.) and further purified using the *RNeasy* method (Qiagen, Inc.). RNA was diluted to 1 µg/ml and labeled as a probe for Affymetrix GeneChip hybridization according to Affymetrix protocol for synthesizing labeled copy RNA (cRNA) (see Example 1). Labeled cRNA for each virus or mock treatment was hybridized to an Affymetrix GeneChip containing sequences corresponding to 8775 *Arabidopsis* genes. The hybridization data was then analyzed using Affymetrix GeneChip software.

Arabidopsis genes that were induced by at least 2-fold in all virus treatments were identified by importing the data into Microsoft Excel and then subjecting the data to selection criteria. Within each time point, the expression level of a gene exceeded 25 and the fold change was greater than 2 by comparison with the mock-infected treatment. Thus, for genes that were induced by all five viruses, the expression level exceeded 25 and the fold change was greater than 2 for all five

viruses. For genes that were repressed by at least 2-fold, the expression level of the gene must exceed 25 in the mock-infected treatment and the fold change must be less than 2 in all of the five virus treatments.

Results

5 A gene chip from Affymetrix having oligonucleotides corresponding to approximately 8,100 *Arabidopsis* genes was used with labeled cRNA obtained from plant cells infected with a selected viruses at different days post-infection (dpi). For example, for *Arabidopsis*, the RNA may be obtained from *Arabidopsis* infected with potyvirus, tobamovirus, tobnavirus, cucumovirus or geminivirus. After
10 hybridization, laser scanning is employed to detect expression levels and the data obtained is then analyzed. For genes that are induced in response to viral infection, genes that are expressed at levels greater than, for example, 2 fold over control, are selected. Alternatively, for genes that are suppressed in response to viral infection, genes that are expressed at levels lower than control are selected. The advantages of
15 a gene chip in such an analysis include a global gene expression analysis, quantitative results, a highly reproducible system, and a higher sensitivity than Northern blot analyses. Moreover, a gene chip with *Arabidopsis* DNA has a further advantage in that the *Arabidopsis* genome is well characterized.

 Data obtained from probe sets which correspond to genes upregulated or
20 downregulated in response to infection by all 5 viruses revealed forty-six genes that were downregulated and 126 that were upregulated in response to viral infection (Tables 17 and 18). Once the induced and/or suppressed genes are identified, the functions of the genes are then characterized by standard methodology.

 Therefore, the expression of genes comprising SEQ ID NOs:14, 48, 53, 98,
25 217, 226, 295, 327, 343, 352, 369, 404, 407, 418, 453, 458, 465, 472, 480, 488, 495, 507, 509, 513, 514, 559, 561, 581, 604, 607, 613, 641, 652, 672, 720, 735, 739, 743, 745, 754, 773, 803, 832, 849, 948, and 949 is downregulated after viral infection, and the expression of genes comprising SEQ ID NOs:3, 51, 54, 60, 61, 66, 75, 76, 78, 88, 95, 96, 101, 106, 108, 123, 126, 128, 129, 131, 137, 145-147, 150, 158, 169,
30 170, 172, 173, 197, 200, 216, 219, 224, 230, 233, 237, 249, 250, 263, 274, 275, 276, 299, 307, 323, 333, 342, 346, 359, 382, 383, 387, 391, 393, 401, 411, 415, 427, 442,

455, 459, 466, 477, 481, 485, 487, 502, 511, 515, 525, 534, 539, 542, 560, 571, 577, 579, 584, 587, 595, 600, 627, 638, 645, 654, 659, 668, 681, 688, 695, 696, 706, 708, 730, 742, 753, 775, 785, 786, 792, 797, 800, 801, 809, 817, 819, 820, 823, 827, 847, 856, 875, 885, 896, 902, 910, 921, 922, 923, 925, 926, 928, 946, and 952 is

5 upregulated after viral infection.

The orthologs of these *Arabidopsis* sequences to other plant genes was determined. .

A summary of the probe sets corresponding to genes, the expression of which is altered after infection of *Arabidopsis* with a pathogen is shown in Table 19.

10

Example 7

Identification of Gene Products that are Modulated upon Infection of a *Chenopodium* Cell with a Virus

Of the many disease resistance mechanisms that can be studied, the HR
15 (hypersensitive resistance) system of *Chenopodium* spp. is attractive because of the broad-spectrum virus resistance it confers. This is shown by the ability of members of the bromo-, como-, cucumo-, ilar-, alfamo-, nepo-, sobemo-, tombus-, tymo-, carla-, clostero-, hordei-, potex-, poty-, tobra- and tobamovirus groups to elicit local lesion HR on *Chenopodium* spp. (CMI/AAB Description of Plant Viruses, 1984;
20 Cooper et al., (1995)). In many instances, the HR completely blocks viral spread. However, certain viruses can break through the hypersensitive response and move from one species of *Chenopodium* to another. The ability of some viruses to infect more than one species of *Chenopodium* provides an opportunity to isolate genes that provide a cell with resistance to viral infection.

25 The genetic mechanisms of *Chenopodium* spp. HR involve a number of factors. These factors can be studied to further understand the hypersensitive response and the mechanism through which the response acts. There are some similarities between the products of *Chenopodium* spp. genes and gene products involved in common defense signaling pathways in other plants. These similarities
30 allow comparisons to be made between *Chenopodium* and these other plants. One

example includes genes that are induced upon viral infection during HR in *C. foetidum* (Visedo et al., (1990).

Additionally, some circumstantial experimental evidence suggests that *Chenopodium* HR may be somewhat similar to tobacco *N* gene HR (Whitham et al., 1994). Movement defective tobacco mosaic tobamovirus (TMV) replicates within an inoculated cell of a tobacco plant with an *N* gene, but fails to move from cell to cell (Cooper et al., 1996). Hypersensitivity is not induced, thus replication alone is not sufficient to induce HR despite the *N* gene elicitor being mapped to the replicase gene of TMV (Padgett and Beachy, 1993). Therefore, the process of virus movement may trigger hypersensitivity, which implicates intercellular signaling in this type of HR. Support for this position comes from experiments in which cell-to-cell contacts were disrupted in *N* gene tobacco which resulted in the prevention of necrotic lesion formation in infected leaves (Gulyas and Farkas, 1978). Likewise, TMV will not induce HR cell death in NN tobacco protoplasts where plasmodesmata are not intact (Otsuki et al., 1972), although HR does occur in callus cultures where plasmodesmata are intact (Beachy and Murakishi, 1971). By comparison in *C. quinoa*, movement defective brome mosaic bromovirus (BMV) replicates but fails to move from cell to cell. Initial infection is not sufficient to induce HR since local lesions do not form (Schmitz and Rao, 1996). Similarly, in *C. amaranticolor*, cucumber mosaic cucumovirus (CMV) lacking a movement protein replicates within inoculated cells, fails to move and does not elicit cell death (Canto and Palukaitis, 1999). Therefore, like TMV on *N* gene tobacco, the process of viral spread of BMV and CMV in *C. quinoa* and *C. amaranticolor* may induce HR.

Methods and Materials

Inoculation of Plants

Leaves of 10-week old *C. amaranticolor* or *C. quinoa* were inoculated with *in vitro* transcripts of TMV-MGfus (Heinlein et al., 1995), TMV virions, tobacco rattle tobavirus (TRV), or they were mock-inoculated. TMV-MGfus encodes GFP (green fluorescent protein) fused to the viral movement protein. Infectious spread can be monitored through the detection of GFP. Using an Olympus

stereomicroscope fitted with a U-ULH Olympus lamp, infected *C. amaranticolor* tissue accumulating GFP was excised at 4, 7 and 11 days after inoculation (dai).

Leaves inoculated with TRV or TMV were collected at 4 dai, at which point local lesions were forming. Mock-inoculated tissue was collected at the same time.

- 5 Tissue was frozen in liquid nitrogen and total RNA was purified from it. Three separate sets of plants were inoculated with TMV-MGfus and yielded three independent preparations of RNA.

cDNA-AFLP (complementary DNA-amplified fragment length polymorphism)

- 10 Poly-A+ RNA was isolated from TMV-MGfus infected *C. amaranticolor* using Qiagen's Oligotex mRNA purification system (Qiagen, Valencia, CA) and cDNA was generated using cDNA synthesis reagents from Life Technologies (Rockville, MD). cDNA was used to generate AFLP fragments with the AFLP reagents from Life Technologies and reactions were performed according to the manufacturer's instructions. cDNA made from one microgram of poly-A+ RNA
- 15 was digested with EcoRI and MseI and the supplied compatible linkers were ligated to the ends of the digested molecules. A few modifications were introduced. EcoRI-NN primers (GACTGCGTACCAATTCNN; SEQ ID NO:2134), rather than EcoRI-NNN, were used with the 5' fluorescent label NED (Applied Biosystems, Foster City, CA) and MseI-N and MseI-NN [GATGAGTCCTGAGTAAN(N); SEQ
- 20 ID NO:2135), rather than MseI-NNN, primers were used (Genosys, The Woodlands, TX), to reduce the complexity of the primer sets evaluated. All possible primer combinations (256 + 64) were used for PCR amplification and products were separated on polyacrylamide gels and visualized using a Genomyx SC fluorescent scanner (Beckman Coulter, Fullerton, CA). Gene fragments that appeared to be
- 25 upregulated in infected tissues compared to mock-inoculated tissues were tested to see if they were also upregulated by the same primers from a second preparation of cDNA from RNA from a second set of infected plants. Gene fragments that were upregulated in both RNA preparations were excised from the gel, eluted from the gel in water and reamplified by PCR using the appropriate MseI and EcoRI primers
- 30 and sequenced with 377 ABI sequencers (Applied Biosystems) using dideoxysequencing methods.

Quantitative RT-PCR

DNase treated total RNA (2 ng per reaction) from the third independent preparation of TMV-MGfus infected *C. amaranticolor*, the first preparation of TRV infected *C. amaranticolor*, or the first preparation of TMV *C. quinoa*, was used with
5 TaqMan One-Step RT-PCR reagents for quantitative analysis in an ABI 7700 (Applied Biosystems). Reactions were performed according to the manufacturer's instructions. Primers and 6-FAM 5' end-labeled probes (6-carboxyfluorescein, Applied Biosystems or Genosys) were designed from the sequences from the *C. amaranticolor* upregulated gene fragments using Primer Express software (Applied
10 Biosystems) and are listed in SEQ ID Nos:954-1000 and 2130-2135. Expression levels were interpolated from standard curves with a correlation coefficient of 0.99 or greater and the quantities were normalized to the expression level of actin in each sample.

Results

15 The interaction of the elicitor and the R gene product establishes a cascade of reactions and signaling events that is then manifested in a phenotypic HR. In essence, HR is the end result of disease activated signaling events. In order to detect the early expression of genes induced by viral infection, it was necessary to isolate infected tissue before the onset of local lesion formation. Therefore, *C.*
20 *amaranticolor* was infected with RNA transcripts of TMV-MGfus that express GFP (green fluorescent protein) in infected cells. This allowed the spread of viral infection to be monitored over time. Infection foci comprising over 100 cells could be detected at 4 dai and foci of more than 500 cells could be detected at 7 dai. There was no visible appearances of cell death or chlorotic local lesion formation at the
25 infection foci at 4 and 7 dai. By 11 dai, the infection foci were associated with chlorotic local lesions. Virus infected tissue was excised from leaves at each time point and RNA was purified from the tissue and used for cDNA-AFLP as previously described.

cDNA-AFLP fragments were separated on polyacrylamide sequencing gels
30 and imaged with a fluorescent scanner. Samples derived from mock-inoculated tissue at 7 dai were run next to samples derived from TMV-MGfus infected tissue at

7 dai for comparison. Ninety-eight bands having intensity in the TMV-MGfus lanes that was greater than that of analogous bands in the mock lanes were easily detected. Thirty out of the 98 bands were also upregulated in an independent set of experiments designed to reduce biological variation between experiments. These
5 bands were excised from the gel, reamplified, and sequenced.

The hypothetical protein sequences derived from the reamplified fragments (Seq ID NOs: 1954-1966) translated from all six reading frames were compared to sequences in the GenBank protein sequence database. The results of the BLASTX search (Altschul et al., 1997) are summarized in Table 20a. To confirm that the
10 expression levels of DESCA genes were upregulated in infected tissue compared to mock inoculated tissue, the relative amount of DESCA and actin transcript in a third independent set of samples at 4 dai, 7dai, and 11 dai was quantitatively measured (Table 20b).

The expression level of DESCA1 increased the most in the TMV-MGfus
15 infected plants. The expression level of DESCA1 increased 200 times by 4 dai but tapered off drastically by 11 dai. DESCA1 is unrelated to any protein known at this time.

Two sequences, DESCA4 and DESCA10, are both related to pumps found in *Arabidopsis* and yeast (Sanchez-Fernandez et al., 1998; Smart and Fleming, 1996).
20 DESCA4 is expressed highly at 4 dai but the expression drops off over time whereas DESCA10 is only moderately induced and its expression returns to normal by the time of the visible appearance of local lesions in *C. amaranticolor*.

DESCA7 is similar to a salicylate-induced glucosyltransferase gene in tobacco (Horvath and Chua, 1996). DESCA9 is similar to cytochrome P450-like
25 proteins which can produce cytotoxic compounds including phytoalexins that are deployed by a plant to defend against invading microbes. DESCA12 is related to a proanthranilate benzoyltransferase from carnation that plays a direct role in the phytoalexin biosynthesis in carnation (Yang et al., 1998). DESCA11 is similar to the tryptophan biosynthetic enzyme phosphoribosylanthranilate transferase whose
30 gene expression is induced in the presence of ozone in *Arabidopsis* (Conklin and Last, 1995).

DESCA3 is similar to endo-1,4-betaglucanases that have a role in fruit ripening, abscission, and cell elongation (Lashbrook et al., 1994). DESCA3 is highly expressed in the infected *C. amaranticolor* and remains highly expressed during the appearance of local lesions and necrosis.

Many disease responses are mediated by positive regulators such as transcription factors or kinases that initiate signaling cascades for the activation of defense responses. One gene, DESCA5, is loosely similar to a yeast potential transcriptional regulator. DESCA5 expression is twice as high at the early stages of infection compared to the late stages of infection illustrating an important role played by gene regulation at the early stages of infection. DESCA6 is related to kinases of *Arabidopsis*. Kinases have essential roles in programmed cell death during viral infection (Dunigan and Madlener, 1995). DESCA2 is the most highly expressed of the group suggesting that it is an important regulator at the onset of infection. It is similar to a receptor-like protein kinase in bean that responds to *Fusarium solani* attack (Lange et al., 1999).

Some R genes have kinase-like regions that may function in initiating a signal cascade during the onset of HR (Song et al.; 1995, Zhou et al., 1997). Global amino acid sequence alignment (Henikoff and Henikoff, 1992) of DESCA2 with Pto or Xa21, R genes with ser/thr kinase domains, reveals a 37% similarity. DESCA8 has a nucleotide binding site and a leucine-rich repeat that is common for many R genes. (Meyers et al., 1999; Leister et al., 1998).

To link DESCA genes to a multivirus resistance pathway, *C. amaranticolor* was inoculated with TRV (tobacco rattle virus), a virus that is taxonomically distinct from TMV. Local lesions appeared by 4 dai and RNA was purified from the infected leaves. DESCA gene expression levels in infected tissue were compared to mock inoculated tissue by quantitative RT-PCR and revealed that the same DESCA genes upregulated during a TMV infection are also upregulated during a TRV infection (Table 20b).

The gene expression levels in TMV infected *C. quinoa* were measured using the same *C. amaranticolor*-derived primers in quantitative PCR to determine if DESCA genes were up-regulated during HR in another *Chenopodium* species. Most

of the DESCA genes were upregulated in *C. quinoa* and were expressed at levels many times higher than in *C. amaranticolor* (Table 20b). This may be a result of the infection of *C. quinoa* with the aggressive wild-type virus rather than slower moving TMV-MGfus.

5 The experimental procedure presented here can detect any similar gene involved in the aforementioned signaling pathways such as SA signaling. Except for DESCA1, whose expression is increased the most at 200+ fold, many of the fragments have homology to other genes that have been placed in disease resistance pathways in other plants. DESCA12 and DESCA9 are respectively similar to
10 hypersensitivity related gene 201, possibly a proanthranilate benzoyltransferase, and p450 monooxygenases, both which are expressed during the hypersensitive response in tobacco upon infection with *Pseudomonas solanacearum* but are not regulated by SA (Czernic et al., 1996). DESCA7 is similar to a salicylate-induced glucosyltransferase gene in tobacco (Horvath and Chua, 1996). Thus, the disease
15 resistance response in *C. amaranticolor* involves pathways both dependent and independent of SA signaling.

 The surprising discovery of DESCA4, DESCA7, DESCA9, DESCA10, and DESCA12, reveal the underpinnings of an endogenous detoxification system. Briefly, the activation phase involves cytochrome P450 monooxygenases
20 introducing functional groups (e.g. aromatic rings) to potential toxins. The conjugation phase in plants involves the linking of glutathione or glucose to the toxin at which point the conjugated molecule can be recognized by an ATP-binding cassette transporter and pumped into the vacuole, or possibly the neighboring cells, during the elimination phase. The final phase includes either storage or breakdown
25 of such molecules. DESCA9, similar to cytochrome P450, and DESCA12, similar to a gene associated with the production of phytoalexin, may produce potential toxins. In fact, *C. amaranticolor* produces many such compounds that are antiviral to TMV. DESCA7, similar to a glucosyltransferase, may conjugate such toxins to be transported by the ABC-transporters encoded by DESCA4 or DESCA10. In this
30 particular case, the transported compound could then be deployed by the infected plant cell as an antiviral agent or cytotoxic compound, stored by noninfected cells in

anticipation of infection, or eliminated by noninfected cells neighboring infected cells. Since all of these genes are induced by TMV and TRV in *C. amaranticolor*, their induced expressions are a result of a specific or general multivirus or disease resistance pathway.

5 Possessing the R genes that allow *C. amaranticolor* to initially recognize multiple viruses provides an opportunity to use these genes, and the regulatory elements associated with these genes, to transfer viral resistance to other plants. In addition, possession of genes that produce and transport antiviral and cytotoxic products allows for the transfer of viral resistance through a mechanism involving
10 induced cell death upon viral infection.

 Two genes that may be used for early recognition of viral infection are DESCA8 and DESCA2, as these genes may act as signaling components to initiate the resistance cascade. DESCA8 has a nucleotide binding site and a leucine-rich repeat that is common for many R genes and that can be found in other plants
15 (Meyers et al., 1999; Leister et al., 1998). DESCA2 is induced in both *Chenopodium* species and is similar to other R genes, Xa21 and Pto, which have similar ser/thr kinase domains.

 Resistance to viral spread may be transferred between *Chenopodium* spp. For example, BMV (brome mosaic virus) induces local lesions in the green variety of *C.*
20 *hybridum*, however lesion formation does not limit the systemic spread of the virus (Verduin, 1978). The systematic spread of the BMV virus may be restricted in the green variety of *C. hybridum* by transformation with a gene from the purple variety that does limit spread (Komari, 1990). Thus, genes that confer viral resistance may be used for complementation, reverse genetics, overexpression, and gene silencing.
25 Furthermore, as indicated by the functionality of the R genes N and Pto after being transferred into heterologous species, (Whitham et al., 1996; Rommens et al., 1995), the *Chenopodium* genes may function to initiate hypersensitivity in crops, *Arabidopsis* or other useful plants.

Example 8

Other Plant-Pathogen Interactions

The methods set out hereinabove can be used for any type of comparable resistance interaction. For example any of the following plant/pathogen interactions will be produced as compatible and incompatible interactions. The RNA from such an interaction is isolated and subject to a protocol such as one outlined in Example 1, e.g., using a Genechip with a specific plant's genes or microarray, differential display PCR or cDNA-ALFP (Example 7). A four-way analysis is performed and genes which are expressed differently are identified. The plant/pathogen interactions in Table 21 are well known in the art. However, any type of plant/pathogen interaction that involves this type of resistance can be used.

Table 21

Plant	Pathogen
Tomato	Cladosporium fulvum
Maize	Rust fungus
Antirrhinium	Rust fungus
Flax	<i>Melampsora lini</i>
Lettuce	Downy mildew
Arabidopsis	<i>Peronospora parasitica</i>
Tomato	Nematode
Corn	<i>Cochliobolus carbonum</i>
Tomato	<i>Pseudomonas syringae</i>
Rice	<i>Xanthomonas oryzae</i> pv. <i>Oryzae</i>
Rice	<i>Pyricularia oryzae</i>
Tobacco	Tobacco Mosaic Virus

15

Genes that are upregulated and cause resistance in a wide variety of plants are particularly useful in methods which upregulate or overexpress the gene. One method is to add an exogenous copy, thus providing more of the gene product or allowing for a different induction from that used by the plant. Alternatively, the endogenous gene can be upregulated using a known inducer or using artificial

20

methods such as using an artificial induction signal in the endogenous promoter. Examples of the two methods are provided in Examples 9 and 10.

Accordingly, embodiments of the invention provide the sequences disclosed herein, which sequences can be used in genetic engineering of crops, as probes and markers to study the dynamics of plant/pathogen interactions, and as markers in marker-assisted breeding protocols to identify plants carrying particularly useful combinations of genes associated with pathogen resistance, as well as in plant defense.

10

Example 9

Transformation of Resistance Genes into Plants

To produce resistant plants, resistance genes such as those identified herein can be introduced into plant cells to generate transgenic plants having enhanced resistance. While HSF4 is any preferred gene for this embodiment of the invention, the invention can be employed with other genes, alone or in combination, whose regulation is strongly responsive to plant/pathogen interactions, such as the genes identified herein. Since some genes are strongly induced and others are strongly repressed in plant/pathogen interactions, and since some genes that are strongly induced in one ecotype can be strongly repressed in another, the invention contemplates use of any of the genes and sequences, or fragments thereof, disclosed herein, in a construct adapted to cause overexpression, repression, or knock out, of the genes in a transgenic plant.

Transgenic downregulation of genes associated with pathogen resistance can have several useful applications. In one embodiment, transgenic downregulation of genes that are strongly repressed in resistance interactions can enhance resistance. Such transgenic downregulation can employ the genes disclosed herein, or fragments thereof, in an antisense orientation to interfere with accumulation of the products of those genes. Likewise, any other methodology capable of lowering expression of such genes is also included within these embodiments of the invention.

Plant transformation can be carried out by conventional means, and can include *Agrobacterium*-mediated transformation, electroporation, particle acceleration, abrasion, and any other useful means leading to expression of a transgene in a plant of interest. Transformed plant cell are then used to regenerate one or more plants in tissue culture. Subsequent generations of transgenic plants can be used directly or bred with other lines to generate plants having enhanced pathogen resistance.

Example 10

Upregulation of Resistance Genes in Crops

Because many or most *Arabidopsis* genes have orthologs in other plants, the genes and sequences disclosed herein are generally useful in constructs to be up-regulated and cause resistance in a wide variety of plants. As examples, the heat shock proteins, and particularly HSF4, are found throughout the plant kingdom. For many such regulatory and responsive genes it is well known that there exist substances that can induce expression. Chemicals such as dexamethasone have been found to induce mammalian HSF proteins. Likewise, a chemical induction of key plant defense genes can be chemically induced. High throughput screening for chemical inducers of the plant HSF4 or other resistance gene is performed.

Potentially useful substances are then tested on crop plants and eventually used as a soil additive or sprayed onto plants when needed to induce resistance. Accordingly, embodiments of the invention usefully employ the genes disclosed herein, or fragments thereof, for screening to identify useful chemical inducers and/or repressors of gene responsive to pathogenic infections.

Example 11

Identification of Inducers and Repressors of Resistance Genes

The yeast two-hybrid method and many methods which use its basic idea, provide a technique to identify proteins which interact with a protein of interest.

The method relies on the fact that a protein contains domains which can be separated. Thus the protein of interest is fused to the GAL4 DNA binding region of

a known protein. The GAL4 (or another) activation signal is fused in a library to produce a library of fused proteins. If one of the proteins from the library interacts with the protein of interest the protein binds and a signal protein is produced, such as luciferase. There are a number of such systems presently, some of which can be
5 used in mammalian cells, allowing for correct processing and folding of certain proteins and others which allow the interaction to occur in the cytoplasm allowing for the identification of other types of proteins.

cDNA from HSF4 and any other protein of interest is cloned in fusion to the yeast GAL4 DNA binding domain on a vector. A library containing cDNA from
10 Arabidopsis is fused to the GAL4 or an activation domain of choice. Expression of luciferase correlates with identification of an interacting protein. This protein is then analyzed as to its action as an inducer or repressor.

Example 12

Determination of the Minimal Promoter Fragment

The full-length promoter sequence as given in SEQ ID Nos: 1001-1095,
5 2137-2661 and 4738-6813, or the promoter orthologs thereof is fused to the β -
glucuronidase (GUS) gene at the native ATG to obtain a chimeric gene cloned into
plasmid DNA. The plasmid DNA is then digested with restriction enzymes to
release a fragment comprising the full-length promoter sequence and the GUS gene,
which is then used to construct the binary vector. This binary vector is transformed
10 into *Agrobacterium tumefaciens*, which is in turn used to transform *Arabidopsis*
plants (for further details of the binary vector construction see above Example 9).

The above plasmid can also be used to form a series of 5' end deletion
mutants having increasingly shorter promoter fragments fused to the GUS gene at
the native ATG. Various restriction enzymes are used to digest the plasmid DNA to
15 obtain the binary vectors with different lengths of promoter fragments. In particular,
a binary vector 1 is constructed with a 1,900-bp long promoter fragment; a binary
vector 2 is constructed with a 1,300-bp long promoter fragment; a binary vector 3 is
constructed with a 1000-bp long promoter fragment; a binary vector 4 is constructed
with a 800-bp long promoter fragment; a binary vector 5 is constructed with a 700-
20 bp long promoter fragment; a binary vector 6 is constructed with a 600-bp long
promoter fragment; a binary vector 6 is constructed with a 500-bp long promoter
fragment; and a binary vector 7 is constructed with a 100-bp long promoter
fragment. Like the binary vector comprising the full-length promoter fragment,
these 5' end deletion mutants are also transformed into *Agrobacterium tumefaciens*
25 and, in turn, *Arabidopsis* plants (for further details of *Arabidopsis* transformation
and promoter assay procedures see Example 5 above) .

The presence of the correct hybrid construct in the transgenic lines is
confirmed by PCR amplification.

By using the above protocol it can be determined, which portion of the
30 promoter sequences given in SEQ ID Nos: 1001-1095, 2137-2661 and 4738-6813,
or the promoter orthologs thereof is required for gene expression.

Minimal promoter fragments having lengths substantially less than the full-length promoter can therefore be operatively linked to coding sequences to form smaller constructs than can be formed using the full-length promoter. As noted earlier, shorter DNA fragments are often more amenable to manipulation than longer fragments. The chimeric gene constructs thus formed can then be transformed into hosts such as crop plants to enable at-will regulation of coding sequences in the hosts.

Example 13

Determination of Promoter Motifs

While a deletion analysis characterizes regions in a promoter that are required overall for its regulation, linker-scanning mutagenesis allows for the identification of short defined motifs whose mutation alters the promoter activity. Accordingly, a set of linker-scanning mutant promoters fused to the coding sequence of the GUS reporter gene are constructed. Each of them contains a 8-10-bp mutation located between defined positions and included in a promoter fragment as given in SEQ ID Nos: 1001-1095, 2137-2661 and 4738-6813, or the promoter orthologs thereof.

Each construct is transformed into *Arabidopsis* and GUS activity is assayed for 19 to 30 independent transgenic lines. The presence of the correct hybrid construct in transgenic lines is confirmed by PCR amplification of all lines containing the mutant constructs and by random sampling of lines containing the other constructs. Amplified fragments are digested with restriction enzyme (e.g. XbaI) and separated on high resolution agarose gels to distinguish between the different mutant constructs. The effect of each mutation on promoter activity is compared to an equivalent number of transgenic lines containing the unmutated construct. Two repetitions resulting from independent plating of seeds are carried out in every case.

The sequences mutated in the linker-scanning constructs, in particular those that showed marked differences from the control construct, are then examined more closely.

5

Example 14

Identifying Orthologs

Orthologs were identified through use of BLAST and SCAN software with some additional filters. For the Arabidopsis search, a BLAST database was created that was a subset of GenBank ver 123.0 (released April 15, 2001) that contained all
10 of the plant translated regions excluding Arabidopsis thaliana sequences. The subset was created with PERL script. A BLAST search with all of the peptide sequences was performed against the GenBank subset. Each query was executed using the "blastall" command with the parameters " -p blastp", "-v 50", "-b 50", "-F F". The BLAST search results were then processed with SCAN (Sequence Comparison
15 Analysis program, version 1.0k, Los Alamos National Laboratories) using default settings and the orthologs were identified following implementation of an E-value cutoff of $\leq 1e-4$. The candidate orthologs were further filtered by comparing words in the description to the text of the annotation fields: product, function and note. The sequence was considered to have the same or similar function if any of the words
20 matched. Words excluded from the filter included: the, like, protein, related, unknown, subunit, hypothetical, and, putative, precursor, clone, homolog, small, beta, class, dna, rna, alpha, gamma, has, not, been, from, to, by, long, type and induced.

For the rice search, amino acid sequences were used that resulted from
25 FGENESH (version 1.C) gene prediction results. The peptide sequences were obtained from gene predictions and formatted into a BLAST database. A BLASTP comparison was then performed against the Arabidopsis sequences. The BLASTP results were then filtered through use of SCAN with the following parameters: "-a 60 60" with an E-value cutoff of $1e-4$. This produced orthologs having 60 or more
30 identities and where 60% of the alignments were made up of identities.

The following pages compile Tables 3 to 20 referred to in the Examples above.

TABLE 3 TO 20

Table 3 Probe Sets corresponding to genes, the expression of which is increased after infection of wild-type *Arabidopsis* with *Pseudomonas syringae*

ProbeSet	Description	Blast Score	EC #	Family
11997_at (AC005967.4_AT)	gb AAD03372.1 (AC005967) unknown protein [Arabidopsis thaliana]	0		
12002_at (AF069442.47_AT)	gb AAC79112.1 (AF069442) hypothetical protein [Arabidopsis thaliana]	0		
12004_at (AL022023.132_AT)	emb CAA17771.1 (AL022023) putative protein [Arabidopsis thaliana]	8E-86		
12007_at (Z99708.249_AT)	emb CAB16829.1 (Z99708) putative protein [Arabidopsis thaliana]	1E-168		
12037_at (AC004005.174_AT)	gb AAC23417.1 (AC004005) unknown protein [Arabidopsis thaliana]	0		
12051_at (AL021889.94_AT)	emb CAA17133.1 (AL021889) putative protein [Arabidopsis thaliana]	1E-143		
12062_at (AC006069.147_AT)	gb AAD12706.1 (AC006069) unknown protein [Arabidopsis thaliana]	0		
12068_at (AF118223.24_AT)	gb AAD03449.1 (AF118223) contains similarity to Methanobacterium thermoautotrophicum transcriptional regulator (GB:AE000850) [Arabidopsis thaliana]	1E-162		
12072_at (AL035396.4_AT)	emb CAA23058.1 (AL035396) putative protein [Arabidopsis thaliana]	1E-158		
12079_s_at (A71597.1_S_AT)	emb CAB42594.1 (A71597) unnamed protein product [Arabidopsis thaliana]	5E-64		
12081_at (AC001645.140_AT)	gb AAB63644.1 (AC001645) unknown protein [Arabidopsis thaliana]	1E-117		

ProbeSet	Description	Blast Score	EC #	Family
12092_at (AC004793.13_AT)	gb AAD21694.1 (AC004793) ESTs gb T20423, gb AA712864, gb H76323 and gb Z25560 come from this gene. [Arabidopsis thaliana]	1E-150		
12115_at (AL033545.26_AT)	emb CAA22152.1 (AL033545) extensin-like protein [Arabidopsis thaliana]	1E-87		
12136_at (AC007591.60_AT)	gb AAD39663.1 AC007591_2 8 (AC007591) ESTs gb R65145, gb N96612 and gb R90096 come from this gene. [Arabidopsis thaliana]	1E-60		
12150_at (AC004005.151_AT)	gb AAC23415.1 (AC004005) unknown protein [Arabidopsis thaliana]	5E-32		
12187_at (AC005489.31_AT)	gb AAD32893.1 AC005489_3 1 (AC005489) F14N23.31 [Arabidopsis thaliana]	0		
12198_at (AC006954.90_AT)	gb AAD23890.1 AC006954_1 1 (AC006954) unknown protein [Arabidopsis thaliana]	1E-70		
12203_at (AL021710.268_AT)	emb CAA16738.1 (AL021710) hypothetical protein [Arabidopsis thaliana]	7E-55		
12216_at (AC007119.56_AT)	gb AAD23641.1 AC007119_7 (AC007119) unknown protein [Arabidopsis thaliana]	8E-55		
12217_at (AJ223804.1_AT)	gb AAF34796.1 AF228640_1 (AF228640) lipoamide dehydrogenase precursor [Arabidopsis thaliana]	0		
12227_at (AC007576.18_AT)	gb AAD39285.1 AC007576_8 (AC007576) Unknown protein [Arabidopsis thaliana]	1E-102		
12233_at (AJ001807.1_AT)	emb CAA05023.1 (AJ001807) succinyl-CoA- ligase alpha subunit [Arabidopsis thaliana]	0	EC_6.2.1.5	synthetase
12278_at (AJ011674.2_AT)	emb CAA09731.1 (AJ011674) receptor-like protein kinase, RLK3 [Arabidopsis thaliana]	0		kinase

ProbeSet	Description	Blast Score	EC #	Family
12307_at (AC002392.162_AT)	gb AAD12037.1 (AC002392) putative receptor-like protein kinase [Arabidopsis thaliana]	0		kinase
12314_at (AC001229.28_AT)	gb AAB60922.1 (AC001229) F5I14.14 [Arabidopsis thaliana]	0		
12317_at (AC004138.27_AT)	gb AAC32907.1 (AC004138) putative sucrose-proton symporter [Arabidopsis thaliana]	0		
12323_at (AC002333.18_AT)	gb AAB64019.1 (AC002333) putative polygalacturonase [Arabidopsis thaliana]	0		Polygalactur onase
12332_s_at (AB023448.2_S_AT)	dbj BAA82810.1 (AB023448) basic endochitinase [Arabidopsis thaliana]	0		
12341_s_at (AL021637.176_S_A T)	emb CAA16619.1 (AL021637) vacuolar sorting receptor-like protein [Arabidopsis thaliana]	0		
12347_at (AC007258.28_AT)	gb AAD39325.1 AC007258_1 4 (AC007258) Putative ATPase [Arabidopsis thaliana]	0	EC_3.6.1.-	ATPase
12349_s_at (X84728.6_S_AT)	gb AAA17993.1 (M91192) phenylalanine ammonia-lyase [Trifolium subterraneum]	0		
12369_at (AC002535.59_AT)	gb AAC62871.1 (AC002535) putative Na ⁺ /Ca ²⁺ antiporter [Arabidopsis thaliana]	0		
12400_at (X98453.1_AT)	emb CAA67092.1 (X98453) peroxidase [Arabidopsis thaliana]	0		peroxidase
12438_at (AL021710.83_AT)	emb CAA16723.1 (AL021710) membrane-bound small GTP-binding - like protein [Arabidopsis thaliana]	1E-122		
12449_s_at (AC002343.179_S_A T)	gb AAB63623.1 (AC002343) cellulose synthase isolog [Arabidopsis thaliana]	0		
12454_at (AC006232.164_AT)	gb AAD15602.1 (AC006232) putative ferredoxin [Arabidopsis thaliana]	5E-85		

ProbeSet	Description	Blast Score	EC #	Family
12475_at (Y11794.1_AT)	emb CAA72490.1 (Y11794) peroxidase ATP29a [Arabidopsis thaliana]	3E-67		peroxidase
12487_at (AC004411.126_AT)	gb AAC34225.1 (AC004411) putative ABC transporter [Arabidopsis thaliana]	0		
12497_at (AC006533.51_AT)	gb AAD32284.1 AC006533_8 (AC006533) putative receptor- like protein kinase [Arabidopsis thaliana]	0		
12500_s_at (AF081067.3_S_AT)	gb AAC32192.1 (AF081067) IAA-Ala hydrolase; IAA- amino acid hydrolase [Arabidopsis thaliana]	0		
12521_at (AF049236.28_AT)	gb AAC14413.1 (AF049236) unknown [Arabidopsis thaliana]	0		
12525_at (AC006587.85_AT)	gb AAD21486.1 (AC006587) putative DOF zinc finger protein [Arabidopsis thaliana]	1E-132		
12530_at (Z99707.184_AT)	emb CAB16760.1 (Z99707) hydroxynitrile lyase like protein [Arabidopsis thaliana]	1E-150		LYASE
12535_at (AL035538.156_AT)	emb CAB37540.1 (AL035538) putative protein [Arabidopsis thaliana]	1E-132		
12538_at (AF033205.2_AT)	gb AAC02973.1 (AF033205) putative pectin methylesterase [Arabidopsis thaliana]	6E-38		methyl- esterase
12571_s_at (AF149413.18_S_AT)	gb AAD40138.1 AF149413_1 9 (AF149413) Arabidopsis thaliana ferrochelataase-I (SW:P42043); Pfam	0		
12574_at (X82624.2_AT)	emb CAA57944.1 (X82624) SRG2At [Arabidopsis thaliana]	1E-25		
12584_at (AC004521.233_AT)	gb AAC16096.1 (AC004521) similar to axi 1 protein from Nicotiana tabacum [Arabidopsis thaliana]	0		
12626_at (AC006234.95_AT)	gb AAD20931.1 (AC006234) putative diacylglycerol kinase [Arabidopsis thaliana]	0		kinase

ProbeSet	Description	Blast Score	EC #	Family
12642_at (AC006920.138_AT)	gb AAD22285.1 AC006920_9 (AC006920) unknown protein [Arabidopsis thaliana]	0		
12645_at (AL021712.56_AT)	emb CAA16774.1 (AL021712) fibrillin precursor-like protein [Arabidopsis thaliana]	1E-150		
12698_at (AC000106.42_AT)	gb AAB70413.1 (AC000106) Similar to Beta integral membrane protein (gb U43629). EST gb W43122 comes from this gene. [Arabidopsis thaliana]	0		
12712_f_at (Z95774_F_AT)	emb CAB09206.1 (Z95774) R2R3-MYB transcription factor [Arabidopsis thaliana]	6E-21		
12736_f_at (Z97048_F_AT)	emb CAA90748.1 (Z50869) MYB-related protein [Arabidopsis thaliana]	4E-21		
12744_at (AC001645.15_AT)	gb AAB63630.1 (AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]	0		
12760_g_at (AC005278.32_G_AT)	gb AAC72120.1 (AC005278) Strong similarity to gb D14550 extracellular dermal glycoprotein (EDGP) precursor from Daucus carota. ESTs gb 84105 and gb AI100071 come from this gene. [Arabidopsis thaliana]	0		
12764_f_at (AC004138.69_F_AT)	gb AAC32912.1 (AC004138) putative glutathione S- transferase [Arabidopsis thaliana]	1E-111		

ProbeSet	Description	Blast Score	EC #	Family
12772_at (AC005278.34_AT)	gb AAC72119.1 (AC005278) Strong similarity to gb D14550 extracellular dermal glycoprotein (EDGP) precursor from Daucus carota. ESTs gb H37281, gb T44167, gb T21813, gb N38437, gb Z26470, gb R65072, gb N76373, gb F15470, gb Z35182, gb H76373, gb Z34678 a	0		
12776_at (AL021811.156_AT)	emb CAA16969.1 (AL021811) putative protein [Arabidopsis thaliana]	0		
12797_s_at (AC007138.25_S_AT)	gb AAD22647.1 AC007138_1 1 (AC007138) S- adenosylmethionine synthase 2 [Arabidopsis thaliana]	0		
12802_at (AL022373.153_AT)	emb CAA18498.1 (AL022373) DnaJ-like protein [Arabidopsis thaliana]	2E-74		
12851_s_at (ACCSYN1_S_AT)	emb CAA78260.1 (Z12614) 1-aminocyclopropane 1- carboxylate synthase [Arabidopsis thaliana]	3E-29		
12879_s_at (AIG1_S_AT)	gb AAC49282.1 (U40856) AIG1 [Arabidopsis thaliana]	1E-150		
12880_s_at (AIG2_S_AT)	gb AAC49283.1 (U40857) AIG2 [Arabidopsis thaliana]	3E-97		
12883_s_at (APX_S_AT)	emb CAA67425.1 (X98925) stromal ascorbate peroxidase [Arabidopsis thaliana]	1E-161		
12889_s_at (ASA1_S_AT)	gb AAA32738.1 (M92353) anthranilate synthase alpha subunit [Arabidopsis thaliana]	0		
12891_at (ATACS6_AT)	gb AAC63850.1 (U73786) ACC synthase [Arabidopsis thaliana]	0		synthase
12892_g_at (ATACS6_G_AT)	gb AAC63850.1 (U73786) ACC synthase [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
12904_s_at (ATERF1_S_AT)	dbj BAA32418.1 (AB008103) ethylene responsive element binding factor 1 [Arabidopsis thaliana]	1E-126		
12905_s_at (ATERF2_S_AT)	dbj BAA32419.1 (AB008104) ethylene responsive element binding factor 2 [Arabidopsis thaliana]	1E-112		
12911_s_at (ATG6PDHE5_S_AT)	emb CAA59011.1 (X84229) glucose-6-phosphate 1- dehydrogenase [Arabidopsis thaliana]	0		
12921_s_at (ATHHMGCOAR_S _AT)	emb CAA33139.1 (X15032) hydroxy methylglutaryl CoA reductase (AA 1-592)	0		
12930_s_at (ATLLS1_S_AT)	gb AAC49679.1 (U77347) lethal leaf-spot 1 homolog [Arabidopsis thaliana]	0		
12951_at (AC005489.5_AT)	gb AAD32867.1 AC005489_5 (AC005489) F14N23.5 [Arabidopsis thaliana]	0		
12958_at (AC002332.249_AT)	gb AAB80675.1 (AC002332) putative protein kinase [Arabidopsis thaliana]	0		kinase
12965_at (AL021711.118_AT)	emb CAA16752.1 (AL021711) protein kinase- like protein [Arabidopsis thaliana]	0		kinase
12966_s_at (AL023094.197_S_A T)	emb CAA18838.1 (AL023094) bZIP transcription factor ATB2 [Arabidopsis thaliana]	2E-67		
12989_s_at (AC004077.149_S_A T)	gb AAC26690.1 (AC004077) putative cytochrome P450 [Arabidopsis thaliana]	0		
13003_s_at (AB021936.1_S_AT)	dbj BAA74591.1 (AB021936) nicotianamine synthase [Arabidopsis thaliana]	0		
13005_at (AC004683.61_AT)	gb AAC28763.1 (AC004683) unknown protein [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
13014_at (U93215.87_AT)	gb AAB63082.1 (U93215) putative lipase [Arabidopsis thaliana]	0		lipase
13015_s_at (X98673.2_S_AT)	emb CAA67232.1 (X98674) zinc finger protein [Arabidopsis thaliana]	7E-90		
13025_at (AL050400.20_AT)	emb CAB43695.1 (AL050400) putative protein [Arabidopsis thaliana]	0		
13040_at (AC002392.134_AT)	gb AAD12039.1 (AC002392) unknown protein [Arabidopsis thaliana]	0		
13070_at (AC006919.171_AT)	gb AAD24640.1 AC006919_2 0 (AC006919) putative pyruvate kinase [Arabidopsis thaliana]	0		kinase
13094_at (AL035523.163_AT)	emb CAB36745.1 (AL035523) putative protein [Arabidopsis thaliana]	1E-172		
13100_at (AC003680.50_AT)	gb AAC06158.1 (AC003680) putative cytochrome P450 [Arabidopsis thaliana]	0		mono- oxygenase
13110_at (AF074021.34_AT)	gb AAD29776.1 AF074021_8 (AF074021) putative symbiosis-related protein [Arabidopsis thaliana]	1E-65		
13115_at (AC000375.44_AT)	gb AAB60774.1 (AC000375) ESTs gb U75592,gb T13956,gb T43 869 come from from this gene. [Arabidopsis thaliana]	0		
13119_at (AC007260.23_AT)	gb AAD30579.1 AC007260_1 0 (AC007260) Similar to dTDP-D-glucose 4,6- dehydratase [Arabidopsis thaliana]	0	EC_4.2.1.46	dehydratase
13128_at (AL049607.47_AT)	emb CAB40756.1 (AL049607) protein phosphatase 2C-like protein [Arabidopsis thaliana]	0		
13134_s_at (AC002337.9_S_AT)	gb AAB63818.1 (AC002337) putative galactinol synthase [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
13137_at (AC007169.86_AT)	gb AAD26480.1 AC007169_1 2 (AC007169) putative fructokinase [Arabidopsis thaliana]	0		fructokinase
13152_s_at (AC005322.24_S_AT)	gb AAC97998.1 (AC005322) Identical to 1- aminocyclopropane-1- carboxylate oxidase (ACC oxidase) gb X66719 (EAT1). ESTs gb T43073, gb T5714, gb R90435, gb R44023, gb AA597926, gb AI099676, gb AA650810 and gb 29725 come from this gene. [Arabidopsis thaliana]	1E-177		
13154_s_at (AC002333.210_S_A T)	gb AAB64047.1 (AC002333) putative endochitinase [Arabidopsis thaliana]	1E-148		
13157_at (AC002409.35_AT)	gb AAB86449.1 (AC002409) putative cytochrome P450 [Arabidopsis thaliana]	0		
13163_s_at (AC005560.223_S_A T)	gb AAD12692.2 (AC006069) unknown protein [Arabidopsis thaliana]	0		
13176_at (AL031394.56_AT)	emb CAA20567.1 (AL031394) putative protein [Arabidopsis thaliana]	0		
13177_at (AL049640.42_AT)	emb CAB40989.1 (AL049640) growth factor like protein [Arabidopsis thaliana]	1E-164		
13187_i_at (ATTHIREDA4_I_AT)	gb AAC49356.1 (U35829) thioredoxin h [Arabidopsis thaliana]	2E-63		
13188_r_at (ATTHIREDA4_R_AT)	gb AAC49356.1 (U35829) thioredoxin h [Arabidopsis thaliana]	2E-63		
13189_s_at (ATTHIREDA4_S_AT)	gb AAC49356.1 (U35829) thioredoxin h [Arabidopsis thaliana]	2E-63		
13190_s_at (ATTHIREDA4_S_A T)	emb CAA80655.1 (Z23108) NADPH thioredoxin reductase [Arabidopsis thaliana]	1E-174		

ProbeSet	Description	Blast Score	EC #	Family
13211_s_at (BCHI_S_AT)	dbj BAA82816.1 (AB023454) basic endochitinase [Arabidopsis thaliana]	2E-72		
13212_s_at (BGL2_S_AT)	emb CAB68132.1 (AL137080) beta-1, 3- glucanase 2 (BG2) [Arabidopsis thaliana]	0		
13215_s_at (CAFFEROYLCOA METHYLTRANS_S _AT)	gb AAF16576.1 AC012563_2 9 (AC012563) putative S- adenosyl-L-methionine:trans- caffeoyl-Coenzyme A 3-O- methyltransferase [Arabidopsis thaliana]	1E-121		
13217_s_at (CALMODULINLIK E_S_AT)	emb CAB42906.1 (AL049862) calmodulin-like protein [Arabidopsis thaliana]	6E-99		
13219_s_at (CHI4_S_AT)	emb CAA74930.1 (Y14590) class IV chitinase [Arabidopsis thaliana]	5E-78		
13243_r_at (ELI32_R_AT)	emb CAB37539.1 (AL035538) cinnamyl-alcohol dehydrogenase ELI3-2 [Arabidopsis	0		
13244_s_at (ELI32_S_AT)	emb CAB37539.1 (AL035538) cinnamyl-alcohol dehydrogenase ELI3-2 [Arabidopsis	0		
13246_at (ERECTAL_AT)	gb AAF26067.1 AC012562_2 2 (AC012562) putative protein kinase [Arabidopsis thaliana]	1E-40		kinase
13255_i_at (GAMMAGLUTAM YLTRANSPEPTI_I _AT)	emb CAA89206.1 (Z49240) gamma-glutamyl transpeptidase [Arabidopsis thaliana]	0	EC_2.3.2.2	glutamyl- trans- peptidase
13259_s_at (GLUTATHIONEPE ROXIDASE1_S_AT)	gb AAD24836.1 AC007071_8 (AC007071) putative glutathione peroxidase [Arabidopsis thaliana]	4E-95		
13261_s_at (GLUTATHIONERE DUCTASE1_S_AT)	gb AAB67841.1 (U37697) glutathione reductase [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
13263_s_at (GST1_RC_S_AT)	emb CAA10060.1 (AJ012571) glutathione transferase [Arabidopsis thaliana]	3E-49		
13266_s_at (GST4_S_AT)	emb CAB51026.1 (AJ243812) glutathione synthetase [Arabidopsis thaliana]	0		
13273_s_at (HSF4_S_AT)	gb AAC31756.1 (U68017) heat shock transcription factor 4 [Arabidopsis thaliana]	1E-113		
13275_f_at (HSP174_F_AT)	emb CAA35182.1 (X17293) heat shock protein (AA 1 - 156) [Arabidopsis thaliana]	8E-80		
13277_i_at (HSP176A_I_AT)	emb CAA74399.1 (Y14070) Heat Shock Protein 17.6A [Arabidopsis thaliana]	2E-75		
13285_s_at (HSP83_S_AT)	gb AAA32822.1 (M62984) heat shock protein 83 [Arabidopsis thaliana]	0		
13312_at (AC006223.75_AT)	gb AAD15391.1 (AC006223) putative disease resistance protein [Arabidopsis thaliana]	1E-126		disease
13367_at (AC004680.97_AT)	gb AAC31853.1 (AC004680) putative NADH dehydrogenase (ubiquinone oxidoreductase) [Arabidopsis thaliana]	0	EC_1.6.5.3	oxido- reductase
13370_at (AC005322.4_AT)	gb AAC97990.1 (AC005322) Strong similarity to Dsor1 protein kinase gb D13782 from Drosophila melanogaster. [Arabidopsis thaliana]	0		kinase
13381_at (AC006580.8_AT)	gb AAD22369.1 AC006580_1 (AC006580) NAM (no apical meristem)-like protein [Arabidopsis thaliana]	1E-169		
13395_at (AL035528.202_AT)	emb CAB36843.1 (AL035528) SAUR-AC-like protein (small auxin up RNA) [Arabidopsis thaliana]	1E-48		

ProbeSet	Description	Blast Score	EC #	Family
13435_at (AF003102.3_AT)	gb AAC49775.1 (AF003102) AP2 domain containing protein RAP2.9 [Arabidopsis thaliana]	1E-33		
13437_at (AF096371.8_AT)	gb AAC62791.1 (AF096371) contains similarity to D- isomer specific 2-hydroxyacid dehydrogenases (Pfam: 2- Hacid_DH.hmm, score: 19.11) [Arabidopsis thaliana]	0		
13450_at (AL049657.33_AT)	emb CAB41122.1 (AL049657) putative proteasome regulatory subunit [Arabidopsis thaliana]	0		
13467_at (AL096860.198_AT)	emb CAB51214.1 (AL096860) putative protein [Arabidopsis thaliana]	0		permease
13480_at (AC005223.15_AT)	gb AAD10644.1 (AC005223) 40409 [Arabidopsis thaliana]	1E-169		
13534_at (AF149413.36_AT)	gb AAD40124.1 AF149413_5 (AF149413) contains similarity to soybean early nodulin 93 (N-93) (SW:Q02921) [Arabidopsis thaliana]	2E-38		
13536_at (AL021636.47_AT)	emb CAA16575.1 (AL021636) putative protein [Arabidopsis thaliana]	0		
13538_at (AL080254.75_AT)	emb CAB45844.1 (AL080254) calcium-binding protein-like [Arabidopsis thaliana]	1E-105		
13564_at (AC005312.113_AT)	gb AAC78521.1 (AC005312) putative glutathione S- transferase [Arabidopsis thaliana]	1E-127		transferase
13565_at (AL035601.21_AT)	emb CAB38206.1 (AL035601) auxin-responsive GH3-like protein [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
13584_at (AC007127.23_AT)	gb AAD25137.1 AC007127_3 (AC007127) putative ubiquitin-like protein [Arabidopsis thaliana]	0		
13588_at (AL021961.24_AT)	emb CAA17552.1 (AL021961) Phosphoglycerate dehydrogenase - like protein [Arabidopsis thaliana]	0		dehydro- genase
13589_at (AC000132.24_AT)	gb AAB60745.1 (AC000132) ESTs gb ATT51236,gb T43334,gb N 97019,gb AA395203 come from this gene. [Arabidopsis thaliana]	2E-91		
13604_at (AC000104.20_AT)	gb AAB70431.1 (AC000104) F19P19.10 [Arabidopsis thaliana]	0	EC_2.7.1.-	
13605_at (AL078470.75_AT)	emb CAB43918.1 (AL078470) 26S proteasome subunit 4-like protein [Arabidopsis thaliana]	0		ATPase
13617_at (AC006592.64_AT)	gb AAD22351.1 AC006592_8 (AC006592) putative mitochondrial dicarboxylate carrier protein [Arabidopsis thaliana]	1E-152		
13627_at (AL035394.196_AT)	emb CAA23036.1 (AL035394) putative Na ⁺ /H ⁺ - exchanging protein [Arabidopsis thaliana]	0		
13645_at (AC000098.8_AT)	gb AAB71443.1 (AC000098) EST gb ATT50295 comes from this gene. [Arabidopsis thaliana]	6E-19		
13647_at (AF000657.22_AT)	gb AAB72161.1 (AF000657) unknown protein [Arabidopsis thaliana]	0		
13656_at (AC007138.31_AT)	gb AAD22649.1 AC007138_1 3 (AC007138) predicted protein of unknown function [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
13659_at (AL022347.46_AT)	emb CAA18462.1 (AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana]	0		
13666_s_at (INDOLE3GPS_S_AT)	gb AAD25838.1 AC006951_1 7 (AC006951) putative indole- 3-glycerol phosphate synthase [Arabidopsis thaliana]	0		
13680_s_at (LOX1_S_AT)	gb AAA17036.1 (U01843) lipoxygenase 1 [Arabidopsis thaliana]	0		
13685_s_at (MLOLIKE2_S_AT)	gb AAD25552.1 AC005850_9 (AC005850) Highly Similar to Mlo proteins [Arabidopsis thaliana]	0		
13688_s_at (MONOPTEROS_S_AT)	gb AAC60794.1 (AF037229) transcription factor [Arabidopsis thaliana]	0		
13697_at (NI16_AT)	No hits found.			
13705_s_at (AC003671X_S_AT)	gb AAC18810.1 (AC003671) Strong similarity to trehalose- 6-phosphate synthase homolog from A. thaliana chromosome 4 contig gb Z97344. ESTs gb H37594, gb R65023, gb H37578 and gb R64855 come from this gene. [Arabidopsis thaliana]	0		
13706_s_at (AC005724X_S_AT)	gb AAD08939.1 (AC005724) putative trehalose-6-phosphate synthase [Arabidopsis thaliana]	0		
13716_at (NOVARTIS103_RC_AT)	emb CAA62665.1 (X91259) lectin like protein [Arabidopsis thaliana]	6E-70		
13718_at (NOVARTIS105_RC_AT)	emb CAA96522.1 (Z72152) AMP-binding protein [Brassica napus]	6E-19		
13746_at (NOVARTIS121_RC_AT)	gb AAF18699.1 AC010795_1 4 (AC010795) hypothetical protein [Arabidopsis thaliana]	8E-80		

ProbeSet	Description	Blast Score	EC #	Family
13751_at (NOVARTIS127_AT)	gb AAF16751.1 AC010155_4 (AC010155) F3M18.8 [Arabidopsis thaliana]	2E-27		
13755_at (NOVARTIS15_AT)	emb CAA16797.1 (AL021713) receptor serine/threonine kinase-like protein [Arabidopsis thaliana]	1E-114		
13763_at (NOVARTIS21_AT)	gb AAF24849.1 AC012679_2 0 (AC012679) putative calmodulin-binding protein [Arabidopsis thaliana]	1E-105		
13764_at (NOVARTIS22_AT)	gb AAD39641.1 AC007591_6 (AC007591) F9L1.6 [Arabidopsis thaliana]	2E-30		
13789_at (AJ132436.2_AT)	emb CAB41008.1 (AJ132436) GA 2-oxidase [Arabidopsis thaliana]	0		oxidase
13803_at (Z97341.376_AT)	emb CAB10444.1 (Z97341) cyanohydrin lyase like protein [Arabidopsis thaliana]	1E-154		
13818_s_at (AC006218.175_S_A T)	gb AAD15433.1 (AC006218) putative aspartate aminotransferase [Arabidopsis thaliana]	0		
13825_s_at (AF104919.22_S_AT)	gb AAC72875.1 (AF104919) Arabidopsis thaliana ABC1 protein (GB:AJ001158)	0		
13834_at (AL080237.29_AT)	emb CAB45784.1 (AL080237) cyclic nucleotide gated channel (CNGC4) like protein [Arabidopsis thaliana]	0		
13842_at (AC002396.12_AT)	gb AAC00572.1 (AC002396) similar to zinc metalloproteinases [Arabidopsis thaliana]	0		metallo- proteinase
13848_at (AC003981.31_AT)	gb AAC14057.1 (AC003981) F22O13.31 [Arabidopsis thaliana]	0		
13880_s_at (AL049480.183_S_A T)	emb CAB39611.1 (AL049480) possible apospory-associated like protein [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
13896_at (AC004473.8_AT)	gb AAC24048.1 (AC004473) Strong similarity to trehalose-6-phosphate synthase homolog gb 2245136 from A. thaliana chromosome 4 contig gb Z97344. [Arabidopsis thaliana]	0		
13908_s_at (A71590.1_S_AT)	emb CAB42588.1 (A71590) unnamed protein product [Arabidopsis thaliana]	9E-62		
13918_at (AC005388.29_AT)	gb AAC64884.1 (AC005388) Strong similarity to F21B7.33 gi 2809264 from A. thaliana BAC gb AC002560. EST gb N65119 comes from this gene. [Arabidopsis thaliana]	0		
13920_at (AC005990.53_AT)	gb AAC98026.1 (AC005990) EST gb AA597511 comes from this gene. [Arabidopsis thaliana]	1E-131		
13944_at (U89959.24_AT)	gb AAC24380.1 (U89959) Unknown protein [Arabidopsis thaliana]	0		
13949_s_at (Z97343.352_S_AT)	emb CAB10528.1 (Z97343) thioesterase like protein [Arabidopsis thaliana]	1E-167		
13963_at (AL021711.26_AT)	emb CAA16746.1 (AL021711) putative protein [Arabidopsis thaliana]	1E-137		
13964_at (AL021889.3_AT)	emb CAA17126.2 (AL021889) N-acetylmethionine deacetylase-like protein, fragment [Arabidopsis thaliana]	0		
13966_at (AL022023.172_AT)	emb CAA17775.1 (AL022023) putative protein [Arabidopsis thaliana]	1E-173		
13999_at (AF071527.56_AT)	gb AAD11584.1 AAD11584 (AF071527) hypothetical protein [Arabidopsis thaliana]	1E-173		
14015_s_at (A71588.1_S_AT)	emb CAB42612.1 (A71639) unnamed protein product [Arabidopsis thaliana]	1E-63		

ProbeSet	Description	Blast Score	EC #	Family
14016_s_at (A71596.1_S_AT)	emb CAB42592.1 (A71596) unnamed protein product [Arabidopsis thaliana]	3E-58		
14025_s_at (AC007293.3_S_AT)	gb AAD12260.1 (AF098632) subtilisin-like protease [Arabidopsis thaliana]	0		
14026_at (AC000106.5_AT)	gb AAB70397.1 (AC000106) Similar to probable Mg- dependent ATPase (pir S56671). ESTs gb T46782,gb AA04798 come from this gene. [Arabidopsis thaliana]	0		
14030_at (AC005970.225_AT)	gb AAC95171.1 (AC005970) putative protein kinase [Arabidopsis thaliana]	0		kinase
14032_at (AL035601.11_AT)	emb CAB38204.1 (AL035601) cytochrome P450-like protein [Arabidopsis thaliana]	0		
14041_at (AC003970.28_AT)	gb AAC33208.1 (AC003970) Highly similar to cinnamyl alcohol dehydrogenase, gi 1143445 [Arabidopsis thaliana]	0		dehydro- genase
14052_at (AC004122.24_AT)	gb AAC34333.1 (AC004122) Highly Similar to branched- chain amino acid aminotransferase [Arabidopsis thaliana]	1E-174		
14068_s_at (AC006922.197_S_A T)	gb AAD31580.1 AC006922_1 2 (AC006922) putative farnesylated protein [Arabidopsis thaliana]	1E-132		
14070_at (AL049658.217_AT)	emb CAB41143.1 (AL049658) putative peptide transporter [Arabidopsis thaliana]	0		
14083_at (AC005662.56_AT)	gb AAC78535.1 (AC005662) putative embryo-abundant protein [Arabidopsis thaliana]	1E-155		

ProbeSet	Description	Blast Score	EC #	Family
14089_at (AC006223.65_AT)	gb AAD15390.1 (AC006223) putative hydrolase [Arabidopsis thaliana]	1E-135		
14100_at (AF002109.108_AT)	gb AAB95282.1 (AF002109) putative peroxisomal membrane carrier protein [Arabidopsis thaliana]	1E-166		
14110_i_at (AL035528.279_I_A T)	emb CAB36854.1 (AL035528) putative disease resistance protein [Arabidopsis thaliana]	0		disease
14116_at (AF077407.30_AT)	gb AAC26243.1 (AF077407) contains similarity to sugar transporters (Pfam: sugar_tr.hmm, score: 395.39) [Arabidopsis thaliana]	0		
14122_at (AF058826.23_AT)	gb AAC13608.1 (AF058826) similar to eukaryotic protein kinase domains (Pfam: pkinase.hmm, score: 189.74) [Arabidopsis thaliana]	0		kinase
14139_at (NOVARTIS30_AT)	gb AAD09343.1 (AF026538) ABA-responsive protein [Hordeum vulgare]	7E-36		
14141_at (NOVARTIS31_AT)				
14148_at (NOVARTIS38_AT)	gb AAF34713.1 AF224762_1 (AF224762) SigA binding protein [Arabidopsis thaliana]	4E-53		
14170_at (NOVARTIS51_AT)	gb AAF29406.1 AC022354_5 (AC022354) unknown protein [Arabidopsis thaliana]	9E-26		
14197_at (NOVARTIS71_AT)				
14214_at (NOVARTIS83_AT)	gb AAF24849.1 AC012679_2 0 (AC012679) putative calmodulin-binding protein [Arabidopsis thaliana]	2E-92		
14223_at (NOVARTIS9_AT)	emb CAA19683.1 (AL024486) putative protein [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
14240_s_at (NR1_S_AT)	gb AAF08556.1 AC012193_5 (AC012193) nitrate reductase 1 (NR1) [Arabidopsis thaliana]	1E-148		
14242_s_at (NRA_S_AT)	gb AAF19225.1 AC007505_1 (AC007505) nitrate reductase [Arabidopsis thaliana]	0		
14248_at (PAD3_AT)	gb AAD31062.1 AC007357_1 1 (AC007357) Strong similarity to gb X97864 cytochrome P450 from Arabidopsis thaliana and is a member of the PF 00067 Cytochrome P450 family. ESTs gb N65665, gb T14112, gb T76255, gb T20906 and gb AI100027 come from this gene.	0		
14249_i_at (PAD4_I_AT)	emb CAB43438.1 (AL050300) putative protein [Arabidopsis thaliana]	0		
14254_s_at (PAL1- MRNA_S_AT)	gb AAD18156.2 (AC006260) phenylalanine ammonia lyase (PAL1) [Arabidopsis	1E-134		
14256_f_at (PAL1- INTRON_F_AT)	gb AAD18156.2 (AC006260) phenylalanine ammonia lyase (PAL1) [Arabidopsis thaliana]	7E-77		
14257_s_at (PAL2- MRNA_S_AT)	gb AAC18871.1 (L33678) phenylalanine ammonia lyase [Arabidopsis thaliana]	0		
14320_at (AC005956.54_AT)	gb AAD23719.1 AC005956_8 (AC005956) putative RING zinc finger protein [Arabidopsis thaliana]	1E-110		
14381_at (AC002521.68_AT)	gb AAC05341.1 (AC002521) unknown protein [Arabidopsis thaliana]	0		
14408_at (AC002291.14_AT)	gb AAC00635.1 (AC002291) Unknown protein [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
14448_at (AC002387.243_AT)	gb AAB82641.1 (AC002387) putative auxin-regulated protein [Arabidopsis thaliana]	2E-94		
14450_at (AC002986.49_AT)	gb AAC17046.1 (AC002986) EST gb N65759 comes from this gene. [Arabidopsis thaliana]	4E-78		
14459_at (AC006200.69_AT)	gb AAD14519.1 (AC006200) unknown protein [Arabidopsis thaliana]	0		kinase
14460_at (AC006201.21_AT)	gb AAD20117.1 (AC006201) unknown protein [Arabidopsis thaliana]	0		
14461_at (AC006202.73_AT)	gb AAD29832.1 AC006202_1 0 (AC006202) putative carbonic anhydrase [Arabidopsis thaliana]	1E-134		
14468_at (AC007576.62_AT)	gb AAD39306.1 AC007576_2 9 (AC007576) Unknown protein [Arabidopsis thaliana]	2E-89		
14475_at (AL021811.121_AT)	emb CAA16965.1 (AL021811) putative protein [Arabidopsis thaliana]	0		
14487_at (Z97341.343_AT)	emb CAB46039.1 (Z97341) HSP like protein [Arabidopsis thaliana]	1E-160		
14498_at (AC004261.51_AT)	gb AAD11996.1 (AC004261) unknown protein [Arabidopsis thaliana]	2E-43		
14584_at (AC007658.25_AT)	gb AAD32844.1 AC007658_3 (AC007658) unknown protein [Arabidopsis thaliana]	2E-74		
14591_at (AL035440.107_AT)	emb CAB36521.1 (AL035440) putative protein [Arabidopsis thaliana]	1E-178		
14609_at (AC002340.147_AT)	gb AAC02748.1 (AC002340) putative cytochrome P450 [Arabidopsis thaliana]	0		
14614_at (AC004165.66_AT)	gb AAC16958.1 (AC004165) putative glucosyltransferase [Arabidopsis thaliana]	0		glucosy- ltransferase

ProbeSet	Description	Blast Score	EC #	Family
14620_s_at (PAT1_S_AT)	gb AAA32835.1 (M96073) phosphoribosylanthranilate transferase [Arabidopsis thaliana]	0		
14635_s_at (PR.1_S_AT)	gb AAC69381.1 (AC005398) pathogenesis-related PR-1-like protein [Arabidopsis thaliana]	1E-94		
14638_s_at (PRXCB_S_AT)	emb CAA50677.1 (X71794) peroxidase [Arabidopsis thaliana]	0		
14640_s_at (PUTATIVEMLOHI _S_AT)	gb AAC28997.1 (AC004697) similar to Mlo proteins from H. vulgare [Arabidopsis thaliana]	0		
14643_s_at (RAR047_S_AT)	gb AAD20078.1 (AC006836) putative steroid sulfotransferase [Arabidopsis thaliana]	1E-162		
14660_s_at (THIOREDOXL_S_ AT)	gb AAB86519.1 (AC002329) putative thioredoxin reductase [Arabidopsis thaliana]	2E-34		
14663_s_at (TREHALASEPREC USOR_RC_S_AT)	gb AAB63620.1 (AC002343) trehalase precursor isolog [Arabidopsis thaliana]	0		
14667_s_at (TRPB_S_AT)	gb AAA32878.1 (M23872) tryptophan synthase beta subunit [Arabidopsis thaliana]	0		
14672_s_at (TSA1_S_AT)	gb AAC49117.1 (U18993) tryptophan synthase alpha chain [Arabidopsis thaliana]	1E-158		
14673_s_at (TSB2_S_AT)	gb AAA32879.1 (M81620) tryptophan synthase beta- subunit [Arabidopsis thaliana] thaliana]	0		
14675_s_at (VSP_S_AT)	dbj BAA22096.1 (D85191) vegetative storage protein [Arabidopsis thaliana]	1E-146		
14682_i_at (WT1012A_RC_I_A T)				

ProbeSet	Description	Blast Score	EC #	Family
14686_s_at (WT1073_S_AT)	gb AAB60752.1 (AC000132) Similar to A. thaliana receptor-like protein kinase (gb RLK5_ARATH). ESTs gb ATTS0475,gb ATTS4362 come from this gene. [Arabidopsis thaliana]	1E-116		
14696_at (WT740_RC_AT)	gb AAD23643.1 AC007119_9 (AC007119) unknown protein [Arabidopsis thaliana]	5E-45		
14697_g_at (WT740_RC_G_AT)	gb AAD23643.1 AC007119_9 (AC007119) unknown protein [Arabidopsis thaliana]	5E-45		
14705_i_at (WT77_RC_I_AT)	emb CAB69849.1 (AL137189) anthranilate N- benzoyltransferase-like protein [Arabidopsis thaliana]	1E-38		
14706_r_at (WT77_RC_R_AT)	emb CAB69849.1 (AL137189) anthranilate N- benzoyltransferase-like protein [Arabidopsis thaliana]	1E-38		
14711_s_at (ZFPL_S_AT)	gb AAD25930.1 AF085279_3 (AF085279) hypothetical Cys- 3-His zinc finger protein [Arabidopsis thaliana]	3E-37		
14735_s_at (AF008124_S_AT)	gb AAB71832.1 (AF008125) multidrug resistance- associated protein homolog [Arabidopsis thaliana]	0		
14750_s_at (AF096370.12_S_AT)	gb AAC62777.1 (AF096370) contains similarity to NAM (no apical meristem) -like proteins [Arabidopsis thaliana]	1E-175		
14763_at (X86958.1_AT)	emb CAA60521.1 (X86958) protein kinase catalytic domain (fragment) [Arabidopsis thaliana]	1E-25		kinase
14779_at (AC004680.71_AT)	gb AAC31851.1 (AC004680) hypothetical protein [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
14780_at (AC004683.103_AT)	gb AAC28770.1 (AC004683) DREB-like AP2 domain transcription factor [Arabidopsis thaliana]	1E-126		
14786_at (AC005397.115_AT)	gb AAC62908.1 (AC005397) putative desiccation related protein [Arabidopsis thaliana]	2E-90		
14793_at (AC006202.10_AT)	emb CAB67652.1 (AL132966) putative protein [Arabidopsis thaliana]	2E-79		
14838_s_at (M96073.6_S_AT)	gb AAA32835.1 (M96073) phosphoribosylanthranilate transferase [Arabidopsis thaliana]	0		
14882_at (AL022605.63_AT)	emb CAA18753.1 (AL022605) putative protein [Arabidopsis thaliana]	1E-103		
14884_at (AL031032.95_AT)	emb CAA19873.1 (AL031032) putative protein [Arabidopsis thaliana]	1E-149		
14895_s_at (Z97344.138_S_AT)	emb CAB10562.1 (Z97344) acetylornithine deacetylase [Arabidopsis thaliana]	4E-68		
14900_at (AC000348.12_AT)	gb AAB61488.1 (AC000348) T7N9.12 [Arabidopsis thaliana]	0		
14923_at (AC006283.158_AT)	gb AAD20693.1 (AC006283) unknown protein [Arabidopsis thaliana]	0		
14924_at (AC006283.46_AT)	gb AAD20686.1 (AC006283) hypothetical protein [Arabidopsis thaliana]	7E-85		
14928_at (AC006569.88_AT)	gb AAD21756.1 (AC006569) unknown protein [Arabidopsis thaliana]	0		
14959_at (AC007202.26_AT)	gb AAD30230.1 AC007202_1 2 (AC007202) T8K14.13 [Arabidopsis thaliana]	0		
14972_at (AC005499.38_AT)	gb AAC67344.1 (AC005499) unknown protein [Arabidopsis thaliana]	1E-123		

ProbeSet	Description	Blast Score	EC #	Family
14978_at (AC002333.49_AT)	gb AAB64024.1 (AC002333) putative glucosyltransferase [Arabidopsis thaliana]	0		glucosyl- transferase
15032_at (AC002294.8_AT)	gb AAB71471.1 (AC002294) Unknown protein [Arabidopsis thaliana]	1E-115		
15042_at (AL021961.3_AT)	emb CAA17549.1 (AL021961) cinnamyl alcohol dehydrogenase - like protein [Arabidopsis thaliana]	1E-167		
15052_at (AC002332.103_AT)	gb AAB80656.1 (AC002332) putative calcium-binding EF- hand protein [Arabidopsis thaliana]	1E-120		
15073_at (AC007069.93_AT)	gb AAD21785.1 (AC007069) putative purple acid phosphatase [Arabidopsis thaliana]	0		
15085_s_at (AL031018.274_S_A T)	emb CAA19817.1 (AL031018) putative protein [Arabidopsis thaliana]	0		
15088_s_at (AC002311.37_S_AT)	gb AAB72158.1 (AF000657) unknown protein [Arabidopsis thaliana]	9E-48		
15091_at (AC004683.97_AT)	gb AAC28768.1 (AC004683) unknown protein [Arabidopsis thaliana]	1E-101		
15098_s_at (ATU26945_S_AT)	emb CAA21463.1 (AL031986) senescence- associated protein sen1 [Arabidopsis thaliana]	1E-103		
15116_f_at (AF121356_F_AT)	gb AAD28243.1 AF121356_1 (AF121356) peroxiredoxin TPx2 [Arabidopsis thaliana]	6E-81		
15123_s_at (ATU40857_S_AT)	gb AAC49283.1 (U40857) AIG2 [Arabidopsis thaliana]	3E-97		
15124_s_at (ATU59508_S_AT)	gb AAB40615.1 (U59508) osmotic stress-induced proline dehydrogenase [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
15125_f_at (D85190_F_AT)	dbj BAA22095.1 (D85190) vegetative storage protein [Arabidopsis thaliana]	1E-142		
15129_s_at (AF030386_S_AT)	gb AAB86938.1 (AF030386) NOI protein [Arabidopsis thaliana]	1E-30		
15132_s_at (AF121878_S_AT)	gb AAD30449.1 AF121878_1 (AF121878) cytidine deaminase [Arabidopsis thaliana]	1E-169		
15137_s_at (ATU57320_S_AT)	gb AAB47973.1 (U57320) blue copper-binding protein II [Arabidopsis thaliana]	5E-70		
15140_s_at (ATU93845_S_AT)	gb AAB52420.1 (U93845) Arabidopsis thaliana ER-type calcium pump protein, complete sequence	0		
15141_s_at (D85191_S_AT)	dbj BAA22096.1 (D85191) vegetative storage protein [Arabidopsis thaliana]	1E-146		
15154_s_at (ATHMTGDAS_S_AT)	emb CAB51206.1 (AL096860) glutamine- dependent asparagine synthetase [Arabidopsis thaliana]	0		
15161_s_at (ATU90522_S_AT)	gb AAB53975.1 (U90522) lysine-ketoglutarate reductase/saccharopine dehydrogenase [Arabidopsis thaliana]	0		
15162_s_at (U01880_S_AT)	gb AAA20642.1 (U01880) pre-hevein-like protein [Arabidopsis thaliana]	1E-113		
15188_s_at (AF081202_S_AT)	gb AAC31606.1 (AF081202) villin 2 [Arabidopsis thaliana]	0		
15192_s_at (ATHERD1_S_AT)	dbj BAA04506.1 (D17582) ERD1 protein [Arabidopsis thaliana]	0		
15196_s_at (ATU43412_S_AT)	gb AAC49573.1 (U43412) 3'- phosphoadenosine 5'- phosphosulfate reductase [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
15197_s_at (ATU52851_S_AT)	gb AAB09723.1 (U52851) arginine decarboxylase [Arabidopsis thaliana]	0		
15199_s_at (AB005804_S_AT)	dbj BAA28624.1 (AB005804) aldehyde oxidase [Arabidopsis thaliana]	0		
15211_s_at (ATH243813_S_AT)	emb CAB51027.1 (AJ243813) glutathione synthetase [Arabidopsis thaliana]	0		
15216_s_at (ATU75191_S_AT)	gb AAB51576.1 (U75198) germin-like protein [Arabidopsis thaliana]	8E-97		
15342_at (AC006593.101_AT)	gb AAD20671.1 (AC006593) unknown protein [Arabidopsis thaliana]	0		
15379_at (AC002335.182_AT)	gb AAB64323.1 (AC002335) unknown protein [Arabidopsis thaliana]	7E-75		
15389_at (AC004786.100_AT)	gb AAC32433.1 (AC004786) unknown protein [Arabidopsis thaliana]	2E-37		
15406_at (AC006931.179_AT)	gb AAD21731.1 (AC006931) unknown protein [Arabidopsis thaliana]	2E-98		
15431_at (AL030978.64_AT)	emb CAA19722.1 (AL030978) putative protein [Arabidopsis thaliana]	2E-51		
15463_at (AL031326.226_AT)				
15479_at (AL049483.205_AT)	emb CAB39671.1 (AL049483) putative protein [Arabidopsis thaliana]	4E-68		
15483_s_at (AC005819.20_S_AT)	gb AAC69922.1 (AC005819) putative cytochrome b5 [Arabidopsis thaliana]	4E-58		
15485_at (AC006233.109_AT)	gb AAD41998.1 AC006233_1 0 (AC006233) unknown protein [Arabidopsis thaliana]	1E-169		
15496_at (AC006282.167_AT)	gb AAD20156.1 (AC006282) putative glucosyl transferase [Arabidopsis thaliana]	0		transferase

ProbeSet	Description	Blast Score	EC #	Family
15518_at (AC005322.28_AT)	gb AAC97999.1 (AC005322) ESTs gb H36249, gb AA59732 and gb AA651219 come from this gene. [Arabidopsis thaliana]	1E-125		
15522_i_at (AL078637.213_I_A T)	emb CAB45071.1 (AL078637) putative protein [Arabidopsis thaliana]	8E-48		
15523_s_at (AL078637.213_S_A T)	emb CAB45071.1 (AL078637) putative protein [Arabidopsis thaliana]	8E-48		
15524_at (AC005508.25_AT)	gb AAD14499.1 (AC005508) 44123 [Arabidopsis thaliana]	0		
15526_at (AC004122.16_AT)	gb AAC34332.1 (AC004122) Unknown protein [Arabidopsis thaliana]	0		
15531_i_at (AL078637.191_I_A T)	emb CAB45069.1 (AL078637) putative protein [Arabidopsis thaliana]	0		
15532_r_at (AL078637.191_R_A T)	emb CAB45069.1 (AL078637) putative protein [Arabidopsis thaliana]	0		
15540_at (AC006585.205_AT)	gb AAD18030.1 (AF118129) Tsil-interacting protein TSIP1 [Nicotiana tabacum]	1E-33		
15543_at (AF096371.10_AT)	gb AAC62794.1 (AF096371) T2L5.6 gene product [Arabidopsis thaliana]	1E-108		
15544_at (AL021633.110_AT)	emb CAA16532.1 (AL021633) predicted protein [Arabidopsis thaliana]	1E-147		
15547_at (AC005970.122_AT)	gb AAC95168.1 (AC005970) unknown protein [Arabidopsis thaliana]	1E-110		
15551_at (AL035440.289_AT)	emb CAB36537.1 (AL035440) putative dihydrolipoamide succinyltransferase [Arabidopsis thaliana]	0	EC_2.3.1.61	succinyl- transferase
15580_s_at (AF057043_S_AT)	gb AAC13497.1 (AF057043) acyl-CoA oxidase [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
15582_s_at (ATH131392_S_AT)	emb CAA10364.1 (AJ131392) alternative oxidase [Arabidopsis thaliana]	0		
15594_s_at (ATU56635_S_AT)	gb AAB01222.1 (U56635) glutamate dehydrogenase 2 [Arabidopsis thaliana]	0		
15613_s_at (ATHHOMEOA_S_AT)	emb CAA79670.1 (Z19602) HAT4 [Arabidopsis thaliana]	1E-144		
15614_s_at (ATHMERI5B_S_AT)	emb CAB52471.1 (AL109796) xyloglucan endo- 1, 4-beta-D-glucanase precursor [Arabidopsis thaliana]	1E-162		
15617_s_at (ATHSAR1_S_AT)	gb AAA56991.1 (M90418) formerly called HAT24; synaptobrevin-related protein [Arabidopsis thaliana]	1E-112		
15622_s_at (ATU43945_S_AT)	gb AAB40594.1 (U43945) strictosidine synthase [Arabidopsis thaliana]	0		
15625_s_at (ATU74610_S_AT)	gb AAB17995.1 (U74610) glyoxalase II [Arabidopsis thaliana]	1E-141		
15629_s_at (AB003280_S_AT)	dbj BAA24440.1 (AB010407) phosphoglycerate dehydrogenase [Arabidopsis thaliana]	0		
15632_s_at (AB012570_S_AT)	dbj BAA37112.1 (AB012570) ATHP3 [Arabidopsis thaliana]	7E-77		
15641_s_at (AF117063_S_AT)	gb AAD10829.1 (AF117063) putative inositol polyphosphate 5-phosphatase At5P2 [Arabidopsis thaliana]	0		
15646_s_at (ATHSAT1G_S_AT)	gb AAC37474.1 (L42212) serine acetyltransferase [Arabidopsis thaliana]	0		
15665_s_at (AF022658_S_AT)	gb AAB80922.1 (AF022658) putative c2h2 zinc finger transcription factor [Arabidopsis thaliana]	3E-94		

ProbeSet	Description	Blast Score	EC #	Family
15669_s_at (AF047834_S_AT)	gb AAF24813.1 AC007592_6 (AC007592) F12K11.9 [Arabidopsis thaliana]	0		
15670_s_at (AF061638_S_AT)	gb AAC64005.1 (AF061638) branched-chain alpha-keto acid decarboxylase E1 beta subunit [Arabidopsis thaliana]	0		
15672_s_at (AF082299_S_AT)				
15674_s_at (AF091844_S_AT)	gb AAC61769.1 (AF091844) aminoalcoholphosphotransfera se [Arabidopsis thaliana]	0		
15680_s_at (ATHATPK19B_S_AT)	dbj BAA07661.1 (D42061) ribosomal-protein S6 kinase homolog [Arabidopsis thaliana]	0		
15778_at (X98676.2_AT)	emb CAA67234.1 (X98676) zinc finger protein [Arabidopsis thaliana]	8E-87		
15779_g_at (X98676.2_G_AT)	emb CAA67234.1 (X98676) zinc finger protein [Arabidopsis thaliana]	8E-87		
15792_at (AC002341.106_AT)	gb AAB67625.1 (AC002341) hypothetical protein [Arabidopsis thaliana]	1E-174		
15798_at (AC002521.173_AT)	gb AAC05351.1 (AC002521) putative receptor-like protein kinase [Arabidopsis thaliana]	0		
15815_s_at (Z97342.366_S_AT)	emb CAB10487.1 (Z97342) hypothetical protein [Arabidopsis thaliana]	1E-175		
15839_at (AC005662.203_AT)	gb AAC78548.1 (AC005662) unknown protein [Arabidopsis thaliana]	8E-22		
15859_at (AC006587.164_AT)	gb AAD21491.1 (AC006587) unknown protein [Arabidopsis thaliana]	4E-17		
15866_s_at (AC007133.59_S_AT)	gb AAC79625.1 (AC005770) unknown protein [Arabidopsis thaliana]	5E-27		

ProbeSet	Description	Blast Score	EC #	Family
15874_at (AL022223.106_AT)	emb CAA18223.1 (AL022223) putative protein [Arabidopsis thaliana]	1E-133		
15886_at (AL078637.204_AT)	emb CAB45070.1 (AL078637) putative protein [Arabidopsis thaliana]	1E-126		phosphorylase
15900_at (AC005311.74_AT)				
15919_at (AC007060.42_AT)	gb AAD25764.1 AC007060_2 2 (AC007060) EST gb AA721821 comes from this gene. [Arabidopsis thaliana]	0		
15921_s_at (AC007067.1_S_AT)	gb AAD39561.1 AC007067_1 (AC007067) T10024.1 [Arabidopsis thaliana]	1E-24		
15924_at (AC007138.61_AT)	gb AAD22658.1 AC007138_2 2 (AC007138) predicted protein of unknown function [Arabidopsis thaliana]	8E-94		
15970_s_at (X71794.2_S_AT)	emb CAA50677.1 (X71794) peroxidase [Arabidopsis thaliana]	0		
15978_at (X68592.6_AT)	emb CAA48579.1 (X68592) adenosine nucleotide translocator [Arabidopsis thaliana]	0		translocase
15982_s_at (AC006260.78_S_AT)	emb CAA66863.1 (X98190) peroxidase ATP2a [Arabidopsis thaliana]	0		
16001_at (AF035385.2_AT)	gb AAC39468.1 (AF035385) unknown [Arabidopsis thaliana]	4E-72		
16003_s_at (AL021749.64_S_AT)	emb CAA16877.1 (AL021749) ADP, ATP carrier-like protein [Arabidopsis thaliana]	0		
16021_s_at (AL022224.182_S_A T)	emb CAA18251.1 (AL022224) endomembrane- associated protein [Arabidopsis thaliana]	3E-63		

ProbeSet	Description	Blast Score	EC #	Family
16203_at (AC007519.53_AT)	gb AAD46036.1 AC007519_2 1 (AC007519) Contains similarity to gb M74161 inositol polyphosphate 5- phosphatase from Homo sapiens and contains a PF 00783 inositol polyphosphate phosphatase catalytic domain. [Arabidopsis thaliana]	0		
16230_at (AL049655.78_AT)	emb CAB41089.1 (AL049655) putative protein [Arabidopsis thaliana]	0		
16232_s_at (AL080252.77_S_AT)	emb CAB45796.1 (AL080252) putative protein [Arabidopsis thaliana]	1E-119		
16233_at (AL080254.83_AT)	emb CAB45846.1 (AL080254) putative protein [Arabidopsis thaliana]	0		
16236_g_at (X92657.3_G_AT)	emb CAA63346.1 (X92657) cationic amino acid transporter [Arabidopsis thaliana]	1E-37		
16272_at (AC006304.136_AT)	gb AAD20108.1 (AC006304) hypothetical protein [Arabidopsis thaliana]	0		
16288_at (AF024504.17_AT)	gb AAB80790.2 (AF024504) similar to prolyl 4-hydroxylase alpha subunit [Arabidopsis thaliana]	1E-143		hydroxylase
16298_at (AL021890.71_AT)	emb CAA17152.1 (AL021890) putative protein [Arabidopsis thaliana]	1E-68		
16299_at (AL024486.185_AT)	emb CAA19705.1 (AL024486) putative protein [Arabidopsis thaliana]	1E-170		
16301_s_at (AL031018.105_S_A T)	emb CAA19807.1 (AL031018) hypothetical protein [Arabidopsis thaliana]	1E-149		
16306_at (AL049751.112_AT)	emb CAB41935.1 (AL049751) putative protein [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
16329_s_at (AF013294.17_S_AT)	emb CAA10659.1 (AJ132387) Ca ²⁺ -ATPase [Arabidopsis thaliana] [Arabidopsis thaliana]	0		
16335_at (AL079347.105_AT)	emb CAB45450.1 (AL079347) xanthine dehydrogenase-like protein [Arabidopsis thaliana]	0		dehydro- genase
16340_at (AC004255.15_AT)	gb AAC13905.1 (AC004255) T1F9.15 [Arabidopsis thaliana]	0		
16357_at (AF149413.38_AT)	gb AAD40144.1 AF149413_2 5 (AF149413) contains similarity to protein kinase domains (Pfam F00069, Score=162.6, E=6.8e-45, N=1) and leucien rich repeats (Pfam PF00560, Score=210.7, E=2.2e-59, N=10) [Arabidopsis thaliana]	0		kinase
16363_at (AC004255.14_AT)	gb AAC13904.1 (AC004255) T1F9.14 [Arabidopsis thaliana]	0		
16383_at (AC006300.64_AT)	gb AAD20719.1 (AC006300) putative disease resistance protein [Arabidopsis thaliana]	0		disease
16391_at (AL050351.194_AT)	emb CAB43642.1 (AL050351) receptor protein kinase-like protein [Arabidopsis thaliana]	0		
16398_s_at (AL022603.3_S_AT)	emb CAA20204.1 (AL031187) serine/threonine kinase-like protein [Arabidopsis thaliana]	0		
16405_at (AC005850.9_AT)	gb AAD25549.1 AC005850_6 (AC005850) Putative serine/threonine kinase [Arabidopsis thaliana]	0		kinase
16409_at (AC004393.2_AT)	gb AAC18783.1 (AC004393) Strong similarity to receptor kinase gb M80238 from A.	0		kinase

ProbeSet	Description	Blast Score	EC #	Family
16440_s_at (AF002109.137_S_AT)	gb AAB95285.1 (AF002109) putative nematode-resistance protein [Arabidopsis thaliana]	0		
16457_s_at (AC005397.17_S_AT)	gb AAD23036.1 AC006526_2 (AC006526) unknown protein [Arabidopsis thaliana]	3E-29		
16461_i_at (AC004683.79_I_AT)	gb AAC28766.1 (AC004683) peroxidase [Arabidopsis thaliana]	0		peroxidase
16462_s_at (AC004683.79_S_AT)	gb AAC28766.1 (AC004683) peroxidase [Arabidopsis thaliana]	0		
16465_at (Y08892.1_AT)	emb CAA70105.1 (Y08892) Hsc70-G8 protein [Arabidopsis thaliana]	4E-46		
16470_s_at (AF068299.4_S_AT)	gb AAD14544.1 (AF068299) gamma-glutamylcysteine synthetase [Arabidopsis thaliana]	0		
16483_at (X68053_AT)	emb CAA48189.1 (X68053) transcription factor [Arabidopsis thaliana]	0		
16496_s_at (AF030386.1_S_AT)	gb AAB86938.1 (AF030386) NOI protein [Arabidopsis thaliana]	1E-30		
16510_at (AL034567.198_AT)	emb CAA22575.1 (AL034567) putative protein [Arabidopsis thaliana]	1E-168		
16522_at (X77500.2_AT)	emb CAA54631.1 (X77500) amino acid transporter [Arabidopsis thaliana]	0		
16524_at (AC006577.38_AT)	gb AAD25783.1 AC006577_1 9 (AC006577) Strong similarity to gb S77096 aldehyde dehydrogenase homolog from Brassica napus and is a member of PF 00171 Aldehyde dehydrogenase family. ESTs gb T46213, gb T42164, gb T43682, gb N96380, gb T42973, gb Z34663, gb Z4	0		dehydro- genase

ProbeSet	Description	Blast Score	EC #	Family
16526_at (Z49227.1_AT)	emb CAA89201.2 (Z49227) adenine nucleotide translocase [Arabidopsis thaliana]	0		translocase
16538_s_at (AB010259_S_AT)	dbj BAA28347.1 (AB010259) DRH1 [Arabidopsis thaliana]	0		
16541_s_at (AB023423_S_AT)	dbj BAA75015.1 (AB023423) sulfate transporter [Arabidopsis thaliana]	0		
16545_s_at (AF037229_S_AT)	gb AAC60794.1 (AF037229) transcription factor [Arabidopsis thaliana]	0		
16553_f_at (AF078821_F_AT)	gb AAC68670.1 (AF078821) RING-H2 finger protein RHA1b [Arabidopsis thaliana]	2E-93		
16568_s_at (ATHATCDPK_S_AT)	gb AAB03246.1 (U31835) calmodulin-domain protein kinase CDPK isoform 6 [Arabidopsis thaliana]	0		
16570_s_at (ATHCDPKA_S_AT)	gb AAF27092.1 AC011809_1 (AC011809) calcium- dependent protein kinase 1 [Arabidopsis thaliana]	0		
16578_s_at (ATHRPRP1B_S_AT)	emb CAB68132.1 (AL137080) beta-1, 3- glucanase 2 (BG2) [Arabidopsis thaliana]	0		
16589_s_at (ATU26937_S_AT)	gb AAD24605.1 AC005825_1 2 (AC005825) putative MYB family transcription factor [Arabidopsis thaliana]	1E-143		
16594_s_at (ATU39783_S_AT)	gb AAB82307.1 (U39783) amino acid transport protein [Arabidopsis thaliana]	0		
16603_s_at (ATU81293_S_AT)	gb AAB58497.1 (U81293) UDP-glucose:indole-3-acetate beta-D-glucosyltransferase [Arabidopsis thaliana]	0		
16609_s_at (AB008104_S_AT)	dbj BAA32419.1 (AB008104) ethylene responsive element binding factor 2 [Arabidopsis thaliana]	1E-112		

ProbeSet	Description	Blast Score	EC #	Family
16611_s_at (AB008782_S_AT)	dbj BAA23424.1 (AB008782) sulfate transporter [Arabidopsis thaliana]	0		
16635_s_at (AF126057_S_AT)	emb CAB43670.1 (AL050352) putative protein [Arabidopsis thaliana]	0		
16638_s_at (AF139098_S_AT)	gb AAD37511.1 AF139098_1 (AF139098) putative zinc finger protein [Arabidopsis thaliana]	1E-103		
16646_s_at (ATHDHS1_S_AT)	gb AAA32784.1 (M74819) 3- deoxy-D-arabino- heptulosonate y-phosphate synthase [Arabidopsis thaliana]	0		
16649_s_at (ATHORF_S_AT)	gb AAF16576.1 AC012563_2 9 (AC012563) putative S- adenosyl-L-methionine:trans- caffeoyl-Coenzyme A 3-O- methyltransferase [Arabidopsis thaliana]	1E-121		
16701_at (AC005312.61_AT)	gb AAC78514.1 (AC005312) putative phloem-specific lectin [Arabidopsis thaliana]	1E-170		
16721_at (AC006533.58_AT)	gb AAD32285.1 AC006533_9 (AC006533) putative poly(ADP-ribose) glycohydrolase [Arabidopsis thaliana]	0		kinase
16747_at (AL021713.3_AT)	emb CAA16788.1 (AL021713) DNA binding- like protein [Arabidopsis thaliana]	0		
16753_at (AL031032.110_AT)	emb CAA19874.1 (AL031032) putative protein [Arabidopsis thaliana]	0		
16781_at (AC002392.100_AT)	gb AAD12030.1 (AC002392) putative receptor-like protein kinase [Arabidopsis thaliana]	0		kinase
16810_at (AC002339.46_AT)	gb AAC02763.1 (AC002339) putative polygalacturonase [Arabidopsis thaliana]	0		Polygalactur onase

ProbeSet	Description	Blast Score	EC #	Family
16817_s_at (AL096882.91_S_AT)	emb CAB51412.1 (AL096882) ACC synthase (AtACS-6) [Arabidopsis thaliana]	0		
16859_at (AL035523.135_AT)	emb CAB36742.1 (AL035523) alpha-amylase- like protein [Arabidopsis thaliana]	0		
16864_i_at (AF037367.4_I_AT)	emb CAB66108.1 (AL133248) endo- polygalacturonase [Arabidopsis thaliana]	0		polygalac- turonase
16865_s_at (AF037367.4_S_AT)	emb CAB66108.1 (AL133248) endo- polygalacturonase [Arabidopsis thaliana]	0		
16888_s_at (AC004684.174_S_A T)	gb AAC23647.1 (AC004684) putative alcohol dehydrogenase [Arabidopsis thaliana]	1E-170		
16902_at (AC007119.67_AT)	gb AAD23643.1 AC007119_9 (AC007119) unknown protein [Arabidopsis thaliana]	6E-91		
16903_g_at (AC007119.67_G_A T)	gb AAD23643.1 AC007119_9 (AC007119) unknown protein [Arabidopsis thaliana]	6E-91		
16908_at (AC002396.22_AT)	gb AAC00577.1 (AC002396) pyruvate dehydrogenase E1 alpha subunit [Arabidopsis thaliana]	0		
16914_s_at (AL049500.57_S_AT)	emb CAB39936.1 (AL049500) osmotin precursor [Arabidopsis thaliana]	1E-143		
16916_s_at (X77199.8_S_AT)	emb CAA54420.1 (X77199) heat shock cognate 70-2 [Arabidopsis thaliana]	3E-52		
16927_s_at (AF035384.2_S_AT)	gb AAC39467.1 (AF035384) endo-xyloglucan transferase [Arabidopsis thaliana]	2E-65		
16940_g_at (AC002334.110_G_ AT)	gb AAC04922.1 (AC002334) putative synaptobrevin [Arabidopsis thaliana]	1E-123		

ProbeSet	Description	Blast Score	EC #	Family
16951_i_at (AC005662.30_I_AT)	gb AAC78532.1 (AC005662) calmodulin-like protein [Arabidopsis thaliana]	1E-88		
16952_s_at (AC005662.30_S_AT)	gb AAC78532.1 (AC005662) calmodulin-like protein [Arabidopsis thaliana]	1E-88		
16955_at (AL031326.215_AT)	emb CAA20468.1 (AL031326) putative protein [Arabidopsis thaliana]	4E-87		
16968_at (AL021961.93_AT)	emb CAA17559.1 (AL021961) glucosyltransferase -like protein [Arabidopsis thaliana]	0		
16970_s_at (Y18291.5_S_AT)	emb CAA77109.1 (Y18291) uncoupling protein [Arabidopsis thaliana]	1E-175		
16972_at (AC004261.89_AT)	gb AAA87347.1 (M88307) calmodulin [Brassica juncea]	5E-81		
16981_s_at (U35829.2_S_AT)	gb AAC49356.1 (U35829) thioredoxin h [Arabidopsis thaliana]	4E-64		
16989_at (AL030978.46_AT)	emb CAA19720.1 (AL030978) GH3 like protein [Arabidopsis thaliana]	0		
16995_at (AC002391.188_AT)	gb AAB87114.1 (AC002391) unknown protein [Arabidopsis thaliana]	0		
17007_at (AC005896.26_AT)	gb AAC98046.1 (AC005896) putative adenylate kinase [Arabidopsis thaliana]	1E-155		kinase
17008_at (AC006585.212_AT)	gb AAD23027.1 AC006585_2 (AC006585) putative tyrosine aminotransferase [Arabidopsis thaliana]	0		transaminase
17009_at (AL021633.163_AT)	emb CAA16537.1 (AL021633) putative protein [Arabidopsis thaliana]	0		
17039_s_at (D78602_S_AT)	dbj BAA28534.1 (D78602) cytochrome P450 monooxygenase [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
17041_s_at (D89631_S_AT)	gb AAC14417.1 (AF049236) unknown [Arabidopsis thaliana]	0		
17051_s_at (AF098947_S_AT)	gb AAD09952.1 (AF098947) CTF2B [Arabidopsis thaliana]	0		
17066_s_at (ATHLIPOXY_S_AT)	gb AAA17036.1 (U01843) lipoxygenase 1 [Arabidopsis thaliana]	0		
17073_s_at (ATTS4391_S_AT)	gb AAD20078.1 (AC006836) putative steroid sulfotransferase [Arabidopsis thaliana]	1E-162		
17075_s_at (ATU09961_S_AT)	gb AAA19628.1 (U09961) nitrilase [Arabidopsis thaliana]	0		
17083_s_at (ATU18770_S_AT)	gb AAD25838.1 AC006951_1 7 (AC006951) putative indole- 3-glycerol phosphate synthase [Arabidopsis thaliana]	0		
17104_s_at (D88541_S_AT)	dbj BAA13640.1 (D88541) phosphoserine aminotransferase [Arabidopsis thaliana]	0		
17111_s_at (ATHACSC_S_AT)	emb CAA78260.1 (Z12614) 1-aminocyclopropane 1- carboxylate synthase [Arabidopsis	0		
17119_s_at (AF132212_S_AT)	gb AAD38925.1 AF132212_1 (AF132212) OPDA-reductase homolog [Arabidopsis thaliana]	0		
17128_s_at (ATHRPRP1A_S_AT)	gb AAC69381.1 (AC005398) pathogenesis-related PR-1-like protein [Arabidopsis	1E-94		
17180_at (AF007270.30_AT)	gb AAB61058.1 (AF007270) contains similarity to GATA- type zinc fingers (PS:PS00344) [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
17187_at (AF128396.2_AT)	gb AAD17371.1 (AF128396) similar to arginases (Pfam: PF00491, Score=353.2, E=1.4e-119, N=1) [Arabidopsis thaliana]	0		arginase
17300_at (X66017.2_AT)	emb CAA46815.1 (X66017) NADPH-ferrihemoprotein reductase [Arabidopsis thaliana]	0		reductase
17303_s_at (AC004683.25_S_AT)	gb AAC67339.2 (AC005499) putative WRKY-type DNA binding protein [Arabidopsis thaliana]	0		
17323_at (U95973.69_AT)	gb AAB65477.1 (U95973) Ser/Thr protein kinase isolog [Arabidopsis thaliana]	0		kinase
17338_at (AC002535.97_AT)	gb AAC62855.1 (AC002535) putative pectinesterase [Arabidopsis thaliana]	0		pectin- esterase
17341_at (AL021713.89_AT)	emb CAA16797.1 (AL021713) receptor serine/threonine kinase-like protein [Arabidopsis thaliana]	0		
17352_at (AC007127.33_AT)	gb AAD25140.1 AC007127_6 (AC007127) putative protein kinase [Arabidopsis thaliana]	0		kinase
17356_s_at (Z97338.190_S_AT)	emb CAB10307.1 (Z97338) UTP-glucose glucosyltransferase [Arabidopsis thaliana]	0		
17371_at (AF076243.44_AT)	gb AAD29762.1 AF076243_9 (AF076243) putative receptor- like protein kinase [Arabidopsis thaliana]	0		
17376_at (AL021890.218_AT)	emb CAA17164.1 (AL021890) putative protein [Arabidopsis thaliana]	1E-119		
17379_at (AF085279.9_AT)	gb AAF18728.1 AC018721_3 (AC018721) putative CCCH- type zinc finger protein [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
17380_at (AL021961.39_AT)	emb CAA17554.1 (AL021961) putative protein [Arabidopsis thaliana]	0		
17398_at (AC002535.143_AT)	gb AAC62863.1 (AC002535) putative protein disulfide- isomerase [Arabidopsis thaliana]	0		isomerase
17413_s_at (AJ006961.4_S_AT)	emb CAA67551.1 (X99097) peroxidase [Arabidopsis thaliana]	2E-84		
17451_at (AC002343.47_AT)	gb AAB63613.1 (AC002343) unknown protein [Arabidopsis thaliana]	0		
17452_g_at (AC002343.47_G_A T)	gb AAB63613.1 (AC002343) unknown protein [Arabidopsis thaliana]	0		
17458_at (AC006260.91_AT)	gb AAD18148.1 (AC006260) unknown protein [Arabidopsis thaliana]	1E-138		
17464_at (AC000132.72_AT)	gb AAB60752.1 (AC000132) Similar to A. thaliana receptor-like protein kinase (gb RLK5_ARATH). ESTs gb ATTS0475,gb ATTS4362 come from this gene. [Arabidopsis thaliana]	0		kinase
17482_s_at (Z97343.441_S_AT)	emb CAB10533.1 (Z97343) GTP-binding RAB1C like protein [Arabidopsis thaliana]	1E-112		
17484_at (X79052.2_AT)	emb CAA55654.1 (X79052) SRG1 [Arabidopsis thaliana]	0		
17485_s_at (Z97340.345_S_AT)	emb CAB10405.1 (Z97340) beta-1, 3-glucanase class I precursor [Arabidopsis thaliana]	1E-169		
17487_s_at (U18993.2_S_AT)	gb AAC49117.1 (U18993) tryptophan synthase alpha chain [Arabidopsis thaliana]	1E-158		

ProbeSet	Description	Blast Score	EC #	Family
17490_s_at (M90416.2_S_AT)	gb AAF01532.1 AC009325_2 (AC009325) homeobox- leucine zipper protein HAT5 (HD-ZIP protein 5) (HD-ZIP protein ATHB-1) [Arabidopsis thaliana]	4E-52		
17500_s_at (ATHCALLGA_S_AT)	emb CAB42906.1 (AL049862) calmodulin-like protein [Arabidopsis thaliana]	6E-99		
17511_s_at (AF067605_S_AT)	gb AAB71482.1 (AC002294) similar to S-linalool synthase gp U58314 1491939 [Arabidopsis thaliana]	0		
17514_s_at (AF076277_S_AT)	gb AAD03545.1 (AF076278) ethylene response factor 1 [Arabidopsis thaliana]	1E-104		
17516_s_at (AF072536_S_AT)	gb AAC24592.1 (AF072536) H-protein promoter binding factor-1 [Arabidopsis thaliana]	0		
17522_s_at (D78606_S_AT)	dbj BAA28538.1 (D78606) cytochrome P450 monooxygenase [Arabidopsis thaliana]	0		
17533_s_at (ATU43488_S_AT)	gb AAB18367.1 (U43488) xyloglucan endotransglycosylase-related protein [Arabidopsis thaliana]	1E-171		
17544_s_at (ATU40856_S_AT)	gb AAC49282.1 (U40856) AIG1 [Arabidopsis thaliana]	1E-150		
17548_s_at (AF118823_S_AT)	gb AAD20613.1 (AF118823) senescence-associated protein [Arabidopsis thaliana]	2E-26		
17578_at (AF093604_AT)	gb AAF00071.1 AF093604_1 (AF093604) apyrase [Arabidopsis thaliana]	0		
17585_s_at (AF134487_S_AT)	emb CAA06460.1 (AJ005261) cytidine deaminase [Arabidopsis thaliana]	1E-168		

ProbeSet	Description	Blast Score	EC #	Family
17595_s_at (AF166352_S_AT)	gb AAC28764.1 (AC004683) putative beta-alanine-pyruvate aminotransferase [Arabidopsis thaliana]	0		
17636_at (AF077409.7_AT)	gb AAC28219.1 (AF077409) contains similarity to C3HC4- type zinc fingers (Pfam: zf- C3HC4.hmm, score: 32.94) [Arabidopsis thaliana]	1E-138		
17648_at (AL021684.43_AT)	emb CAA16674.1 (AL021684) predicted protein [Arabidopsis thaliana]	0		
17653_at (AL035679.144_AT)	emb CAB38823.1 (AL035679) putative protein [Arabidopsis thaliana]	0		
17702_at (AC005700.212_AT)	gb AAC69951.1 (AC005700) Mutator-like transposase [Arabidopsis thaliana]	0		
17719_at (AC006592.17_AT)	gb AAD22346.1 AC006592_3 (AC006592) hypothetical protein [Arabidopsis thaliana]	0		
17744_s_at (AC004684.168_S_A T)	gb AAC23646.1 (AC004684) putative alcohol dehydrogenase [Arabidopsis thaliana]	1E-170		
17752_at (AC003974.37_AT)	gb AAC04483.1 (AC003974) putative protein kinase [Arabidopsis thaliana]	0		kinase
17758_at (AF076243.41_AT)	gb AAD29761.1 AF076243_8 (AF076243) putative receptor- like protein kinase [Arabidopsis thaliana]	0		
17775_at (AC004392.2_AT)	gb AAC28500.1 (AC004392) Similar to glucose-6- phosphate/phosphate- translocator (GPT) gb AF020814 from Pisum sativum. [Arabidopsis thaliana]	0		
17781_at (AL049746.177_AT)	emb CAB41861.1 (AL049746) ABC transporter- like protein [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
17840_s_at (AC002333.223_S_AT)	gb AAB64049.1 (AC002333) putative endochitinase [Arabidopsis thaliana]	1E-161		
17854_at (Z99707.366_AT)	emb CAB16762.1 (Z99707) caltractin-like protein [Arabidopsis thaliana]	1E-91		
17860_at (AL078467.4_AT)	emb CAB43873.1 (AL078467) putative protein [Arabidopsis thaliana]	1E-177		
17876_at (AJ007587.2_AT)	emb CAA07574.1 (AJ007587) monooxygenase [Arabidopsis thaliana]	0		mono- oxygenase
17877_g_at (AJ007587.2_G_AT)	emb CAA07574.1 (AJ007587) monooxygenase [Arabidopsis thaliana]	0		
17881_at (AC002391.54_AT)	gb AAB87100.1 (AC002391) putative WRKY-type DNA- binding protein [Arabidopsis thaliana]	1E-133		
17882_at (AL035523.49_AT)	emb CAB36734.1 (AL035523) PROTEIN TRANSPORT PROTEIN SEC61 GAMMA SUBUNIT- like [Arabidopsis thaliana]	1E-24		
17893_at (AC004401.135_AT)	gb AAC17827.1 (AC004401) similar to late embryogenesis abundant proteins [Arabidopsis thaliana]	2E-43		
17894_at (AC005724.44_AT)	gb AAD08938.1 (AC005724) unknown protein [Arabidopsis thaliana]	1E-147		
17899_at (Z97339.197_AT)	emb CAB10339.1 (Z97339) hypothetical protein [Arabidopsis thaliana]	5E-55		
17900_s_at (AC000106.13_S_AT)	gb AAB70401.1 (AC000106) Similar to Glycine SRC2 (gb AB000130). ESTs gb H76869,gb T21700,gb ATT S5089 come from this gene. [Arabidopsis thaliana]	2E-97		
17907_s_at (AC004684.165_S_AT)	gb AAC23645.1 (AC004684) unknown protein [Arabidopsis thaliana]	4E-24		

ProbeSet	Description	Blast Score	EC #	Family
17930_s_at (AJ006960.4_S_AT)	emb CAA07352.1 (AJ006960) peroxidase [Arabidopsis thaliana]	1E-111		
17945_at (Z97341.411_AT)	emb CAB10448.1 (Z97341) limonene cyclase like protein [Arabidopsis thaliana]	0		
17955_at (AL021768.242_AT)	emb CAA16940.1 (AL021768) small GTP- binding protein-like [Arabidopsis thaliana]	1E-110		
17956_i_at (AC005967.32_I_AT)	gb AAD03381.1 (AC005967) putative leucine aminopeptidase [Arabidopsis thaliana]	0	EC_3.4.11.1	amino- peptidase
17963_at (AL049730.88_AT)	emb CAB41717.1 (AL049730) pEARLI 1-like protein [Arabidopsis thaliana]	6E-46		
17967_at (AL096859.32_AT)	emb CAB51172.1 (AL096859) protein kinase 6- like protein [Arabidopsis thaliana]	0		
18010_s_at (AJ001264_S_AT)	emb CAA77109.1 (Y18291) uncoupling protein [Arabidopsis thaliana]	1E-175		
18012_s_at (AJ002295_S_AT)	emb CAB59428.1 (AJ002295) inositol-1,4,5-trisphosphate 5- Phosphatase [Arabidopsis thaliana]	0		
18045_at (AJ011976_AT)	emb CAA71798.1 (Y10845) O-acetylserine(thiol) lyase [Brassica juncea]	1E-148		
18054_at (AJ238846_AT)	emb CAB54517.1 (AJ238846) SGP1 monomeric G-protein [Arabidopsis thaliana]	1E-150		
18109_s_at (AC002391.206_S_A T)	gb AAB87118.1 (AC002391) putative metal ion transporter (NRAMP) [Arabidopsis thaliana]	0		
18121_s_at (AC002337.21_S_AT)	gb AAB63819.1 (AC002337) MYB transcription factor (Atmyb2) [Arabidopsis thaliana]	1E-167		

ProbeSet	Description	Blast Score	EC #	Family
18122_at (AC002338.110_AT)	gb AAC16938.1 (AC002338) putative protein kinase [Arabidopsis thaliana]	0		kinase
18140_at (Z97341.319_AT)	emb CAB10440.1 (Z97341) growth regulator like protein [Arabidopsis thaliana]	0		
18148_at (AC004669.25_AT)	gb AAC20719.1 (AC004669) putative dioxygenase [Arabidopsis thaliana]	0		
18176_at (AL035540.31_AT)	emb CAB37503.1 (AL035540) protein kinase like protein [Arabidopsis thaliana]	0		kinase
18194_i_at (AL096859.227_I_A T)	emb CAB51196.1 (AL096859) glucuronosyl transferase-like protein [Arabidopsis thaliana]	0		glucosyl- transferase
18213_at (AL022140.126_AT)	emb CAA18110.1 (AL022140) putative protein [Arabidopsis thaliana]	1E-174		
18216_at (X95573.2_AT)	gb AAF24959.1 AC012375_2 2 (AC012375) T22C5.18 [Arabidopsis thaliana]	1E-119		
18217_g_at (X95573.2_G_AT)	gb AAF24959.1 AC012375_2 2 (AC012375) T22C5.18 [Arabidopsis thaliana]	1E-119		
18224_s_at (AL021890.57_S_AT)	emb CAA17150.1 (AL021890) putative protein [Arabidopsis thaliana]	4E-81		
18226_s_at (AC002343.142_S_A T)	emb CAB51645.1 (AL109619) putative protein [Arabidopsis thaliana]	0		
18228_at (X91259.1_AT)	emb CAA62665.1 (X91259) lectin like protein [Arabidopsis thaliana]	1E-142		
18234_at (AC000348.3_AT)	gb AAB61479.1 (AC000348) T7N9.3 [Arabidopsis thaliana]	1E-154		
18236_s_at (AC004683.69_S_AT)	gb AAC28764.1 (AC004683) putative beta-alanine-pyruvate aminotransferase [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
18241_at (AC006580.71_AT)	gb AAD21720.1 (AC006931) putative RNA-binding protein [Arabidopsis thaliana]	0		
18242_g_at (AC006580.71_G_AT)	gb AAD21720.1 (AC006931) putative RNA-binding protein [Arabidopsis thaliana]	0		
18255_at (AC005770.25_AT)	gb AAC79625.1 (AC005770) unknown protein [Arabidopsis thaliana]	0		
18258_s_at (AC006439.222_S_AT)	gb AAD15515.1 (AC006439) unknown protein [Arabidopsis thaliana]	4E-58		
18263_at (AC005724.36_AT)	gb AAD08937.1 (AC005724) unknown protein [Arabidopsis thaliana]	1E-139		
18266_at (AC004684.33_AT)	gb AAC23628.1 (AC004684) unknown protein [Arabidopsis thaliana]	0		
18267_at (AC006223.23_AT)	gb AAD15384.1 (AC006223) unknown protein [Arabidopsis thaliana]	2E-38		
18268_s_at (AC006418.38_S_AT)	gb AAD20161.1 (AC006418) putative ubiquitin [Arabidopsis thaliana]	0		
18280_at (AC007369.2_AT)	gb AAD30591.1 AC007369_1 (AC007369) Unknown protein [Arabidopsis thaliana]	1E-135		
18284_at (AL021961.67_AT)	emb CAA17557.1 (AL021961) putative protein [Arabidopsis thaliana]	6E-97		
18287_at (AC007661.142_AT)	gb AAD32777.1 AC007661_1 4 (AC007661) unknown protein [Arabidopsis thaliana]	0		
18299_s_at (M23872.2_S_AT)	gb AAA32878.1 (M23872) tryptophan synthase beta subunit [Arabidopsis thaliana]	0		
18314_i_at (AL078579.83_I_AT)	emb CAB43971.1 (AL078579) putative beta- glucosidase [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
18348_at (AL022603.104_AT)	emb CAA18711.1 (AL022603) putative protein [Arabidopsis thaliana]	1E-160		
18456_s_at (AC004697.159_S_AT)	gb AAC28997.1 (AC004697) similar to Mlo proteins from H. vulgare [Arabidopsis thaliana]	0		
18508_s_at (AC006532.89_S_AT)	gb AAA33709.1 (L16797) glutamate decarboxylase [Petunia x hybrida]	0		
18544_at (AC007060.14_AT)	gb AAD25749.1 AC007060_7 (AC007060) Strong similarity to F19I3.8 gi 3033381 putative UDP-galactose-4-epimerase from Arabidopsis thaliana BAC gb AC004238 and is a member of PF 01370 the NAD dependent epimerase/dehydratase family. EST gb AA597338 comes fro	0	EC_5.1.3.2	epimerase
18582_s_at (AC003671.36_S_AT)	gb AAC18810.1 (AC003671) Strong similarity to trehalose- 6-phosphate synthase homolog from A. thaliana chromosome 4 contig gb Z97344. ESTs gb H37594, gb R65023, gb H37578 and gb R64855 come from this gene. [Arabidopsis thaliana]	0		
18587_s_at (AC007166.53_S_AT)	gb AAF18667.1 AC007166_9 (AC007166) unknown protein [Arabidopsis thaliana]	0		
18590_at (AJ222713.4_AT)	emb CAA10955.1 (AJ222713) unnamed protein product [Arabidopsis thaliana]	1E-151		
18591_at (X74756.2_AT)	emb CAA52772.1 (X74756) ATAF2 [Arabidopsis thaliana]	2E-99		
18596_at (AC005698.13_AT)	gb AAD43614.1 AC005698_1 3 (AC005698) T3P18.13 [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
18597_at (AL080282.74_AT)	emb CAB45881.1 (AL080282) berberine bridge enzyme-like protein [Arabidopsis thaliana]	0		
18601_s_at (AC002387.279_S_AT)	gb AAF18602.1 AC002387_1 (AC002387) putative microtubule-associated protein [Arabidopsis thaliana]	8E-45		
18604_at (AF069298.31_AT)	gb AAC19273.1 (AF069298) similar to several small proteins (~100 aa) that are induced by heat, auxin, ethylene and wounding such as Phaseolus aureus indole-3- acetic acid induced protein ARG (SW:32292) [Arabidopsis thaliana]	3E-82		
18622_g_at (AJ005902.2_G_AT)	emb CAA06759.1 (AJ005902) vag2 [Arabidopsis thaliana]	3E-47		
18625_at (AC005278.22_AT)	gb AAC72125.1 (AC005278) ESTs gb H36966, gb R65511, gb T42324 and gb T20569 come from this gene. [Arabidopsis thaliana]	0		
18631_at (AC002510.112_AT)	gb AAB84346.1 (AC002510) unknown protein [Arabidopsis thaliana]	0		
18636_at (AC006577.22_AT)	gb AAD25775.1 AC006577_1 1 (AC006577) Belongs to the PF00657 Lipase/Acylhydrolase with GDSL-motif family. ESTs gb T75865, gb R30449, gb AI239373, gb F19931 and gb F19930 come from this gene. [Arabidopsis thaliana]	0		
18650_s_at (AF013294.25_S_AT)	gb AAB62867.1 (AF013294) AT0ZII gene product [Arabidopsis thaliana]	3E-41		
18662_s_at (AC002343.20_S_AT)	gb AAB63608.1 (AC002343) unknown protein [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
18668_at (AJ249794_AT)	emb CAB56692.1 (AJ249794) lipoxygenase [Arabidopsis thaliana]	0		
18681_at (L23573_AT)	gb AAD02548.1 (AF049922) PGP169-12 [Petunia x hybrida]	8E-94		
18686_s_at (U18126_S_AT)	gb AAA57314.1 (U18126) inner mitochondrial membrane protein [Arabidopsis thaliana]	2E-78		
18698_s_at (X17528_S_AT)	emb CAA35570.1 (X17528) citrate synthetase [Arabidopsis thaliana]	0		
18720_s_at (X92419_S_AT)	emb CAB52583.1 (X92420) SNAP25AB protein [Arabidopsis thaliana]	1E-157		
18735_s_at (Z29490_S_AT)	emb CAA82626.1 (Z29490) gamma-glutamylcysteine synthetase [Arabidopsis thaliana]	0		
18753_s_at (AF118222.28_S_AT)	gb AAD03425.1 (AF118222) contains similarity to Iron/Ascorbate family of oxidoreductases (Pfam: PF00671, Score=297.8, E=1.3e-85, N=1) [Arabidopsis thaliana]	0		
18782_at (AC003040.90_AT)	gb AAC23760.1 (AC003040) putative protein kinase [Arabidopsis thaliana]	0		kinase
18803_at (AC005315.94_AT)	gb AAC33232.1 (AC005315) putative SCARECROW gene regulator [Arabidopsis thaliana]	0		
18885_at (AC006921.147_AT)	gb AAD21443.1 (AC006921) unknown protein [Arabidopsis thaliana]	1E-126		
18888_at (AC007591.68_AT)	gb AAD39666.1 AC007591_3 1 (AC007591) Is a member of the PF 00903 glyoxalase family. ESTs gb T44721, gb T21844 and gb AA395404 come from this gene. [Arabidopsis thaliana]	1E-101		

ProbeSet	Description	Blast Score	EC #	Family
18899_s_at (X13434.1_S_AT)	emb CAA79494.1 (Z19050) nitrate reductase [Arabidopsis thaliana]	0		
18908_i_at (AF055848.2_I_AT)	gb AAC62611.1 (AF055848) subtilisin-like protease [Arabidopsis thaliana]	0		protease
18909_s_at (AF055848.2_S_AT)	gb AAC62611.1 (AF055848) subtilisin-like protease [Arabidopsis thaliana]	0		
18928_at (AC002333.181_AT)	gb AAB64044.1 (AC002333) putative endochitinase [Arabidopsis thaliana]	1E-157		endo-chitinase
18930_at (AC005990.57_AT)	gb AAC98028.1 (AC005990) Similar to gb L19255 carbonic anhydrase from Nicotiana tabacum and a member of the prokaryotic-type carbonic anhydrase family PF 00484. EST gb Z235745 comes from this gene. [Arabidopsis thaliana]	1E-149		anhydrase
18933_at (AC007020.48_AT)	gb AAD25665.1 AC007020_7 (AC007020) putative ferritin [Arabidopsis thaliana]	1E-129		
18936_at (AJ003119.4_AT)	emb CAA05875.1 (AJ003119) protein phosphatase 2C [Arabidopsis thaliana]	0	EC_3.1.3.16	phosphatase
18949_at (Z54136.1_AT)	emb CAA90809.1 (Z54136) MYB-related protein [Arabidopsis thaliana]	1E-145		
18953_at (AF077955.1_AT)	gb AAC69851.1 (AF077955) branched-chain alpha keto-acid dehydrogenase E1 alpha subunit [Arabidopsis thaliana]	0		dehydro-genase
18963_at (AC004561.99_AT)	gb AAC95194.1 (AC004561) putative glutathione S-transferase [Arabidopsis thaliana]	1E-127		transferase
18966_at (AC004561.106_AT)	gb AAC95196.1 (AC004561) putative glutathione S-transferase [Arabidopsis thaliana]	1E-128		transferase

ProbeSet	Description	Blast Score	EC #	Family
18980_at (U78721.20_AT)	gb AAC69126.1 (U78721) putative protein phosphatase 2C [Arabidopsis thaliana]	0	EC_3.1.3.16	phosphatase
19019_i_at (X82623.2_I_AT)	emb CAA57943.1 (X82623) SRG2At [Arabidopsis thaliana]	7E-33		
19060_at (AC003671.34_AT)	gb AAC18809.1 (AC003671) Similar to high affinity potassium transporter, HAK1 protein gb U22945 from Schwanniomycetes occidentalis. [Arabidopsis thaliana]	0		
19092_at (AL078606.188_AT)	emb CAB44327.1 (AL078606) protein kinase- like protein [Arabidopsis thaliana]	0		kinase
19110_s_at (X86947.2_S_AT)	emb CAA60510.1 (X86947) Protein Kinase catalytic domain (fragment) [Arabidopsis thaliana]	4E-27		
19132_s_at (AL022603.298_S_A T)	emb CAA18722.1 (AL022603) putative NADPH quinone oxidoreductase [Arabidopsis thaliana]	0		
19137_at (X74755.2_AT)	emb CAA52771.1 (X74755) ATAF1 [Arabidopsis thaliana]	1E-138		
19140_at (AC005170.24_AT)	gb AAC63657.1 (AC005170) unknown protein [Arabidopsis thaliana]	9E-83		
19161_at (AL078579.9_AT)	emb CAB43966.1 (AL078579) putative acyl- CoA binding protein [Arabidopsis thaliana]	0		
19171_at (AC002335.160_AT)	gb AAB64325.1 (AC002335) putative trypsin inhibitor [Arabidopsis thaliana]	7E-40		
19178_at (Y18227.2_AT)	dbj BAA86999.1 (AB035137) blue copper binding protein [Arabidopsis thaliana]	2E-57		

ProbeSet	Description	Blast Score	EC #	Family
19181_s_at (AF053065.2_S_AT)	gb AAC39464.1 (AF053065) late embryogenesis abundant protein homolog [Arabidopsis thaliana]	3E-34		
19182_at (AL031804.245_AT)	emb CAA21214.1 (AL031804) putative protein [Arabidopsis thaliana]	0		
19207_at (AC006069.117_AT)	gb AAD12704.1 (AC006069) unknown protein [Arabidopsis thaliana]	1E-104		
19230_at (AC003113.15_AT)	gb AAB96860.1 (AC003113) F25O1.15 [Arabidopsis thaliana]	1E-134		
19247_at (AF071527.44_AT)	gb AAD11587.1 AAD11587 (AF071527) hypothetical protein [Arabidopsis thaliana]	0		
19257_s_at (AC000104.57_S_AT)	emb CAA44318.1 (X62461) H1flk [Arabidopsis thaliana] [Arabidopsis thaliana]	0		
19284_at (AC003028.196_AT)	gb AAC27173.1 (AC003028) putative anthocyanidin synthase [Arabidopsis thaliana]	0		
19288_at (AC005824.130_AT)	gb AAC73031.1 (AC005824) putative cytochrome P450 [Arabidopsis thaliana]	0		
19325_at (AL022604.42_AT)	emb CAA18731.1 (AL022604) putative protein [Arabidopsis thaliana]	0		
19364_at (AL022023.142_AT)	emb CAA17779.1 (AL022023) putative protein [Arabidopsis thaliana]	1E-126		
19376_at (AF024504.11_AT)	gb AAB80784.2 (AF024504) putative chloroplast nucleoid DNA binding protein [Arabidopsis thaliana]	0		peptidase
19383_at (AC006200.203_AT)	gb AAD14534.1 (AC006200) unknown protein [Arabidopsis thaliana]	1E-101		

ProbeSet	Description	Blast Score	EC #	Family
19395_at (AF007270.32_AT)	gb AAB61059.1 (AF007270) contains similarity to DNA polymerase III, alpha chain (SP:P47277) [Arabidopsis thaliana]	1E-179		polymerase
19405_at (AJ223803.1_AT)	emb CAA11553.1 (AJ223803) 2-oxoglutarate dehydrogenase E2 subunit [Arabidopsis thaliana]	0	EC_2.3.1.61	succinyl- transferase
19407_at (AC004697.81_AT)	gb AAC28981.1 (AC004697) putative adenylate kinase [Arabidopsis thaliana]	1E-142	EC_2.7.4.3	kinase
19409_at (AC007357.56_AT)	gb AAD31077.1 AC007357_2 6 (AC007357) EST gb T21221 comes from this gene. [Arabidopsis thaliana]	2E-17		
19411_at (AC007661.104_AT)	gb AAD32774.1 AC007661_1 1 (AC007661) unknown protein [Arabidopsis thaliana]	1E-110		
19421_at (X70990.4_AT)	emb CAA50317.1 (X70990) sucrose synthase [Arabidopsis thaliana]	0		synthase
19432_s_at (AL035680.11_S_AT)	gb AAA32879.1 (M81620) tryptophan synthase beta- subunit [Arabidopsis thaliana]	0		
19451_at (AC004392.6_AT)	gb AAC28502.1 (AC004392) Similar to F4I1.26 putative beta-glucosidase gi 3128187 from A. thaliana BAC gb AC004521. ESTs gb N97083, gb F19868 and gb F15482 come from this gene. [Arabidopsis thaliana]	0		glucosidase
19460_s_at (AC000132.66_S_AT)	gb AAB60749.1 (AC000132) Identical to A. thaliana HEMA2 (gb U27118). [Arabidopsis thaliana]	0		
19462_s_at (AF001168.2_S_AT)	emb CAB75467.1 (AL138659) serine/threonine- specific kinase lecRK1 precursor, lectin	0		

ProbeSet	Description	Blast Score	EC #	Family
19464_at (AC005560.51_AT)	gb AAC67338.1 (AC005560) putative MAP kinase [Arabidopsis thaliana]	0	EC_2.7.1.37	kinase
19465_at (AL021768.96_AT)	emb CAA16929.1 (AL021768) resistance protein RPP5-like [Arabidopsis thaliana]	0		
19531_at (AL021960.91_AT)	emb CAA17531.1 (AL021960) amino acid transport protein AAT1 [Arabidopsis thaliana]	0		
19546_at (AC005398.172_AT)	gb AAC69380.1 (AC005398) putative endoxyloglucan glycosyltransferase [Arabidopsis thaliana]	0		transferase
19555_at (AF058919.48_AT)	gb AAC13630.1 (AF058919) F6N23.8 gene product [Arabidopsis thaliana]	0		
19591_at (AJ010735.4_AT)	emb CAA09330.1 (AJ010735) gr1-protein [Arabidopsis thaliana]	0	EC_3.5.-.-	amido- hydrolase
19614_at (AC003970.32_AT)	gb AAC33210.1 (AC003970) Highly similar to cinnamyl alcohol dehydrogenase, gi 1143445 [Arabidopsis thaliana]	0		dehydro- genase
19623_at (AF000657.40_AT)	gb AAB72175.1 (AF000657) cytochrome C [Arabidopsis thaliana]	2E-63		
19624_at (AL049481.196_AT)	emb CAB39628.1 (AL049481) cytochrome c [Arabidopsis thaliana]	4E-63		
19625_s_at (AC002311.26_S_AT)	gb AAC00610.1 (AC002311) Putative sulphate transporter protein#protein [Arabidopsis thaliana]	0		
19635_at (AL049746.38_AT)	emb CAB41856.1 (AL049746) ABC-type transport-like protein [Arabidopsis thaliana]	0		
19639_at (AL080252.22_AT)	emb CAB45788.1 (AL080252) putative protein [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
19640_at (AC004561.78_AT)	gb AAC95192.1 (AC004561) putative glutathione S- transferase [Arabidopsis thaliana]	1E-118		transferase
19641_at (AC004561.66_AT)	gb AAC95189.1 (AC004561) putative glutathione S- transferase [Arabidopsis thaliana]	1E-128		transferase
19645_at (AC004561.70_AT)	gb AAC95190.1 (AC004561) putative glutathione S- transferase [Arabidopsis thaliana]	1E-130		transferase
19646_s_at (AC005819.55_S_AT)	gb AAC69925.1 (AC005819) homeodomain transcription factor (ATHB-7) [Arabidopsis thaliana]	9E-57		
19655_at (Y14199.1_AT)	emb CAA74591.1 (Y14199) MAP3K delta-1 protein kinase [Arabidopsis thaliana]	0		kinase
19667_at (AL021710.5_AT)	emb CAA16716.1 (AL021710) glycolate oxidase - like protein [Arabidopsis thaliana]	0	EC_1.1.2.3	dehydro- genase
19672_at (AC005687.19_AT)	gb AAC36019.1 (AC005687) RAP2.6 [Arabidopsis thaliana]	1E-105		
19673_g_at (AC005687.19_G_A T)	gb AAC36019.1 (AC005687) RAP2.6 [Arabidopsis thaliana]	1E-105		
19700_s_at (AL031326.154_S_A T)	emb CAA20463.1 (AL031326) putative protein [Arabidopsis thaliana]	8E-85		
19701_s_at (AC005724.67_S_AT)	gb AAD08939.1 (AC005724) putative trehalose-6-phosphate synthase [Arabidopsis thaliana]	0		
19704_i_at (AJ005927.2_I_AT)	emb CAA06769.1 (AJ005927) squalene epoxidase homologue [Arabidopsis thaliana]	0		epoxidase
19707_s_at (Z95768.3_S_AT)	emb CAB09200.1 (Z95768) R2R3-MYB transcription factor [Arabidopsis thaliana]	4E-21		

ProbeSet	Description	Blast Score	EC #	Family
19741_at (AL049171.72_AT)	emb CAB38956.1 (AL049171) pyrophosphate- dependent phosphofructo-1- kinase [Arabidopsis thaliana]	0		kinase
19755_at (AC006593.64_AT)	gb AAD20668.1 (AC006593) ethylene reponse factor-like AP2 domain transcription factor [Arabidopsis thaliana]	8E-97		
19762_at (AL035527.204_AT)	emb CAB36812.1 (AL035527) peptide transporter-like protein [Arabidopsis thaliana]	0		
19818_i_at (AL021749.33_I_AT)	emb CAA16876.2 (AL021749) hypothetical protein [Arabidopsis thaliana]	0		
19819_s_at (AL021749.33_S_AT)	emb CAA16876.2 (AL021749) hypothetical protein [Arabidopsis thaliana]	0		
19844_at (AJ007588.2_AT)	emb CAB37510.1 (AL035540) monooxygenase 2 (MO2) [Arabidopsis thaliana]	0		mono- oxygenase
19845_g_at (AJ007588.2_G_AT)	emb CAB37510.1 (AL035540) monooxygenase 2 (MO2) [Arabidopsis thaliana]	0		
19848_s_at (AC004261.94_S_AT)	dbj BAA08282.1 (D45848) calmodulin-related protein [Arabidopsis thaliana]	0		
19851_at (U23794.3_AT)	gb AAB60293.1 (U23794) ILR1 [Arabidopsis thaliana]	0	EC_3.5.-.-	amido- hydrolase
19878_at (AL080252.102_AT)	emb CAB45799.1 (AL080252) nodulin-like protein [Arabidopsis thaliana]	0		
19879_s_at (Z97338.342_S_AT)	emb CAB10321.1 (Z97338) UFD1 like protein [Arabidopsis thaliana]	0		
19881_at (AC004077.49_AT)	gb AAC26705.1 (AC004077) putative trans- prenyltransferase [Arabidopsis thaliana]	1E-154		synthetase

ProbeSet	Description	Blast Score	EC #	Family
19892_at (AC005770.30_AT)	gb AAC79626.1 (AC005770) putative protease inhibitor [Arabidopsis thaliana]	2E-36		protease
19894_at (AJ001809.1_AT)	emb CAA05025.1 (AJ001809) succinate dehydrogenase flavoprotein alpha subunit [Arabidopsis thaliana]	0		dehydro- genase
19895_s_at (U77347.4_S_AT)	gb AAC49679.1 (U77347) lethal leaf-spot 1 homolog [Arabidopsis thaliana]	0		
19916_at (AC006577.34_AT)	gb AAD25781.1 AC006577_1 7 (AC006577) EST gb R64848 comes from this gene. [Arabidopsis thaliana]	0		
19944_at (AC002130.4_AT)	gb AAB95233.1 (AC002130) FIN21.4 [Arabidopsis thaliana]	1E-128		
19946_at (AC004482.14_AT)	gb AAF18611.1 AC005170_1 (AC005170) similar to senescence-associated protein [Arabidopsis thaliana]	4E-92		
19956_at (AC006282.11_AT)	gb AAD20139.1 (AC006282) unknown protein [Arabidopsis thaliana]	1E-123		
19960_at (AL035527.360_AT)	emb CAB36823.1 (AL035527) putative protein [Arabidopsis thaliana]	1E-128		
19970_s_at (AC003674.10_S_AT)	gb AAB97120.1 (AC003674) unknown protein [Arabidopsis thaliana]	1E-154		
19982_at (AC002986.28_AT)	gb AAC17040.1 (AC002986) Similarity to A. thaliana gene product F21M12.20, gb AC000132. EST gb Z25651 comes from this gene. [Arabidopsis thaliana]	0		
19991_at (AC007017.124_AT)	gb AAD21459.1 (AC007017) similar to harpin-induced protein hin1 from tobacco [Arabidopsis thaliana]	1E-112		

ProbeSet	Description	Blast Score	EC #	Family
20017_at (AC004521.66_AT)	gb AAC16079.1 (AC004521) unknown protein [Arabidopsis thaliana]	1E-101		
20023_at (AC006577.46_AT)	gb AAD25787.1 AC006577_23 (AC006577) Similar to gi 1653162 (p)ppGpp 3-pyrophosphohydrolase from Synechocystis sp genome gb D90911. EST gb W43807 comes from this gene. [Arabidopsis thaliana]	0	EC_2.7.6.5	pyro-phospho-kinase
20030_at (AL078637.51_AT)	emb CAB45058.1 (AL078637) putative protein [Arabidopsis thaliana]	1E-168		
20051_at (AC000106.38_AT)	gb AAB70412.1 (AC000106) Similar to Saccharomyces hypothetical protein YDR051c (gb Z49209). ESTs gb T44436,gb 42252 come from this gene. [Arabidopsis thaliana]	1E-166		
20053_at (AC002292.27_AT)	gb AAB71973.1 (AC002292) Unknown protein [Arabidopsis thaliana]	0		
20096_at (AC004238.31_AT)	gb AAC12821.1 (AC004238) putative berberine bridge enzyme [Arabidopsis thaliana]	0		
20098_at (AC004697.123_AT)	gb AAC28986.1 (AC004697) similar to latex allergen from Hevea brasiliensis [Arabidopsis thaliana]	0		
20133_i_at (AC007178.71_I_AT)	gb AAD28682.1 AC007178_2 (AC007178) hypothetical protein [Arabidopsis thaliana]	0		
20134_s_at (AC007178.71_S_AT)	gb AAD28682.1 AC007178_2 (AC007178) hypothetical protein [Arabidopsis thaliana]	0		
20142_at (AL035521.155_AT)	emb CAB36716.1 (AL035521) extra-large G-protein-like [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
20144_at (AL079350.68_AT)	emb CAB45516.1 (AL079350) receptor kinase- like protein [Arabidopsis thaliana]	0		kinase
20165_at (AC002311.16_AT)	gb AAC00605.1 (AC002311) Unknown protein [Arabidopsis thaliana]	6E-75		
20179_at (AL035538.229_AT)	emb CAB37546.1 (AL035538) putative protei [Arabidopsis thaliana]	2E-63		
20189_at (AC005489.2_AT)	gb AAD32864.1 AC005489_2 (AC005489) F14N23.2 [Arabidopsis thaliana]	2E-57		
20194_at (AC007584.48_AT)	gb AAD32907.1 AC007584_5 (AC007584) unknown protein [Arabidopsis thaliana]	0		
20200_at (AL050400.67_AT)	emb CAB43700.1 (AL050400) hypothetical protein [Arabidopsis thaliana]	4E-95		
20215_s_at (AF117125.2_S_AT)	gb AAD29957.1 (AF117125) endoplasmic reticulum-type calcium-transporting ATPase 4 [Arabidopsis thaliana]	0		
20223_at (AL022347.145_AT)	emb CAA18469.1 (AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana]	0		kinase
20238_at (X74514.2_AT)	emb CAA52619.1 (X74514) beta-fructofuranosidase [Arabidopsis thaliana]	0	EC_3.2.1.26	hydrolase
20239_g_at (X74514.2_G_AT)	emb CAA52619.1 (X74514) beta-fructofuranosidase [Arabidopsis thaliana]	0		
20245_s_at (AC005309.97_S_AT)	emb CAA05625.1 (AJ002584) AtMRP4 [Arabidopsis thaliana] thaliana]	0		
20246_s_at (AF084037.3_S_AT)	gb AAC95354.1 (AF084037) receptor-like protein kinase [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
20247_at (AC004392.4_AT)	gb AAC28501.1 (AC004392) Similar to beta-glucosidase BGQ60 precursor gb L41869 from <i>Hordeum vulgare</i> . [<i>Arabidopsis thaliana</i>]	0	EC_3.2.1.21	glucosidase
20258_at (AF130252.1_AT)	gb AAD28759.1 AF130252_1 (AF130252) calcium dependent protein kinase CP4 [<i>Arabidopsis thaliana</i>]	0		kinase
20262_at (AC002294.26_AT)	gb AAB71480.1 (AC002294) Similar to transcription factor gb Z46606 1658307 and others [<i>Arabidopsis thaliana</i>]	0		
20263_at (AB004798.1_AT)	dbj BAA20519.1 (AB004798) ascorbate oxidase [<i>Arabidopsis thaliana</i>]	0		oxidase
20269_at (AC002387.237_AT)	gb AAB82640.1 (AC002387) putative pectinesterase [<i>Arabidopsis thaliana</i>]	0		pectin- esterase
20271_at (Z99707.27_AT)	emb CAB16771.1 (Z99707) cytochrome P450-like protein [<i>Arabidopsis thaliana</i>]	0		
20285_s_at (AC003674.18_S_AT)	gb AAB97121.1 (AC003674) putative protein kinase [<i>Arabidopsis thaliana</i>]	0		
20287_at (Y14590.5_AT)	emb CAA74930.1 (Y14590) class IV chitinase [<i>Arabidopsis thaliana</i>]	1E-166		chitinase
20288_g_at (Y14590.5_G_AT)	emb CAA74930.1 (Y14590) class IV chitinase [<i>Arabidopsis thaliana</i>]	1E-166		
20291_s_at (M92353.4_S_AT)	gb AAA32738.1 (M92353) anthranilate synthase alpha subunit [<i>Arabidopsis thaliana</i>]	0		
20297_at (AC007153.27_AT)	gb AAD30627.1 AC007153_1 9 (AC007153) Similar to indole-3-acetate beta- glucosyltransferase [<i>Arabidopsis thaliana</i>]	0		glucosyl- transferase
20323_at (AC004561.62_AT)	gb AAC95188.1 (AC004561) putative small heat shock protein [<i>Arabidopsis thaliana</i>]	1E-67		

ProbeSet	Description	Blast Score	EC #	Family
20346_at (AL031135.156_AT)	emb CAA20030.1 (AL031135) protein kinase - like protein [Arabidopsis thaliana]	0		
20348_at (AC005967.35_AT)	gb AAD03382.1 (AC005967) putative limonene cyclase [Arabidopsis thaliana]	0		cyclase
20356_at (AC004561.74_AT)	gb AAC95191.1 (AC004561) putative glutathione S- transferase [Arabidopsis thaliana]	1E-128		transferase
20365_s_at (AC005850.19_S_AT)	gb AAD25552.1 AC005850_9 (AC005850) Highly Similar to Mlo proteins [Arabidopsis thaliana]	0		
20370_at (AC004561.263_AT)	gb AAC95219.1 (AC004561) putative tropinone reductase [Arabidopsis thaliana]	1E-151		reductase
20382_s_at (AC002338.35_S_AT)	gb AAC16930.1 (AC002338) putative WRKY-type DNA binding protein [Arabidopsis thaliana]	0		
20420_at (AL024486.131_AT)	emb CAA19698.1 (AL024486) putative chitinase [Arabidopsis thaliana]	0		chitinase
20421_at (U81294.2_AT)	emb CAB10242.1 (Z97336) germin precursor oxalate oxidase [Arabidopsis thaliana]	8E-98		
20422_g_at (U81294.2_G_AT)	emb CAB10242.1 (Z97336) germin precursor oxalate oxidase [Arabidopsis thaliana]	8E-98		
20432_at (U43486.2_AT)	gb AAB18365.1 (U43486) xyloglucan endotransglycosylase-related protein [Arabidopsis thaliana]	1E-174		trans- glycosylase
20433_at (AC006232.147_AT)	gb AAD15611.1 (AC006232) putative beta-1,3-glucanase [Arabidopsis thaliana]	0		glucanase
20450_at (AJ005930.2_AT)	emb CAA06772.1 (AJ005930) squalene epoxidase homologue [Arabidopsis thaliana]	0		epoxidase

ProbeSet	Description	Blast Score	EC #	Family
20461_at (AL049480.157_AT)	emb CAB39609.1 (AL049480) pumilio-like protein [Arabidopsis thaliana]	0		
20462_at (U82399.2_AT)	gb AAB40725.1 (U82399) putative protein kinase PK1 [Arabidopsis thaliana]	3E-38		kinase
20479_i_at (AF069495.2_I_AT)	emb CAB38908.1 (AL035708) cytochrome P450-like protein [Arabidopsis thaliana]	0		
20480_s_at (AF069495.2_S_AT)	emb CAB38908.1 (AL035708) cytochrome P450-like protein [Arabidopsis thaliana]	0		
20485_at (AC007660.131_AT)	gb AAD32811.1 AC007660_1 2 (AC007660) putative two- component response regulator protein [Arabidopsis thaliana]	1E-80		
20491_at (AC004561.146_AT)	gb AAC95203.1 (AC004561) putative tropinone reductase [Arabidopsis thaliana]	1E-153	EC_1.1.1.10 0	reductase
20511_at (AC007290.24_AT)	gb AAD26884.1 AC007290_3 (AC007290) putative nucleotide-binding protein [Arabidopsis thaliana]	0		
20517_at (Y17722.7_AT)	emb CAB50690.1 (Y17722) telomere repeat-binding protein TRP1 [Arabidopsis thaliana]	0		
20529_at (Z97341.125_AT)	emb CAB10426.1 (Z97341) cysteine proteinase inhibitor like protein [Arabidopsis thaliana]	7E-35		
20551_at (AC006081.211_AT)	gb AAD24395.1 AC006081_7 (AC006081) unknown protein [Arabidopsis thaliana]	0		
20572_s_at (AC005560.229_S_A T)	gb AAD12710.1 (AC006069) unknown protein [Arabidopsis thaliana]	1E-114		
20577_at (AL078464.72_AT)	emb CAB43841.1 (AL078464) putative protein [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
20584_at (AC004450.75_AT)	gb AAC64305.1 (AC004450) putative clathrin binding protein (epsin) [Arabidopsis thaliana]	2E-92		
20586_i_at (AC005824.195_I_A T)	gb AAC73042.1 (AC005824) unknown protein [Arabidopsis thaliana]	2E-67		
20587_s_at (AC005824.195_S_A T)	gb AAC73042.1 (AC005824) unknown protein [Arabidopsis thaliana]	2E-67		
20589_at (AF081066.3_AT)	gb AAC31939.1 (AF081066) IAA-amino acid hydrolase homolog ILL3 [Arabidopsis thaliana]	0		hydrolase
20591_at (AL080252.115_AT)	emb CAB45800.1 (AL080252) nodulin-like protein [Arabidopsis thaliana]	0		
20646_at (AC002291.20_AT)	gb AAC00619.1 (AC002291) Unknown protein [Arabidopsis thaliana]	0		
20656_at (AL035396.46_AT)	emb CAA23064.1 (AL035396) putative protein [Arabidopsis thaliana]	0		
20658_s_at (AL050400.70_S_AT)	emb CAB43701.1 (AL050400) beta-carotene hydroxylase [Arabidopsis thaliana]	1E-165		
20669_s_at (AC002388.6_S_AT)	gb AAD32838.1 AC007659_2 0 (AC007659) unknown protein [Arabidopsis thaliana]	0		
20685_at (AL049751.46_AT)	emb CAB41928.1 (AL049751) short-chain alcohol dehydrogenase like protein [Arabidopsis thaliana]	1E-139	EC_1.1.1.-	dehydro- genase
20686_at (Y14424.2_AT)	emb CAA74766.1 (Y14424) hypothetical protein [Arabidopsis thaliana]	0		
20689_s_at (AC002335.19_S_AT)	gb AAB64310.1 (AC002335) putative calcium binding protein [Arabidopsis thaliana]	6E-95		
20715_at (AF079183.1_AT)	gb AAC69857.1 (AF079183) RING-H2 finger protein RHG1a [Arabidopsis thaliana]	4E-99		

Parameter	Unit	Value	Unit	Value
Temperature	°C	25.0	Temperature	°C
Pressure	atm	1.0	Pressure	atm
Flow rate	L/min	1.0	Flow rate	L/min
Concentration	g/L	1.0	Concentration	g/L
pH		7.0	pH	
Time	min	10	Time	min
Distance	cm	10	Distance	cm
Volume	L	1.0	Volume	L
Mass	g	1.0	Mass	g
Energy	J	1.0	Energy	J
Power	W	1.0	Power	W
Frequency	Hz	1.0	Frequency	Hz
Wavelength	nm	1.0	Wavelength	nm
Angle	°	1.0	Angle	°
Area	cm ²	1.0	Area	cm ²
Volume	cm ³	1.0	Volume	cm ³
Mass	g	1.0	Mass	g
Energy	J	1.0	Energy	J
Power	W	1.0	Power	W
Frequency	Hz	1.0	Frequency	Hz
Wavelength	nm	1.0	Wavelength	nm
Angle	°	1.0	Angle	°
Area	cm ²	1.0	Area	cm ²
Volume	cm ³	1.0	Volume	cm ³
Mass	g	1.0	Mass	g
Energy	J	1.0	Energy	J
Power	W	1.0	Power	W
Frequency	Hz	1.0	Frequency	Hz
Wavelength	nm	1.0	Wavelength	nm
Angle	°	1.0	Angle	°
Area	cm ²	1.0	Area	cm ²
Volume	cm ³	1.0	Volume	cm ³
Mass	g	1.0	Mass	g
Energy	J	1.0	Energy	J
Power	W	1.0	Power	W
Frequency	Hz	1.0	Frequency	Hz
Wavelength	nm	1.0	Wavelength	nm
Angle	°	1.0	Angle	°
Area	cm ²	1.0	Area	cm ²
Volume	cm ³	1.0	Volume	cm ³
Mass	g	1.0	Mass	g
Energy	J	1.0	Energy	J
Power	W	1.0	Power	W
Frequency	Hz	1.0	Frequency	Hz
Wavelength	nm	1.0	Wavelength	nm
Angle	°	1.0	Angle	°
Area	cm ²	1.0	Area	cm ²
Volume	cm ³	1.0	Volume	cm ³
Mass	g	1.0	Mass	g
Energy	J	1.0	Energy	J
Power	W	1.0	Power	W
Frequency	Hz	1.0	Frequency	Hz
Wavelength	nm	1.0	Wavelength	nm
Angle	°	1.0	Angle	°
Area	cm ²	1.0	Area	cm ²
Volume	cm ³	1.0	Volume	cm ³
Mass	g	1.0	Mass	g
Energy	J	1.0	Energy	J
Power	W	1.0	Power	W
Frequency	Hz	1.0	Frequency	Hz
Wavelength	nm	1.0	Wavelength	nm
Angle	°	1.0	Angle	°
Area	cm ²	1.0	Area	cm ²
Volume	cm ³	1.0	Volume	cm ³
Mass	g	1.0	Mass	g
Energy	J	1.0	Energy	J
Power	W	1.0	Power	W
Frequency	Hz	1.0	Frequency	Hz
Wavelength	nm	1.0	Wavelength	nm
Angle	°	1.0	Angle	°
Area	cm ²	1.0	Area	cm ²
Volume	cm ³	1.0	Volume	cm ³
Mass	g	1.0	Mass	g
Energy	J	1.0	Energy	J
Power	W	1.0	Power	W
Frequency	Hz	1.0	Frequency	Hz
Wavelength	nm	1.0	Wavelength	nm
Angle	°	1.0	Angle	°
Area	cm ²	1.0	Area	cm ²
Volume	cm ³	1.0	Volume	cm ³
Mass	g	1.0	Mass	g
Energy	J	1.0	Energy	J
Power	W	1.0	Power	W
Frequency	Hz	1.0	Frequency	Hz
Wavelength	nm	1.0	Wavelength	nm
Angle	°	1.0	Angle	°
Area	cm ²	1.0	Area	

Table 4a Probe Sets in addition to those in Table 4b corresponding to genes, the expression of which is induced by *Pseudomonas* infection in wild-type *Arabidopsis* plants and perturbed in at least one mutant plant

ProbeSet	Description	Blast Score
13716_at (NOVARTIS103_RC_AT)	emb CAA62665.1 (X91259) lectin like protein [<i>Arabidopsis thaliana</i>]	6E-70
13751_at (NOVARTIS127_AT)	gb AAF16751.1 AC010155_4 (AC010155) F3M18.8 [<i>Arabidopsis thaliana</i>]	2E-27
13755_at (NOVARTIS15_AT)	emb CAA16797.1 (AL021713) receptor serine/threonine kinase-like protein [<i>Arabidopsis thaliana</i>]	1E-114
13763_at (NOVARTIS21_AT)	gb AAF24849.1 AC012679_20 (AC012679) putative calmodulin-binding protein [<i>Arabidopsis thaliana</i>]	1E-105
13764_at (NOVARTIS22_AT)	gb AAD39641.1 AC007591_6 (AC007591) F9L1.6 [<i>Arabidopsis thaliana</i>]	2E-30
14139_at (NOVARTIS30_AT)	gb AAD09343.1 (AF026538) ABA-responsive protein [<i>Hordeum vulgare</i>]	7E-36
14148_at (NOVARTIS38_AT)	gb AAF34713.1 AF224762_1 (AF224762) SigA binding protein [<i>Arabidopsis thaliana</i>]	4E-53
14170_at (NOVARTIS51_AT)	gb AAF29406.1 AC022354_5 (AC022354) unknown protein [<i>Arabidopsis thaliana</i>]	9E-26
14197_at (NOVARTIS71_AT)	No hits found.	
14214_at (NOVARTIS83_AT)	gb AAF24849.1 AC012679_20 (AC012679) putative calmodulin-binding protein [<i>Arabidopsis thaliana</i>]	2E-92
14223_at (NOVARTIS9_AT)	emb CAA19683.1 (AL024486) putative protein [<i>Arabidopsis thaliana</i>]	0

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Table 4b Probe Sets as referred to in Table 3 corresponding to genes, the expression of which is induced by *Pseudomonas* infection in wild-type *Arabidopsis* plants and perturbed in at least one mutant plant

11997_at (AC005967.4_AT)	12004_at (AL022023.132_AT)
12007_at (Z99708.249_AT)	12037_at (AC004005.174_AT)
12072_at (AL035396.4_AT)	12079_s_at (A71597.1_S_AT)
12081_at (AC001645.140_AT)	12115_at (AL033545.26_AT)
12136_at (AC007591.60_AT)	12150_at (AC004005.151_AT)
12198_at (AC006954.90_AT)	12216_at (AC007119.56_AT)

12233_at (AJ001807.1_AT)	12307_at (AC002392.162_AT)
12314_at (AC001229.28_AT)	12317_at (AC004138.27_AT)
12323_at (AC002333.18_AT)	12332_s_at (AB023448.2_S_AT)
12341_s_at (AL021637.176_S_AT)	12349_s_at (X84728.6_S_AT)
12369_at (AC002535.59_AT)	12400_at (X98453.1_AT)
12438_at (AL021710.83_AT)	12449_s_at (AC002343.179_S_AT)
12454_at (AC006232.164_AT)	12475_at (Y11794.1_AT)
12487_at (AC004411.126_AT)	12497_at (AC006533.51_AT)
12500_s_at (AF081067.3_S_AT)	12525_at (AC006587.85_AT)
12530_at (Z99707.184_AT)	12535_at (AL035538.156_AT)
12538_at (AF033205.2_AT)	12574_at (X82624.2_AT)
12584_at (AC004521.233_AT)	12626_at (AC006234.95_AT)
12645_at (AL021712.56_AT)	12712_f_at (Z95774_F_AT)
12736_f_at (Z97048_F_AT)	12744_at (AC001645.15_AT)
12760_g_at (AC005278.32_G_AT)	12764_f_at (AC004138.69_F_AT)
12772_at (AC005278.34_AT)	12797_s_at (AC007138.25_S_AT)
12851_s_at (ACCSYN1_S_AT)	12879_s_at (AIG1_S_AT)
12880_s_at (AIG2_S_AT)	12883_s_at (APX_S_AT)
12889_s_at (ASA1_S_AT)	12891_at (ATACS6_AT)
12892_g_at (ATACS6_G_AT)	12904_s_at (ATERF1_S_AT)
12905_s_at (ATERF2_S_AT)	12911_s_at (ATG6PDHE5_S_AT)
12921_s_at (ATHHMGCOAR_S_AT)	12951_at (AC005489.5_AT)
12958_at (AC002332.249_AT)	12965_at (AL021711.118_AT)
12966_s_at (AL023094.197_S_AT)	12989_s_at (AC004077.149_S_AT)
13003_s_at (AB021936.1_S_AT)	13014_at (U93215.87_AT)
13040_at (AC002392.134_AT)	13070_at (AC006919.171_AT)
13094_at (AL035523.163_AT)	13134_s_at (AC002337.9_S_AT)
13152_s_at (AC005322.24_S_AT)	13154_s_at (AC002333.210_S_AT)
13157_at (AC002409.35_AT)	13176_at (AL031394.56_AT)
13177_at (AL049640.42_AT)	13190_s_at (ATTHIREDA_S_AT)
13211_s_at (BCHI_S_AT)	13212_s_at (BGL2_S_AT)
13215_s_at (cafferoylcoamethyltrans_S_AT)	13219_s_at (CHI4_S_AT)
13243_r_at (ELI32_R_AT)	13244_s_at (ELI32_S_AT)
13255_i_at (gammaglutamyltranspepti_I_AT)	13266_s_at (GST4_S_AT)
13273_s_at (HSF4_S_AT)	13275_f_at (HSP174_F_AT)
13277_i_at (HSP176A_I_AT)	13285_s_at (HSP83_S_AT)

13312_at (AC006223.75_AT)	13370_at (AC005322.4_AT)
13381_at (AC006580.8_AT)	13395_at (AL035528.202_AT)
13435_at (AF003102.3_AT)	13437_at (AF096371.8_AT)
13467_at (AL096860.198_AT)	13536_at (AL021636.47_AT)
13538_at (AL080254.75_AT)	13565_at (AL035601.21_AT)
13588_at (AL021961.24_AT)	13589_at (AC000132.24_AT)
13617_at (AC006592.64_AT)	13627_at (AL035394.196_AT)
13645_at (AC000098.8_AT)	13656_at (AC007138.31_AT)
13659_at (AL022347.46_AT)	13666_s_at (INDOLE3GPS_S_AT)
13680_s_at (LOX1_S_AT)	13685_s_at (MLOLIKE2_S_AT)
13688_s_at (MONOPTEROS_S_AT)	13697_at (NI16_AT)
13705_s_at (AC003671X_S_AT)	13789_at (AJ132436.2_AT)
13803_at (Z97341.376_AT)	13818_s_at (AC006218.175_S_AT)
13842_at (AC002396.12_AT)	13848_at (AC003981.31_AT)
13880_s_at (AL049480.183_S_AT)	13908_s_at (A71590.1_S_AT)
13918_at (AC005388.29_AT)	13920_at (AC005990.53_AT)
13949_s_at (Z97343.352_S_AT)	13963_at (AL021711.26_AT)
13999_at (AF071527.56_AT)	14015_s_at (A71588.1_S_AT)
14016_s_at (A71596.1_S_AT)	14025_s_at (AC007293.3_S_AT)
14030_at (AC005970.225_AT)	14032_at (AL035601.11_AT)
14041_at (AC003970.28_AT)	14052_at (AC004122.24_AT)
14068_s_at (AC006922.197_S_AT)	14070_at (AL049658.217_AT)
14089_at (AC006223.65_AT)	14100_at (AF002109.108_AT)
14110_i_at (AL035528.279_I_AT)	14240_s_at (NR1_S_AT)
14242_s_at (NRA_S_AT)	14248_at (PAD3_AT)
14249_i_at (PAD4_I_AT)	14254_s_at (PAL1-MRNA_S_AT)
14256_f_at (PAL1-INTRON_F_AT)	14320_at (AC005956.54_AT)
14408_at (AC002291.14_AT)	14448_at (AC002387.243_AT)
14450_at (AC002986.49_AT)	14461_at (AC006202.73_AT)
14468_at (AC007576.62_AT)	14475_at (AL021811.121_AT)
14487_at (Z97341.343_AT)	14584_at (AC007658.25_AT)
14609_at (AC002340.147_AT)	14620_s_at (PAT1_S_AT)
14635_s_at (PR.1_S_AT)	14638_s_at (PRXCB_S_AT)
14640_s_at (putativemloHI_S_AT)	14643_s_at (RAR047_S_AT)
14663_s_at (trehalaseprecursor_RC_S_AT)	14667_s_at (TRPB_S_AT)
14672_s_at (TSA1_S_AT)	14673_s_at (TSB2_S_AT)

14675_s_at (VSP_S_AT)	14705_i_at (WT77_RC_I_AT)
14706_r_at (WT77_RC_R_AT)	14711_s_at (ZFPL_S_AT)
14735_s_at (AF008124_S_AT)	14750_s_at (AF096370.12_S_AT)
14763_at (X86958.1_AT)	14779_at (AC004680.71_AT)
14780_at (AC004683.103_AT)	14786_at (AC005397.115_AT)
14793_at (AC006202.10_AT)	14882_at (AL022605.63_AT)
14900_at (AC000348.12_AT)	14923_at (AC006283.158_AT)
14924_at (AC006283.46_AT)	14928_at (AC006569.88_AT)
14959_at (AC007202.26_AT)	14978_at (AC002333.49_AT)
15052_at (AC002332.103_AT)	15073_at (AC007069.93_AT)
15088_s_at (AC002311.37_S_AT)	15091_at (AC004683.97_AT)
15098_s_at (ATU26945_S_AT)	15116_f_at (AF121356_F_AT)
15123_s_at (ATU40857_S_AT)	15124_s_at (ATU59508_S_AT)
15125_f_at (D85190_F_AT)	15132_s_at (AF121878_S_AT)
15137_s_at (ATU57320_S_AT)	15141_s_at (D85191_S_AT)
15154_s_at (ATHMTGDAS_S_AT)	15161_s_at (ATU90522_S_AT)
15162_s_at (U01880_S_AT)	15188_s_at (AF081202_S_AT)
15196_s_at (ATU43412_S_AT)	15199_s_at (AB005804_S_AT)
15211_s_at (ATH243813_S_AT)	15216_s_at (ATU75191_S_AT)
15342_at (AC006593.101_AT)	15406_at (AC006931.179_AT)
15431_at (AL030978.64_AT)	15479_at (AL049483.205_AT)
15483_s_at (AC005819.20_S_AT)	15485_at (AC006233.109_AT)
15496_at (AC006282.167_AT)	15518_at (AC005322.28_AT)
15522_i_at (AL078637.213_I_AT)	15523_s_at (AL078637.213_S_AT)
15524_at (AC005508.25_AT)	15526_at (AC004122.16_AT)
15531_i_at (AL078637.191_I_AT)	15532_r_at (AL078637.191_R_AT)
15540_at (AC006585.205_AT)	15543_at (AF096371.10_AT)
15544_at (AL021633.110_AT)	15547_at (AC005970.122_AT)
15551_at (AL035440.289_AT)	15594_s_at (ATU56635_S_AT)
15613_s_at (ATHHOMEOA_S_AT)	15622_s_at (ATU43945_S_AT)
15625_s_at (ATU74610_S_AT)	15632_s_at (AB012570_S_AT)
15641_s_at (AF117063_S_AT)	15665_s_at (AF022658_S_AT)
15669_s_at (AF047834_S_AT)	15670_s_at (AF061638_S_AT)
15672_s_at (AF082299_S_AT)	15778_at (X98676.2_AT)
15779_g_at (X98676.2_G_AT)	15792_at (AC002341.106_AT)
15798_at (AC002521.173_AT)	15815_s_at (Z97342.366_S_AT)

15839_at (AC005662.203_AT)	15859_at (AC006587.164_AT)
15866_s_at (AC007133.59_S_AT)	15874_at (AL022223.106_AT)
15886_at (AL078637.204_AT)	15919_at (AC007060.42_AT)
15921_s_at (AC007067.1_S_AT)	15924_at (AC007138.61_AT)
15970_s_at (X71794.2_S_AT)	15978_at (X68592.6_AT)
15982_s_at (AC006260.78_S_AT)	16001_at (AF035385.2_AT)
16003_s_at (AL021749.64_S_AT)	16021_s_at (AL022224.182_S_AT)
16031_at (X94248.1_AT)	16043_at (AC005489.17_AT)
16053_i_at (Y14251.4_I_AT)	16063_s_at (AB008103_S_AT)
16073_f_at (AF062908_F_AT)	16083_s_at (AF153283_S_AT)
16091_s_at (ATHHSP83_S_AT)	16103_s_at (ATU60445_S_AT)
16105_s_at (ATU68017_S_AT)	16108_s_at (D78604_S_AT)
16130_s_at (AF078683_S_AT)	16173_s_at (D78607_S_AT)
16203_at (AC007519.53_AT)	16232_s_at (AL080252.77_S_AT)
16233_at (AL080254.83_AT)	16272_at (AC006304.136_AT)
16298_at (AL021890.71_AT)	16299_at (AL024486.185_AT)
16301_s_at (AL031018.105_S_AT)	16306_at (AL049751.112_AT)
16335_at (AL079347.105_AT)	16340_at (AC004255.15_AT)
16357_at (AF149413.38_AT)	16363_at (AC004255.14_AT)
16383_at (AC006300.64_AT)	16398_s_at (AL022603.3_S_AT)
16405_at (AC005850.9_AT)	16409_at (AC004393.2_AT)
16440_s_at (AF002109.137_S_AT)	16461_i_at (AC004683.79_I_AT)
16462_s_at (AC004683.79_S_AT)	16465_at (Y08892.1_AT)
16470_s_at (AF068299.4_S_AT)	16510_at (AL034567.198_AT)
16522_at (X77500.2_AT)	16526_at (Z49227.1_AT)
16541_s_at (AB023423_S_AT)	16545_s_at (AF037229_S_AT)
16553_f_at (AF078821_F_AT)	16570_s_at (ATHCDPKA_S_AT)
16578_s_at (ATHRPRP1B_S_AT)	16589_s_at (ATU26937_S_AT)
16594_s_at (ATU39783_S_AT)	16603_s_at (ATU81293_S_AT)
16609_s_at (AB008104_S_AT)	16611_s_at (AB008782_S_AT)
16638_s_at (AF139098_S_AT)	16646_s_at (ATHDHS1_S_AT)
16649_s_at (ATHORF_S_AT)	16701_at (AC005312.61_AT)
16721_at (AC006533.58_AT)	16747_at (AL021713.3_AT)
16781_at (AC002392.100_AT)	16810_at (AC002339.46_AT)
16859_at (AL035523.135_AT)	16864_i_at (AF037367.4_I_AT)
16865_s_at (AF037367.4_S_AT)	16888_s_at (AC004684.174_S_AT)

16914_s_at (AL049500.57_S_AT)
 16968_at (AL021961.93_AT)
 16995_at (AC002391.188_AT)
 17008_at (AC006585.212_AT)
 17041_s_at (D89631_S_AT)
 17066_s_at (ATHLIPOXY_S_AT)
 17075_s_at (ATU09961_S_AT)
 17111_s_at (ATHACSC_S_AT)
 17128_s_at (ATHRPRP1A_S_AT)
 17187_at (AF128396.2_AT)
 17303_s_at (AC004683.25_S_AT)
 17338_at (AC002535.97_AT)
 17356_s_at (Z97338.190_S_AT)
 17379_at (AF085279.9_AT)
 17451_at (AC002343.47_AT)
 17484_at (X79052.2_AT)
 17487_s_at (U18993.2_S_AT)
 17514_s_at (AF076277_S_AT)
 17533_s_at (ATU43488_S_AT)
 17548_s_at (AF118823_S_AT)
 17595_s_at (AF166352_S_AT)
 17653_at (AL035679.144_AT)
 17719_at (AC006592.17_AT)
 17758_at (AF076243.41_AT)
 17781_at (AL049746.177_AT)
 17860_at (AL078467.4_AT)
 17877_g_at (AJ007587.2_G_AT)
 17899_at (Z97339.197_AT)
 17945_at (Z97341.411_AT)
 18012_s_at (AJ002295_S_AT)
 18109_s_at (AC002391.206_S_AT)
 18122_at (AC002338.110_AT)
 18176_at (AL035540.31_AT)
 18213_at (AL022140.126_AT)
 18228_at (X91259.1_AT)
 18242_g_at (AC006580.71_G_AT)

16916_s_at (X77199.8_S_AT)
 16989_at (AL030978.46_AT)
 17007_at (AC005896.26_AT)
 17039_s_at (D78602_S_AT)
 17051_s_at (AF098947_S_AT)
 17073_s_at (ATTS4391_S_AT)
 17104_s_at (D88541_S_AT)
 17119_s_at (AF132212_S_AT)
 17180_at (AF007270.30_AT)
 17300_at (X66017.2_AT)
 17323_at (U95973.69_AT)
 17341_at (AL021713.89_AT)
 17371_at (AF076243.44_AT)
 17413_s_at (AJ006961.4_S_AT)
 17452_g_at (AC002343.47_G_AT)
 17485_s_at (Z97340.345_S_AT)
 17511_s_at (AF067605_S_AT)
 17522_s_at (D78606_S_AT)
 17544_s_at (ATU40856_S_AT)
 17585_s_at (AF134487_S_AT)
 17648_at (AL021684.43_AT)
 17702_at (AC005700.212_AT)
 17752_at (AC003974.37_AT)
 17775_at (AC004392.2_AT)
 17840_s_at (AC002333.223_S_AT)
 17876_at (AJ007587.2_AT)
 17893_at (AC004401.135_AT)
 17930_s_at (AJ006960.4_S_AT)
 17963_at (AL049730.88_AT)
 18054_at (AJ238846_AT)
 18121_s_at (AC002337.21_S_AT)
 18148_at (AC004669.25_AT)
 18194_i_at (AL096859.227_I_AT)
 18224_s_at (AL021890.57_S_AT)
 18236_s_at (AC004683.69_S_AT)
 18255_at (AC005770.25_AT)

18258_s_at (AC006439.222_S_AT)
 18266_at (AC004684.33_AT)
 18299_s_at (M23872.2_S_AT)
 18508_s_at (AC006532.89_S_AT)
 18582_s_at (AC003671.36_S_AT)
 18590_at (AJ222713.4_AT)
 18596_at (AC005698.13_AT)
 18604_at (AF069298.31_AT)
 18625_at (AC005278.22_AT)
 18636_at (AC006577.22_AT)
 18686_s_at (U18126_S_AT)
 18735_s_at (Z29490_S_AT)
 18782_at (AC003040.90_AT)
 18885_at (AC006921.147_AT)
 18899_s_at (X13434.1_S_AT)
 18909_s_at (AF055848.2_S_AT)
 18930_at (AC005990.57_AT)
 18949_at (Z54136.1_AT)
 18963_at (AC004561.99_AT)
 19019_i_at (X82623.2_I_AT)
 19092_at (AL078606.188_AT)
 19137_at (X74755.2_AT)
 19181_s_at (AF053065.2_S_AT)
 19247_at (AF071527.44_AT)
 19284_at (AC003028.196_AT)
 19325_at (AL022604.42_AT)
 19383_at (AC006200.203_AT)
 19405_at (AJ223803.1_AT)
 19409_at (AC007357.56_AT)
 19421_at (X70990.4_AT)
 19451_at (AC004392.6_AT)
 19465_at (AL021768.96_AT)
 19555_at (AF058919.48_AT)
 19614_at (AC003970.32_AT)
 19625_s_at (AC002311.26_S_AT)
 19640_at (AC004561.78_AT)

18263_at (AC005724.36_AT)
 18267_at (AC006223.23_AT)
 18456_s_at (AC004697.159_S_AT)
 18544_at (AC007060.14_AT)
 18587_s_at (AC007166.53_S_AT)
 18591_at (X74756.2_AT)
 18597_at (AL080282.74_AT)
 18622_g_at (AJ005902.2_G_AT)
 18631_at (AC002510.112_AT)
 18668_at (AJ249794_AT)
 18698_s_at (X17528_S_AT)
 18753_s_at (AF118222.28_S_AT)
 18803_at (AC005315.94_AT)
 18888_at (AC007591.68_AT)
 18908_i_at (AF055848.2_I_AT)
 18928_at (AC002333.181_AT)
 18933_at (AC007020.48_AT)
 18953_at (AF077955.1_AT)
 18966_at (AC004561.106_AT)
 19060_at (AC003671.34_AT)
 19110_s_at (X86947.2_S_AT)
 19140_at (AC005170.24_AT)
 19207_at (AC006069.117_AT)
 19257_s_at (AC000104.57_S_AT)
 19288_at (AC005824.130_AT)
 19364_at (AL022023.142_AT)
 19395_at (AF007270.32_AT)
 19407_at (AC004697.81_AT)
 19411_at (AC007661.104_AT)
 19432_s_at (AL035680.11_S_AT)
 19460_s_at (AC000132.66_S_AT)
 19546_at (AC005398.172_AT)
 19591_at (AJ010735.4_AT)
 19624_at (AL049481.196_AT)
 19635_at (AL049746.38_AT)
 19641_at (AC004561.66_AT)

19645_at (AC004561.70_AT)	19655_at (Y14199.1_AT)
19667_at (AL021710.5_AT)	19672_at (AC005687.19_AT)
19673_g_at (AC005687.19_G_AT)	19700_s_at (AL031326.154_S_AT)
19704_i_at (AJ005927.2_I_AT)	19707_s_at (Z95768.3_S_AT)
19741_at (AL049171.72_AT)	19755_at (AC006593.64_AT)
19762_at (AL035527.204_AT)	19818_i_at (AL021749.33_I_AT)
19844_at (AJ007588.2_AT)	19848_s_at (AC004261.94_S_AT)
19851_at (U23794.3_AT)	19881_at (AC004077.49_AT)
19892_at (AC005770.30_AT)	19895_s_at (U77347.4_S_AT)
19944_at (AC002130.4_AT)	19956_at (AC006282.11_AT)
19960_at (AL035527.360_AT)	19970_s_at (AC003674.10_S_AT)
19982_at (AC002986.28_AT)	19991_at (AC007017.124_AT)
20017_at (AC004521.66_AT)	20023_at (AC006577.46_AT)
20030_at (AL078637.51_AT)	20051_at (AC000106.38_AT)
20053_at (AC002292.27_AT)	20096_at (AC004238.31_AT)
20098_at (AC004697.123_AT)	20133_i_at (AC007178.71_I_AT)
20134_s_at (AC007178.71_S_AT)	20144_at (AL079350.68_AT)
20179_at (AL035538.229_AT)	20189_at (AC005489.2_AT)
20194_at (AC007584.48_AT)	20223_at (AL022347.145_AT)
20238_at (X74514.2_AT)	20239_g_at (X74514.2_G_AT)
20245_s_at (AC005309.97_S_AT)	20247_at (AC004392.4_AT)
20263_at (AB004798.1_AT)	20269_at (AC002387.237_AT)
20271_at (Z99707.27_AT)	20287_at (Y14590.5_AT)
20288_g_at (Y14590.5_G_AT)	20291_s_at (M92353.4_S_AT)
20297_at (AC007153.27_AT)	20323_at (AC004561.62_AT)
20348_at (AC005967.35_AT)	20356_at (AC004561.74_AT)
20365_s_at (AC005850.19_S_AT)	20370_at (AC004561.263_AT)
20420_at (AL024486.131_AT)	20421_at (U81294.2_AT)
20422_g_at (U81294.2_G_AT)	20432_at (U43486.2_AT)
20433_at (AC006232.147_AT)	20450_at (AJ005930.2_AT)
20461_at (AL049480.157_AT)	20462_at (U82399.2_AT)
20479_i_at (AF069495.2_I_AT)	20480_s_at (AF069495.2_S_AT)
20485_at (AC007660.131_AT)	20529_at (Z97341.125_AT)
20572_s_at (AC005560.229_S_AT)	20589_at (AF081066.3_AT)
20646_at (AC002291.20_AT)	20656_at (AL035396.46_AT)
20658_s_at (AL050400.70_S_AT)	20669_s_at (AC002388.6_S_AT)

20685_at (AL049751.46_AT)
20689_s_at (AC002335.19_S_AT)

20686_at (Y14424.2_AT)

20685_at (AL049751.46_AT)

Table 5 Probe Sets as referred to in Tables 4a and 4b corresponding to genes encoding regulatory proteins, the expression of which is increased after infection of wild-type *Arabidopsis*, and altered after infection of at least one mutant *Arabidopsis*, with *Pseudomonas syringae*

5

ProbeSet	Regulatory factor
12497_at (AC006533.51_AT)	putative receptor-like protein kinase
16409_at (AC004393.2_AT)	putative receptor-like kinase
12307_at (AC002392.162_AT)	putative receptor-like protein kinase
13659_at (AL022347.46_AT)	serine/threonine kinase-like protein
17341_at (AL021713.89_AT)	receptor serine/threonine kinase-like protein
12958_at (AC002332.249_AT)	putative protein kinase
17758_at (AF076243.41_AT)	putative receptor-like protein kinase
16570_s_at (ATHCDPKA_S_AT)	CDPK1 calcium dependent protein kinase 1
19092_at (AL078606.188_AT)	protein kinase-like protein
17371_at (AF076243.44_AT)	putative receptor-like protein kinase
20223_at (AL022347.145_AT)	putative ser/thr protein kinase
19655_at (Y14199.1_AT)	MAP3K delta-1 protein kinase
14030_at (AC005970.225_AT)	putative protein kinase
20462_at (U82399.2_AT)	putative protein kinase PK1
16781_at (AC002392.100_AT)	putative receptor-like protein kinase
14763_at (X86958.1_AT)	protein kinase catalytic domain (fragment)
17752_at (AC003974.37_AT)	putative protein kinase
13755_at (NOVARTIS15_AT)	putative ser/thr kinase
13370_at (AC005322.4_AT)	similar to Dsor1 protein kinase
20144_at (AL079350.68_AT)	receptor kinase-like protein
16357_at (AF149413.38_AT)	putative protein kinase
18176_at (AL035540.31_AT)	putative protein kinase
15798_at (AC002521.173_AT)	putative receptor-like protein kinase
12965_at (AL021711.118_AT)	protein kinase-like protein
16398_s_at (AL022603.3_S_AT)	putative ser/thr protein kinase
18122_at (AC002338.110_AT)	putative protein kinase
17323_at (U95973.69_AT)	putative ser/thr protein kinase
18782_at (AC003040.90_AT)	putative protein kinase
16405_at (AC005850.9_AT)	putative serine/threonine protein kinase

ProbeSet	Regulatory factor
14110_i_at (AL035528.279_I_AT)	putative R protein. Like Hcr9-9A, Lycopersicon pimpinellifolium F18A5_290 chr.4
14214_at (NOVARTIS83_AT)	putative calmodulin-binding protein (duplicate)
13763_at (NOVARTIS21_AT)	putative calmodulin-binding protein (duplicate)
12438_at (AL021710.83_AT)	membrane-bound small GTP-binding - like protein
19848_s_at (AC004261.94_S_AT)	calmodulin-related protein
16103_s_at (ATU60445_S_AT)	GRF7 general regulatory factor encoding 14-3-3 protein
14249_i_at (PAD4_I_AT)	PAD4 phytoalexin deficient 4
19465_at (AL021768.96_AT)	RPP5-like NBS-LRR resistance protein
14640_s_at (putativemloHI_S_AT)	Mlo-like (duplicate)
18456_s_at (AC004697.159_S_AT)	Mlo-like (duplicate)
14320_at (AC005956.54_AT)	putative RING zinc finger protein
18054_at (AJ238846_AT)	SGP1 monomeric G-protein
16130_s_at (AF078683_S_AT)	RHA1a RING-H2 finger protein
20485_at (AC007660.131_AT)	putative two-component response regulator protein
15052_at (AC002332.103_AT)	putative calcium-binding EF-hand protein
15632_s_at (AB012570_S_AT)	ATHP3 two-compoent phosphorelay mediator with a single HPt domain
16553_f_at (AF078821_F_AT)	RHA1b RING-H2 finger protein
13685_s_at (MLOLIKE2_S_AT)	Mlo-like 2 (duplicate)
20365_s_at (AC005850.19_S_AT)	Mlo-like 2 (duplicate)
13312_at (AC006223.75_AT)	putative disease resistance protein
17180_at (AF007270.30_AT)	similar to GATA-type zinc fingers
15779_g_at (X98676.2_G_AT)	zinc finger protein (duplicate)
15778_at (X98676.2_AT)	zinc finger protein (duplicate)
14711_s_at (ZFPL_S_AT)	hypothetical Cys-3-His zinc finger protein
17379_at (AF085279.9_AT)	putative CCCH-type zinc finger protein
12525_at (AC006587.85_AT)	putative DOF zinc finger protein
16589_s_at (ATU26937_S_AT)	AtMYB7 transcription factor
12712_f_at (Z95774_F_AT)	AtMYB51 R2R3 myb transcription factor
13273_s_at (HSF4_S_AT)	HSF4 heat shock transcription factor 4 (duplicate)
16105_s_at (ATU68017_S_AT)	HSF4 heat shock transcription factor 4 (duplicate)
18803_at (AC005315.94_AT)	putative SCARECROW homeobox gene regulator

ProbeSet	Regulatory factor
12905_s_at (ATERF2_S_AT)	EREBP2 ethylene responsive element binding factor 2 (duplicate)
16609_s_at (AB008104_S_AT)	EREBP2 ethylene responsive element binding factor 2 (duplicate)
19755_at (AC006593.64_AT)	ethylene reponse factor-like AP2 domain transcription factor
17514_s_at (AF076277_S_AT)	ERF1 ethylene response factor 1 transcription factor
18121_s_at (AC002337.21_S_AT)	AtMYB2 MYB transcription factor
13688_s_at (monopteros_S_AT)	transcription factor
12904_s_at (ATERF1_S_AT)	EREBP1 ethylene responsive element binding factor 1 (duplicate)
16063_s_at (AB008103_S_AT)	EREBP1 ethylene responsive element binding factor 1 (duplicate)
16638_s_at (AF139098_S_AT)	putative zinc finger protein
16545_s_at (AF037229_S_AT)	transcription factor
13435_at (AF003102.3_AT)	RAP2.9 AP2 domain containing putative transcription factor
15665_s_at (AF022658_S_AT)	putative c2h2 zinc finger transcription factor
19673_g_at (AC005687.19_G_AT)	RAP2.6 AP2 domain containing putative transcription factor (duplicate)
19672_at (AC005687.19_AT)	RAP2.6 AP2 domain containing putative transcription factor (duplicate)
14780_at (AC004683.103_AT)	DREB-like AP2 domain transcription factor
17303_s_at (AC004683.25_S_AT)	WRKY33 transcription factor
18949_at (Z54136.1_AT)	MYB-related protein
19707_s_at (Z95768.3_S_AT)	AtMYB44 transcription factor
16073_f_at (AF062908_F_AT)	putative transcription factor
12966_s_at (AL023094.197_S_AT)	ATB2 bZIP transcription factor
12736 f at (Z97048 F_AT)	AtMYB13 transcription factor

Table 6 Probe Sets as referred to in Tables 4a and 4b corresponding to genes, the expression of which is increased after infection of wild-type *Arabidopsis*, and altered after infection of at least one mutant *Arabidopsis* having a mutation that results in enhanced susceptibility to *Pseudomonas*

12079_s_at (A71597.1_S_AT)	12081_at (AC001645.140_AT)
12115_at (AL033545.26_AT)	12150_at (AC004005.151_AT)
12233_at (AJ001807.1_AT)	12307_at (AC002392.162_AT)
12314_at (AC001229.28_AT)	12332_s_at (AB023448.2_S_AT)
12341_s_at (AL021637.176_S_AT)	12400_at (X98453.1_AT)
12438_at (AL021710.83_AT)	12475_at (Y11794.1_AT)
12487_at (AC004411.126_AT)	12497_at (AC006533.51_AT)
12500_s_at (AF081067.3_S_AT)	12530_at (Z99707.184_AT)
12574_at (X82624.2_AT)	12584_at (AC004521.233_AT)
12712_f_at (Z95774_F_AT)	12760_g_at (AC005278.32_G_AT)
12764_f_at (AC004138.69_F_AT)	12772_at (AC005278.34_AT)
12851_s_at (ACCSYN1_S_AT)	12879_s_at (AIG1_S_AT)
12883_s_at (APX_S_AT)	12889_s_at (ASA1_S_AT)
12891_at (ATACS6_AT)	12892_g_at (ATACS6_G_AT)
12905_s_at (ATERF2_S_AT)	12911_s_at (ATG6PDHE5_S_AT)
12921_s_at (ATHHMGCOAR_S_AT)	12958_at (AC002332.249_AT)
12989_s_at (AC004077.149_S_AT)	13003_s_at (AB021936.1_S_AT)
13014_at (U93215.87_AT)	13040_at (AC002392.134_AT)
13070_at (AC006919.171_AT)	13094_at (AL035523.163_AT)
13157_at (AC002409.35_AT)	13177_at (AL049640.42_AT)
13190_s_at (ATTHIREDA_S_AT)	13211_s_at (BCHI_S_AT)
13212_s_at (BGL2_S_AT)	13219_s_at (CHI4_S_AT)
13266_s_at (GST4_S_AT)	13273_s_at (HSF4_S_AT)
13275_f_at (HSP174_F_AT)	13370_at (AC005322.4_AT)
13381_at (AC006580.8_AT)	13435_at (AF003102.3_AT)
13467_at (AL096860.198_AT)	13538_at (AL080254.75_AT)
13565_at (AL035601.21_AT)	13588_at (AL021961.24_AT)
13589_at (AC000132.24_AT)	13617_at (AC006592.64_AT)
13627_at (AL035394.196_AT)	13656_at (AC007138.31_AT)
13659_at (AL022347.46_AT)	13666_s_at (INDOLE3GPS_S_AT)
13680_s_at (LOX1_S_AT)	13688_s_at (MONOPTEROS_S_AT)

13697_at (NI16_AT)	13716_at (NOVARTIS103_RC_AT)
13751_at (NOVARTIS127_AT)	13755_at (NOVARTIS15_AT)
13763_at (NOVARTIS21_AT)	13764_at (NOVARTIS22_AT)
13818_s_at (AC006218.175_S_AT)	13842_at (AC002396.12_AT)
13880_s_at (AL049480.183_S_AT)	13920_at (AC005990.53_AT)
14015_s_at (A71588.1_S_AT)	14016_s_at (A71596.1_S_AT)
14025_s_at (AC007293.3_S_AT)	14030_at (AC005970.225_AT)
14032_at (AL035601.11_AT)	14041_at (AC003970.28_AT)
14052_at (AC004122.24_AT)	14068_s_at (AC006922.197_S_AT)
14110_i_at (AL035528.279_I_AT)	14139_at (NOVARTIS30_AT)
14148_at (NOVARTIS38_AT)	14170_at (NOVARTIS51_AT)
14214_at (NOVARTIS83_AT)	14242_s_at (NRA_S_AT)
14248_at (PAD3_AT)	14249_i_at (PAD4_I_AT)
14408_at (AC002291.14_AT)	14450_at (AC002986.49_AT)
14461_at (AC006202.73_AT)	14487_at (Z97341.343_AT)
14584_at (AC007658.25_AT)	14609_at (AC002340.147_AT)
14620_s_at (PAT1_S_AT)	14635_s_at (PR.1_S_AT)
14638_s_at (PRXCB_S_AT)	14663_s_at (trehalaseprecursor_RC_S_AT)
14667_s_at (TRPB_S_AT)	14672_s_at (TSA1_S_AT)
14673_s_at (TSB2_S_AT)	14705_i_at (WT77_RC_I_AT)
14706_r_at (WT77_RC_R_AT)	14735_s_at (AF008124_S_AT)
14763_at (X86958.1_AT)	14786_at (AC005397.115_AT)
14882_at (AL022605.63_AT)	14924_at (AC006283.46_AT)
14959_at (AC007202.26_AT)	14978_at (AC002333.49_AT)
15073_at (AC007069.93_AT)	15091_at (AC004683.97_AT)
15098_s_at (ATU26945_S_AT)	15116_f_at (AF121356_F_AT)
15124_s_at (ATU59508_S_AT)	15125_f_at (D85190_F_AT)
15137_s_at (ATU57320_S_AT)	15154_s_at (ATHMTGDAS_S_AT)
15162_s_at (U01880_S_AT)	15196_s_at (ATU43412_S_AT)
15199_s_at (AB005804_S_AT)	15216_s_at (ATU75191_S_AT)
15406_at (AC006931.179_AT)	15431_at (AL030978.64_AT)
15483_s_at (AC005819.20_S_AT)	15496_at (AC006282.167_AT)
15518_at (AC005322.28_AT)	15522_i_at (AL078637.213_I_AT)
15526_at (AC004122.16_AT)	15531_i_at (AL078637.191_I_AT)
15540_at (AC006585.205_AT)	15543_at (AF096371.10_AT)
15544_at (AL021633.110_AT)	15551_at (AL035440.289_AT)

15594_s_at (ATU56635_S_AT)	15622_s_at (ATU43945_S_AT)
15632_s_at (AB012570_S_AT)	15665_s_at (AF022658_S_AT)
15672_s_at (AF082299_S_AT)	15778_at (X98676.2_AT)
15779_g_at (X98676.2_G_AT)	15815_s_at (Z97342.366_S_AT)
15839_at (AC005662.203_AT)	15859_at (AC006587.164_AT)
15866_s_at (AC007133.59_S_AT)	15874_at (AL022223.106_AT)
15886_at (AL078637.204_AT)	15924_at (AC007138.61_AT)
15970_s_at (X71794.2_S_AT)	15978_at (X68592.6_AT)
15982_s_at (AC006260.78_S_AT)	16001_at (AF035385.2_AT)
16003_s_at (AL021749.64_S_AT)	16021_s_at (AL022224.182_S_AT)
16031_at (X94248.1_AT)	16043_at (AC005489.17_AT)
16053_i_at (Y14251.4_I_AT)	16083_s_at (AF153283_S_AT)
16091_s_at (ATHHSP83_S_AT)	16103_s_at (ATU60445_S_AT)
16105_s_at (ATU68017_S_AT)	16108_s_at (D78604_S_AT)
16130_s_at (AF078683_S_AT)	16233_at (AL080254.83_AT)
16272_at (AC006304.136_AT)	16298_at (AL021890.71_AT)
16299_at (AL024486.185_AT)	16306_at (AL049751.112_AT)
16340_at (AC004255.15_AT)	16357_at (AF149413.38_AT)
16363_at (AC004255.14_AT)	16383_at (AC006300.64_AT)
16409_at (AC004393.2_AT)	16461_i_at (AC004683.79_I_AT)
16462_s_at (AC004683.79_S_AT)	16470_s_at (AF068299.4_S_AT)
16545_s_at (AF037229_S_AT)	16570_s_at (ATHCDPKA_S_AT)
16578_s_at (ATHRPRP1B_S_AT)	16589_s_at (ATU26937_S_AT)
16594_s_at (ATU39783_S_AT)	16603_s_at (ATU81293_S_AT)
16609_s_at (AB008104_S_AT)	16701_at (AC005312.61_AT)
16721_at (AC006533.58_AT)	16781_at (AC002392.100_AT)
16810_at (AC002339.46_AT)	16859_at (AL035523.135_AT)
16864_i_at (AF037367.4_I_AT)	16865_s_at (AF037367.4_S_AT)
16914_s_at (AL049500.57_S_AT)	16968_at (AL021961.93_AT)
16989_at (AL030978.46_AT)	16995_at (AC002391.188_AT)
17007_at (AC005896.26_AT)	17051_s_at (AF098947_S_AT)
17066_s_at (ATHLIPOXY_S_AT)	17075_s_at (ATU09961_S_AT)
17128_s_at (ATHRPRP1A_S_AT)	17180_at (AF007270.30_AT)
17338_at (AC002535.97_AT)	17341_at (AL021713.89_AT)
17356_s_at (Z97338.190_S_AT)	17371_at (AF076243.44_AT)
17413_s_at (AJ006961.4_S_AT)	17451_at (AC002343.47_AT)

17452_g_at (AC002343.47_G_AT)
 17485_s_at (Z97340.345_S_AT)
 17533_s_at (ATU43488_S_AT)
 17585_s_at (AF134487_S_AT)
 17752_at (AC003974.37_AT)
 17775_at (AC004392.2_AT)
 17840_s_at (AC002333.223_S_AT)
 17893_at (AC004401.135_AT)
 17930_s_at (AJ006960.4_S_AT)
 17963_at (AL049730.88_AT)
 18109_s_at (AC002391.206_S_AT)
 18176_at (AL035540.31_AT)
 18213_at (AL022140.126_AT)
 18242_g_at (AC006580.71_G_AT)
 18258_s_at (AC006439.222_S_AT)
 18508_s_at (AC006532.89_S_AT)
 18590_at (AJ222713.4_AT)
 18596_at (AC005698.13_AT)
 18622_g_at (AJ005902.2_G_AT)
 18686_s_at (U18126_S_AT)
 18735_s_at (Z29490_S_AT)
 18803_at (AC005315.94_AT)
 18888_at (AC007591.68_AT)
 18909_s_at (AF055848.2_S_AT)
 18930_at (AC005990.57_AT)
 18953_at (AF077955.1_AT)
 19019_i_at (X82623.2_I_AT)
 19140_at (AC005170.24_AT)
 19207_at (AC006069.117_AT)
 19257_s_at (AC000104.57_S_AT)
 19325_at (AL022604.42_AT)
 19383_at (AC006200.203_AT)
 19407_at (AC004697.81_AT)
 19411_at (AC007661.104_AT)
 19432_s_at (AL035680.11_S_AT)
 19460_s_at (AC000132.66_S_AT)

17484_at (X79052.2_AT)
 17487_s_at (U18993.2_S_AT)
 17544_s_at (ATU40856_S_AT)
 17653_at (AL035679.144_AT)
 17758_at (AF076243.41_AT)
 17781_at (AL049746.177_AT)
 17877_g_at (AJ007587.2_G_AT)
 17899_at (Z97339.197_AT)
 17945_at (Z97341.411_AT)
 18054_at (AJ238846_AT)
 18148_at (AC004669.25_AT)
 18194_i_at (AL096859.227_I_AT)
 18228_at (X91259.1_AT)
 18255_at (AC005770.25_AT)
 18267_at (AC006223.23_AT)
 18544_at (AC007060.14_AT)
 18591_at (X74756.2_AT)
 18604_at (AF069298.31_AT)
 18625_at (AC005278.22_AT)
 18698_s_at (X17528_S_AT)
 18753_s_at (AF118222.28_S_AT)
 18885_at (AC006921.147_AT)
 18899_s_at (X13434.1_S_AT)
 18928_at (AC002333.181_AT)
 18933_at (AC007020.48_AT)
 18966_at (AC004561.106_AT)
 19137_at (X74755.2_AT)
 19181_s_at (AF053065.2_S_AT)
 19247_at (AF071527.44_AT)
 19288_at (AC005824.130_AT)
 19364_at (AL022023.142_AT)
 19405_at (AJ223803.1_AT)
 19409_at (AC007357.56_AT)
 19421_at (X70990.4_AT)
 19451_at (AC004392.6_AT)
 19465_at (AL021768.96_AT)

19546_at (AC005398.172_AT)
 19624_at (AL049481.196_AT)
 19645_at (AC004561.70_AT)
 19741_at (AL049171.72_AT)
 19818_i_at (AL021749.33_I_AT)
 19881_at (AC004077.49_AT)
 19944_at (AC002130.4_AT)
 19970_s_at (AC003674.10_S_AT)
 19991_at (AC007017.124_AT)
 20030_at (AL078637.51_AT)
 20098_at (AC004697.123_AT)
 20134_s_at (AC007178.71_S_AT)
 20238_at (X74514.2_AT)
 20245_s_at (AC005309.97_S_AT)
 20263_at (AB004798.1_AT)
 20271_at (Z99707.27_AT)
 20288_g_at (Y14590.5_G_AT)
 20297_at (AC007153.27_AT)
 20348_at (AC005967.35_AT)
 20370_at (AC004561.263_AT)
 20421_at (U81294.2_AT)
 20432_at (U43486.2_AT)
 20461_at (AL049480.157_AT)
 20479_i_at (AF069495.2_I_AT)
 20485_at (AC007660.131_AT)
 20572_s_at (AC005560.229_S_AT)
 20669_s_at (AC002388.6_S_AT)
 20689_s_at (AC002335.19_S_AT)

19555_at (AF058919.48_AT)
 19641_at (AC004561.66_AT)
 19667_at (AL021710.5_AT)
 19755_at (AC006593.64_AT)
 19848_s_at (AC004261.94_S_AT)
 19892_at (AC005770.30_AT)
 19956_at (AC006282.11_AT)
 19982_at (AC002986.28_AT)
 20017_at (AC004521.66_AT)
 20051_at (AC000106.38_AT)
 20133_i_at (AC007178.71_I_AT)
 20144_at (AL079350.68_AT)
 20239_g_at (X74514.2_G_AT)
 20247_at (AC004392.4_AT)
 20269_at (AC002387.237_AT)
 20287_at (Y14590.5_AT)
 20291_s_at (M92353.4_S_AT)
 20323_at (AC004561.62_AT)
 20356_at (AC004561.74_AT)
 20420_at (AL024486.131_AT)
 20422_g_at (U81294.2_G_AT)
 20450_at (AJ005930.2_AT)
 20462_at (U82399.2_AT)
 20480_s_at (AF069495.2_S_AT)
 20529_at (Z97341.125_AT)
 20589_at (AF081066.3_AT)
 20685_at (AL049751.46_AT)

Table 7 Probe Sets as referred to in Tables 4a and 4b corresponding to genes, the expression of which is increased after infection of wild-type *Arabidopsis*, and altered after infection of at least one mutant *Arabidopsis* having a mutation in a gene whose expression is important for resistance to necrotrophic fungi

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11997_at (AC005967.4_AT)	12004_at (AL022023.132_AT)
12037_at (AC004005.174_AT)	12072_at (AL035396.4_AT)
12079_s_at (A71597.1_S_AT)	12081_at (AC001645.140_AT)
12115_at (AL033545.26_AT)	12136_at (AC007591.60_AT)
12150_at (AC004005.151_AT)	12216_at (AC007119.56_AT)
12317_at (AC004138.27_AT)	12323_at (AC002333.18_AT)
12332_s_at (AB023448.2_S_AT)	12369_at (AC002535.59_AT)
12400_at (X98453.1_AT)	12449_s_at (AC002343.179_S_AT)
12475_at (Y11794.1_AT)	12487_at (AC004411.126_AT)
12500_s_at (AF081067.3_S_AT)	12530_at (Z99707.184_AT)
12535_at (AL035538.156_AT)	12538_at (AF033205.2_AT)
12574_at (X82624.2_AT)	12584_at (AC004521.233_AT)
12626_at (AC006234.95_AT)	12645_at (AL021712.56_AT)
12744_at (AC001645.15_AT)	12760_g_at (AC005278.32_G_AT)
12772_at (AC005278.34_AT)	12797_s_at (AC007138.25_S_AT)
12851_s_at (ACCSYN1_S_AT)	12880_s_at (AIG2_S_AT)
12889_s_at (ASA1_S_AT)	12904_s_at (ATERF1_S_AT)
12905_s_at (ATERF2_S_AT)	12921_s_at (ATHHMGCOAR_S_AT)
12951_at (AC005489.5_AT)	12965_at (AL021711.118_AT)
12966_s_at (AL023094.197_S_AT)	12989_s_at (AC004077.149_S_AT)
13040_at (AC002392.134_AT)	13094_at (AL035523.163_AT)
13134_s_at (AC002337.9_S_AT)	13152_s_at (AC005322.24_S_AT)
13176_at (AL031394.56_AT)	13211_s_at (BCHI_S_AT)
13215_s_at (cafferoylcoAmethyltrans_S_AT)	13243_r_at (ELI32_R_AT)
13244_s_at (ELI32_S_AT)	13266_s_at (GST4_S_AT)
13275_f_at (HSP174_F_AT)	13277_i_at (HSP176A_I_AT)
13312_at (AC006223.75_AT)	13370_at (AC005322.4_AT)
13381_at (AC006580.8_AT)	13395_at (AL035528.202_AT)
13435_at (AF003102.3_AT)	13437_at (AF096371.8_AT)
13536_at (AL021636.47_AT)	13538_at (AL080254.75_AT)
13565_at (AL035601.21_AT)	13588_at (AL021961.24_AT)

13680_s_at (LOX1_S_AT)	13688_s_at (monopteros_S_AT)
13751_at (NOVARTIS127_AT)	13755_at (NOVARTIS15_AT)
13764_at (NOVARTIS22_AT)	13803_at (Z97341.376_AT)
13848_at (AC003981.31_AT)	13918_at (AC005388.29_AT)
13949_s_at (Z97343.352_S_AT)	13999_at (AF071527.56_AT)
14015_s_at (A71588.1_S_AT)	14016_s_at (A71596.1_S_AT)
14041_at (AC003970.28_AT)	14052_at (AC004122.24_AT)
14068_s_at (AC006922.197_S_AT)	14070_at (AL049658.217_AT)
14089_at (AC006223.65_AT)	14100_at (AF002109.108_AT)
14197_at (NOVARTIS71_AT)	14240_s_at (NR1_S_AT)
14450_at (AC002986.49_AT)	14461_at (AC006202.73_AT)
14475_at (AL021811.121_AT)	14584_at (AC007658.25_AT)
14609_at (AC002340.147_AT)	14663_s_at (trehalaseprecursor_RC_S_AT)
14667_s_at (TRPB_S_AT)	14673_s_at (TSB2_S_AT)
14675_s_at (VSP_S_AT)	14705_i_at (WT77_RC_I_AT)
14706_r_at (WT77_RC_R_AT)	14735_s_at (AF008124_S_AT)
14750_s_at (AF096370.12_S_AT)	14779_at (AC004680.71_AT)
14786_at (AC005397.115_AT)	14978_at (AC002333.49_AT)
15052_at (AC002332.103_AT)	15073_at (AC007069.93_AT)
15088_s_at (AC002311.37_S_AT)	15091_at (AC004683.97_AT)
15098_s_at (ATU26945_S_AT)	15124_s_at (ATU59508_S_AT)
15125_f_at (D85190_F_AT)	15137_s_at (ATU57320_S_AT)
15141_s_at (D85191_S_AT)	15154_s_at (ATHMTGDAS_S_AT)
15161_s_at (ATU90522_S_AT)	15162_s_at (U01880_S_AT)
15188_s_at (AF081202_S_AT)	15196_s_at (ATU43412_S_AT)
15211_s_at (ATH243813_S_AT)	15342_at (AC006593.101_AT)
15406_at (AC006931.179_AT)	15479_at (AL049483.205_AT)
15483_s_at (AC005819.20_S_AT)	15485_at (AC006233.109_AT)
15496_at (AC006282.167_AT)	15522_i_at (AL078637.213_I_AT)
15523_s_at (AL078637.213_S_AT)	15524_at (AC005508.25_AT)
15526_at (AC004122.16_AT)	15531_i_at (AL078637.191_I_AT)
15532_r_at (AL078637.191_R_AT)	15547_at (AC005970.122_AT)
15594_s_at (ATU56635_S_AT)	15622_s_at (ATU43945_S_AT)
15625_s_at (ATU74610_S_AT)	15632_s_at (AB012570_S_AT)
15665_s_at (AF022658_S_AT)	15670_s_at (AF061638_S_AT)
15792_at (AC002341.106_AT)	15798_at (AC002521.173_AT)

15839_at (AC005662.203_AT)
 15874_at (AL022223.106_AT)
 15982_s_at (AC006260.78_S_AT)
 16073_f_at (AF062908_F_AT)
 16130_s_at (AF078683_S_AT)
 16203_at (AC007519.53_AT)
 16298_at (AL021890.71_AT)
 16306_at (AL049751.112_AT)
 16363_at (AC004255.14_AT)
 16405_at (AC005850.9_AT)
 16462_s_at (AC004683.79_S_AT)
 16510_at (AL034567.198_AT)
 16526_at (Z49227.1_AT)
 16545_s_at (AF037229_S_AT)
 16589_s_at (ATU26937_S_AT)
 16609_s_at (AB008104_S_AT)
 16638_s_at (AF139098_S_AT)
 16649_s_at (ATHORF_S_AT)
 16747_at (AL021713.3_AT)
 16810_at (AC002339.46_AT)
 16865_s_at (AF037367.4_S_AT)
 16968_at (AL021961.93_AT)
 16995_at (AC002391.188_AT)
 17041_s_at (D89631_S_AT)
 17075_s_at (ATU09961_S_AT)
 17111_s_at (ATHACSC_S_AT)
 17187_at (AF128396.2_AT)
 17323_at (U95973.69_AT)
 17356_s_at (Z97338.190_S_AT)
 17511_s_at (AF067605_S_AT)
 17522_s_at (D78606_S_AT)
 17548_s_at (AF118823_S_AT)
 17648_at (AL021684.43_AT)
 17719_at (AC006592.17_AT)
 17860_at (AL078467.4_AT)
 17893_at (AC004401.135_AT)

15859_at (AC006587.164_AT)
 15886_at (AL078637.204_AT)
 16063_s_at (AB008103_S_AT)
 16108_s_at (D78604_S_AT)
 16173_s_at (D78607_S_AT)
 16272_at (AC006304.136_AT)
 16301_s_at (AL031018.105_S_AT)
 16357_at (AF149413.38_AT)
 16398_s_at (AL022603.3_S_AT)
 16461_i_at (AC004683.79_I_AT)
 16470_s_at (AF068299.4_S_AT)
 16522_at (X77500.2_AT)
 16541_s_at (AB023423_S_AT)
 16553_f_at (AF078821_F_AT)
 16603_s_at (ATU81293_S_AT)
 16611_s_at (AB008782_S_AT)
 16646_s_at (ATHDHS1_S_AT)
 16701_at (AC005312.61_AT)
 16781_at (AC002392.100_AT)
 16864_i_at (AF037367.4_I_AT)
 16914_s_at (AL049500.57_S_AT)
 16989_at (AL030978.46_AT)
 17008_at (AC006585.212_AT)
 17066_s_at (ATHLIPOXY_S_AT)
 17104_s_at (D88541_S_AT)
 17119_s_at (AF132212_S_AT)
 17300_at (X66017.2_AT)
 17338_at (AC002535.97_AT)
 17485_s_at (Z97340.345_S_AT)
 17514_s_at (AF076277_S_AT)
 17533_s_at (ATU43488_S_AT)
 17595_s_at (AF166352_S_AT)
 17702_at (AC005700.212_AT)
 17775_at (AC004392.2_AT)
 17877_g_at (AJ007587.2_G_AT)
 17945_at (Z97341.411_AT)

18109_s_at (AC002391.206_S_AT)
 18122_at (AC002338.110_AT)
 18176_at (AL035540.31_AT)
 18224_s_at (AL021890.57_S_AT)
 18236_s_at (AC004683.69_S_AT)
 18266_at (AC004684.33_AT)
 18587_s_at (AC007166.53_S_AT)
 18596_at (AC005698.13_AT)
 18668_at (AJ249794_AT)
 18782_at (AC003040.90_AT)
 18888_at (AC007591.68_AT)
 18908_i_at (AF055848.2_I_AT)
 18949_at (Z54136.1_AT)
 18963_at (AC004561.99_AT)
 19060_at (AC003671.34_AT)
 19137_at (X74755.2_AT)
 19284_at (AC003028.196_AT)
 19325_at (AL022604.42_AT)
 19383_at (AC006200.203_AT)
 19409_at (AC007357.56_AT)
 19451_at (AC004392.6_AT)
 19546_at (AC005398.172_AT)
 19614_at (AC003970.32_AT)
 19640_at (AC004561.78_AT)
 19645_at (AC004561.70_AT)
 19672_at (AC005687.19_AT)
 19700_s_at (AL031326.154_S_AT)
 19707_s_at (Z95768.3_S_AT)
 19762_at (AL035527.204_AT)
 19851_at (U23794.3_AT)
 19956_at (AC006282.11_AT)
 20023_at (AC006577.46_AT)
 20053_at (AC002292.27_AT)
 20133_i_at (AC007178.71_I_AT)
 20144_at (AL079350.68_AT)
 20189_at (AC005489.2_AT)

18121_s_at (AC002337.21_S_AT)
 18148_at (AC004669.25_AT)
 18213_at (AL022140.126_AT)
 18228_at (X91259.1_AT)
 18258_s_at (AC006439.222_S_AT)
 18299_s_at (M23872.2_S_AT)
 18590_at (AJ222713.4_AT)
 18636_at (AC006577.22_AT)
 18735_s_at (Z29490_S_AT)
 18803_at (AC005315.94_AT)
 18899_s_at (X13434.1_S_AT)
 18933_at (AC007020.48_AT)
 18953_at (AF077955.1_AT)
 19019_i_at (X82623.2_I_AT)
 19110_s_at (X86947.2_S_AT)
 19257_s_at (AC000104.57_S_AT)
 19288_at (AC005824.130_AT)
 19364_at (AL022023.142_AT)
 19395_at (AF007270.32_AT)
 19432_s_at (AL035680.11_S_AT)
 19460_s_at (AC000132.66_S_AT)
 19591_at (AJ010735.4_AT)
 19635_at (AL049746.38_AT)
 19641_at (AC004561.66_AT)
 19667_at (AL021710.5_AT)
 19673_g_at (AC005687.19_G_AT)
 19704_i_at (AJ005927.2_I_AT)
 19755_at (AC006593.64_AT)
 19818_i_at (AL021749.33_I_AT)
 19895_s_at (U77347.4_S_AT)
 19960_at (AL035527.360_AT)
 20051_at (AC000106.38_AT)
 20096_at (AC004238.31_AT)
 20134_s_at (AC007178.71_S_AT)
 20179_at (AL035538.229_AT)
 20194_at (AC007584.48_AT)

20247_at (AC004392.4_AT)	20263_at (AB004798.1_AT)
20291_s_at (M92353.4_S_AT)	20297_at (AC007153.27_AT)
20323_at (AC004561.62_AT)	20348_at (AC005967.35_AT)
20356_at (AC004561.74_AT)	20370_at (AC004561.263_AT)
20433_at (AC006232.147_AT)	20450_at (AJ005930.2_AT)
20479_i_at (AF069495.2_I_AT)	20485_at (AC007660.131_AT)
20572_s_at (AC005560.229_S_AT)	20646_at (AC002291.20_AT)
20656_at (AL035396.46_AT)	20658_s_at (AL050400.70_S_AT)
20669_s_at (AC002388.6_S_AT)	20686_at (Y14424.2_AT)

Table 8 Probe Sets as referred to in Table 6 corresponding to genes, the expression of which is increased after infection of wild-type *Arabidopsis* and altered after infection of at least one mutant *Arabidopsis* having a mutation in a gene that interferes with salicylic acid dependent signaling

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12079_s_at (A71597.1_S_AT)	12081_at (AC001645.140_AT)
12115_at (AL033545.26_AT)	12150_at (AC004005.151_AT)
12233_at (AJ001807.1_AT)	12307_at (AC002392.162_AT)
12314_at (AC001229.28_AT)	12332_s_at (AB023448.2_S_AT)
12341_s_at (AL021637.176_S_AT)	12400_at (X98453.1_AT)
12438_at (AL021710.83_AT)	12475_at (Y11794.1_AT)
12487_at (AC004411.126_AT)	12497_at (AC006533.51_AT)
12500_s_at (AF081067.3_S_AT)	12530_at (Z99707.184_AT)
12574_at (X82624.2_AT)	12584_at (AC004521.233_AT)
12712_f_at (Z95774_F_AT)	12760_g_at (AC005278.32_G_AT)
12764_f_at (AC004138.69_F_AT)	12879_s_at (AIG1_S_AT)
12883_s_at (APX_S_AT)	12889_s_at (ASA1_S_AT)
12891_at (ATACS6_AT)	12892_g_at (ATACS6_G_AT)
12905_s_at (ATERF2_S_AT)	12911_s_at (ATG6PDHE5_S_AT)
12921_s_at (ATHHMGCOAR_S_AT)	12958_at (AC002332.249_AT)
12989_s_at (AC004077.149_S_AT)	13003_s_at (AB021936.1_S_AT)
13014_at (U93215.87_AT)	13040_at (AC002392.134_AT)
13070_at (AC006919.171_AT)	13094_at (AL035523.163_AT)
13157_at (AC002409.35_AT)	13190_s_at (ATTHIREDA_S_AT)
13211_s_at (BCHI_S_AT)	13212_s_at (BGL2_S_AT)
13219_s_at (CHI4_S_AT)	13273_s_at (HSF4_S_AT)
13275_f_at (HSP174_F_AT)	13370_at (AC005322.4_AT)

13381_at (AC006580.8_AT)	13538_at (AL080254.75_AT)
13565_at (AL035601.21_AT)	13588_at (AL021961.24_AT)
13589_at (AC000132.24_AT)	13617_at (AC006592.64_AT)
13627_at (AL035394.196_AT)	13656_at (AC007138.31_AT)
13659_at (AL022347.46_AT)	13666_s_at (INDOLE3GPS_S_AT)
13680_s_at (LOX1_S_AT)	13697_at (NI16_AT)
13751_at (NOVARTIS127_AT)	13755_at (NOVARTIS15_AT)
13763_at (NOVARTIS21_AT)	13764_at (NOVARTIS22_AT)
13818_s_at (AC006218.175_S_AT)	13880_s_at (AL049480.183_S_AT)
13920_at (AC005990.53_AT)	14015_s_at (A71588.1_S_AT)
14016_s_at (A71596.1_S_AT)	14025_s_at (AC007293.3_S_AT)
14030_at (AC005970.225_AT)	14032_at (AL035601.11_AT)
14041_at (AC003970.28_AT)	14052_at (AC004122.24_AT)
14068_s_at (AC006922.197_S_AT)	14110_i_at (AL035528.279_I_AT)
14139_at (NOVARTIS30_AT)	14148_at (NOVARTIS38_AT)
14170_at (NOVARTIS51_AT)	14214_at (NOVARTIS83_AT)
14242_s_at (NRA_S_AT)	14248_at (PAD3_AT)
14249_i_at (PAD4_I_AT)	14408_at (AC002291.14_AT)
14450_at (AC002986.49_AT)	14461_at (AC006202.73_AT)
14487_at (Z97341.343_AT)	14584_at (AC007658.25_AT)
14609_at (AC002340.147_AT)	14620_s_at (PAT1_S_AT)
14635_s_at (PR.1_S_AT)	14638_s_at (PRXCB_S_AT)
14663_s_at (trehalaseprecursor_RC_S_AT)	14667_s_at (TRPB_S_AT)
14672_s_at (TSA1_S_AT)	14673_s_at (TSB2_S_AT)
14735_s_at (AF008124_S_AT)	14763_at (X86958.1_AT)
14786_at (AC005397.115_AT)	14882_at (AL022605.63_AT)
14959_at (AC007202.26_AT)	14978_at (AC002333.49_AT)
15073_at (AC007069.93_AT)	15091_at (AC004683.97_AT)
15116_f_at (AF121356_F_AT)	15137_s_at (ATU57320_S_AT)
15162_s_at (U01880_S_AT)	15196_s_at (ATU43412_S_AT)
15199_s_at (AB005804_S_AT)	15216_s_at (ATU75191_S_AT)
15431_at (AL030978.64_AT)	15483_s_at (AC005819.20_S_AT)
15496_at (AC006282.167_AT)	15518_at (AC005322.28_AT)
15526_at (AC004122.16_AT)	15540_at (AC006585.205_AT)
15543_at (AF096371.10_AT)	15544_at (AL021633.110_AT)
15551_at (AL035440.289_AT)	15594_s_at (ATU56635_S_AT)

15622_s_at (ATJ43945_S_AT)
15672_s_at (AF082299_S_AT)
15779_g_at (X98676.2_G_AT)
15839_at (AC005662.203_AT)
15866_s_at (AC007133.59_S_AT)
15924_at (AC007138.61_AT)
15978_at (X68592.6_AT)
16003_s_at (AL021749.64_S_AT)
16031_at (X94248.1_AT)
16053_i_at (Y14251.4_I_AT)
16091_s_at (ATHHSP83_S_AT)
16105_s_at (ATU68017_S_AT)
16130_s_at (AF078683_S_AT)
16272_at (AC006304.136_AT)
16306_at (AL049751.112_AT)
16357_at (AF149413.38_AT)
16383_at (AC006300.64_AT)
16461_i_at (AC004683.79_I_AT)
16470_s_at (AF068299.4_S_AT)
16578_s_at (ATHRPRP1B_S_AT)
16594_s_at (ATU39783_S_AT)
16609_s_at (AB008104_S_AT)
16721_at (AC006533.58_AT)
16810_at (AC002339.46_AT)
16865_s_at (AF037367.4_S_AT)
16968_at (AL021961.93_AT)
17007_at (AC005896.26_AT)
17066_s_at (ATHLIPOXY_S_AT)
17128_s_at (ATHRPRP1A_S_AT)
17338_at (AC002535.97_AT)
17356_s_at (Z97338.190_S_AT)
17451_at (AC002343.47_AT)
17484_at (X79052.2_AT)
17487_s_at (U18993.2_S_AT)
17544_s_at (ATU40856_S_AT)
17653_at (AL035679.144_AT)
15632_s_at (AB012570_S_AT)
15778_at (X98676.2_AT)
15815_s_at (Z97342.366_S_AT)
15859_at (AC006587.164_AT)
15874_at (AL022223.106_AT)
15970_s_at (X71794.2_S_AT)
15982_s_at (AC006260.78_S_AT)
16021_s_at (AL022224.182_S_AT)
16043_at (AC005489.17_AT)
16083_s_at (AF153283_S_AT)
16103_s_at (ATU60445_S_AT)
16108_s_at (D78604_S_AT)
16233_at (AL080254.83_AT)
16299_at (AL024486.185_AT)
16340_at (AC004255.15_AT)
16363_at (AC004255.14_AT)
16409_at (AC004393.2_AT)
16462_s_at (AC004683.79_S_AT)
16570_s_at (ATHCDPKA_S_AT)
16589_s_at (ATU26937_S_AT)
16603_s_at (ATU81293_S_AT)
16701_at (AC005312.61_AT)
16781_at (AC002392.100_AT)
16864_i_at (AF037367.4_I_AT)
16914_s_at (AL049500.57_S_AT)
16995_at (AC002391.188_AT)
17051_s_at (AF098947_S_AT)
17075_s_at (ATU09961_S_AT)
17180_at (AF007270.30_AT)
17341_at (AL021713.89_AT)
17413_s_at (AJ006961.4_S_AT)
17452_g_at (AC002343.47_G_AT)
17485_s_at (Z97340.345_S_AT)
17533_s_at (ATU43488_S_AT)
17585_s_at (AF134487_S_AT)
17752_at (AC003974.37_AT)

17758_at (AF076243.41_AT)	17775_at (AC004392.2_AT)
17781_at (AL049746.177_AT)	17840_s_at (AC002333.223_S_AT)
17893_at (AC004401.135_AT)	17899_at (Z97339.197_AT)
17930_s_at (AJ006960.4_S_AT)	17963_at (AL049730.88_AT)
18054_at (AJ238846_AT)	18148_at (AC004669.25_AT)
18194_i_at (AL096859.227_I_AT)	18213_at (AL022140.126_AT)
18242_g_at (AC006580.71_G_AT)	18255_at (AC005770.25_AT)
18258_s_at (AC006439.222_S_AT)	18508_s_at (AC006532.89_S_AT)
18544_at (AC007060.14_AT)	18590_at (AJ222713.4_AT)
18591_at (X74756.2_AT)	18596_at (AC005698.13_AT)
18604_at (AF069298.31_AT)	18622_g_at (AJ005902.2_G_AT)
18625_at (AC005278.22_AT)	18686_s_at (U18126_S_AT)
18698_s_at (X17528_S_AT)	18735_s_at (Z29490_S_AT)
18753_s_at (AF118222.28_S_AT)	18803_at (AC005315.94_AT)
18885_at (AC006921.147_AT)	18888_at (AC007591.68_AT)
18909_s_at (AF055848.2_S_AT)	18928_at (AC002333.181_AT)
18930_at (AC005990.57_AT)	18933_at (AC007020.48_AT)
18953_at (AF077955.1_AT)	18966_at (AC004561.106_AT)
19019_i_at (X82623.2_I_AT)	19137_at (X74755.2_AT)
19140_at (AC005170.24_AT)	19181_s_at (AF053065.2_S_AT)
19207_at (AC006069.117_AT)	19247_at (AF071527.44_AT)
19257_s_at (AC000104.57_S_AT)	19325_at (AL022604.42_AT)
19364_at (AL022023.142_AT)	19407_at (AC004697.81_AT)
19409_at (AC007357.56_AT)	19411_at (AC007661.104_AT)
19421_at (X70990.4_AT)	19432_s_at (AL035680.11_S_AT)
19451_at (AC004392.6_AT)	19460_s_at (AC000132.66_S_AT)
19465_at (AL021768.96_AT)	19546_at (AC005398.172_AT)
19555_at (AF058919.48_AT)	19624_at (AL049481.196_AT)
19641_at (AC004561.66_AT)	19667_at (AL021710.5_AT)
19741_at (AL049171.72_AT)	19755_at (AC006593.64_AT)
19818_i_at (AL021749.33_I_AT)	19881_at (AC004077.49_AT)
19892_at (AC005770.30_AT)	19944_at (AC002130.4_AT)
19956_at (AC006282.11_AT)	19970_s_at (AC003674.10_S_AT)
19982_at (AC002986.28_AT)	19991_at (AC007017.124_AT)
20017_at (AC004521.66_AT)	20030_at (AL078637.51_AT)
20051_at (AC000106.38_AT)	20098_at (AC004697.123_AT)

20133_i_at (AC007178.71_I_AT)
 20144_at (AL079350.68_AT)
 20247_at (AC004392.4_AT)
 20271_at (Z99707.27_AT)
 20288_g_at (Y14590.5_G_AT)
 20323_at (AC004561.62_AT)
 20370_at (AC004561.263_AT)
 20421_at (U81294.2_AT)
 20432_at (U43486.2_AT)
 20461_at (AL049480.157_AT)
 20479_i_at (AF069495.2_I_AT)
 20529_at (Z97341.125_AT)
 20589_at (AF081066.3_AT)
 20685_at (AL049751.46_AT)

20134_s_at (AC007178.71_S_AT)
 20245_s_at (AC005309.97_S_AT)
 20269_at (AC002387.237_AT)
 20287_at (Y14590.5_AT)
 20291_s_at (M92353.4_S_AT)
 20356_at (AC004561.74_AT)
 20420_at (AL024486.131_AT)
 20422_g_at (U81294.2_G_AT)
 20450_at (AJ005930.2_AT)
 20462_at (U82399.2_AT)
 20480_s_at (AF069495.2_S_AT)
 20572_s_at (AC005560.229_S_AT)
 20669_s_at (AC002388.6_S_AT)
 20689_s_at (AC002335.19_S_AT)

Table 9 Probe Sets corresponding to genes, the expression of which is downregulated (repressed) in an avrRpt-2-dependent manner in *Arabidopsis*

ProbeSet	Description
11991_g_at (AC002387.210_G_AT)	11991_g_at (AC002387.210_G_AT)gb AAB82645.1 (AC002387) unknown protein [Arabidopsis thaliana]
12091_at (AC004450.116_AT)	12091_at (AC004450.116_AT)gb AAC64313.1 (AC004450) unknown protein [Arabidopsis thaliana]
12124_s_at (Z97337.149_S_AT)	12124_s_at (Z97337.149_S_AT)emb CAB10270.1 (Z97337) imidazoleglycerol-phosphate dehydratase [Arabidopsis thaliana]
12125_at (Z97341.99_AT)	12125_at (Z97341.99_AT)emb CAB10421.1 (Z97341) hypothetical protein [Arabidopsis thaliana]
12160_at (AC006284.117_AT)	12160_at (AC006284.117_AT)gb AAD17436.1 (AC006284) unknown protein [Arabidopsis thaliana]
12191_at (AC006068.35_AT)	12191_at (AC006068.35_AT)gb AAD15440.1 (AC006068) unknown protein [Arabidopsis thaliana]
12193_at (AC006072.132_AT)	12193_at (AC006072.132_AT)gb AAD13708.1 (AC006072) unknown protein [Arabidopsis thaliana]
12223_s_at (AC007168.178_S_AT)	12223_s_at (AC007168.178_S_AT)gb AAF18668.1 AC007168_ 1 (AC007168) unknown protein [Arabidopsis thaliana]
12290_at (Y09418.2_AT)	12290_at (Y09418.2_AT)emb CAA70572.1 (Y09418) CDPK-related protein kinase [Arabidopsis thaliana]
12421_at (AJ002414.1_AT)	12421_at (AJ002414.1_AT)emb CAA05398.1 (AJ002414) hnRNP-like protein [Arabidopsis thaliana]
12460_s_at (AC006920.129_S_AT)	12460_s_at (AC006920.129_S_AT)gb AAD22284.1 AC006920_ 8 (AC006920) DNA-directed RNA polymerase II, third largest subunit [Arabidopsis thaliana]
12493_g_at (Y09095.1_G_AT)	12493_g_at (Y09095.1_G_AT)emb CAA70310.1 (Y09095) chloride channel [Arabidopsis thaliana]
12559_at (AC005727.83_AT)	12559_at (AC005727.83_AT)gb AAC79586.1 (AC005727) putative DOF zinc finger protein [Arabidopsis thaliana]

ProbeSet	Description
12560_at (AC005825.57_AT)	12560_at (AC005825.57_AT)gb AAD24598.1 AC005825_5 (AC005825) putative chloroplast outer membrane protein [Arabidopsis thaliana]
12561_at (AL021687.107_AT)	12561_at (AL021687.107_AT)emb CAA16701.1 (AL021687) putative protein [Arabidopsis thaliana]
12855_f_at (ADH_F_AT)	12855_f_at (ADH_F_AT)gb AAC00625.1 (AC002291) Alcohol Dehydrogenase [Arabidopsis thaliana]
12962_at (AC004697.165_AT)	12962_at (AC004697.165_AT)gb AAC28988.1 (AC004697) putative ABC transporter [Arabidopsis thaliana]
13221_at (CHS-WHOLE-SEQ_AT)	13221_at (CHS-WHOLE-SEQ_AT)gb AAF23561.1 AF112086_1 (AF112086) chalcome synthase [Arabidopsis thaliana]
13253_f_at (FPS1_F_AT)	13253_f_at (FPS1_F_AT)gb AAB49290.1 (U80605) farnesyl diphosphate synthase precursor [Arabidopsis thaliana]
13459_at (AF013294.21_AT)	13459_at (AF013294.21_AT)gb AAB62852.1 (AF013294) similar to auxin-induced protein [Arabidopsis thaliana]
13708_s_at (AC007259X_S_AT)	13708_s_at (AC007259X_S_AT)gb AAD50000.1 AC007259_1 3 (AC007259) Similar to protein kinases [Arabidopsis thaliana]
14428_s_at (AL023094.342_S_AT)	14428_s_at (AL023094.342_S_AT)emb CAA18852.1 (AL023094) putative protein [Arabidopsis thaliana]
15175_s_at (ATU28215_S_AT)	15175_s_at (ATU28215_S_AT)gb AAC62130.1 (AC005169) hexokinase (ATHXK2) [Arabidopsis thaliana]
15943_at (AC007202.16_AT)	15943_at (AC007202.16_AT)gb AAD30227.1 AC007202_9 (AC007202) Strong similarity to gb Y14272 3-deoxy-D-manno-2-octulosonate-8-phosphate synthase from Pisum sativum. ESTs gb AA067485 and gb AI100551 come from this gene. [Arabidopsis thaliana]

ProbeSet	Description
19219_at (AC007019.185_AT)	19219_at (AC007019.185_AT)gb AAD20413.1 (AC007019) unknown protein [Arabidopsis thaliana]

19219_at (AC007019.185_AT)

Table 10A: Expression data for 9 probe sets corresponding to genes that are specifically induced during incompatible interaction within 3 hours

ProbeSet	Col					
	3 hr			6 hr		
	Pst	Pst/aR2	cont	Pst	Pst/aR2	cont
12094_at	ud	303	ud	19	28	ud
12128_at	84	255	ud	0	181	ud
12712_f_at	10	278	ud	ud	90	20
13763_at	18	176	16	64	274	40
14882_at	24	385	11	62	457	46
16398_s_at	16	104	5	17	65	18
16536_s_at	24	346	19	ud	19	30
17180_at	50	361	26	93	367	76
19970_s_at	18	175	8	14	65	11
ProbeSet	Ws					
	3 hr			6 hr		
	Pst	Pst/aR2	cont	Pst	Pst/aR2	cont
12094_at	ud	104	ud	ud	29	ud
12128_at	ud	77	ud	ud	29	ud
12712_f_at	ud	146	ud	ud	46	ud
13763_at	ud	90	ud	15	378	25
14882_at	19	255	7	23	291	32
16398_s_at	9	93	7	4	49	ud
16536_s_at	ud	409	ud	ud	4	8
17180_at	ud	200	ud	ud	259	ud
19970_s_at	11	146	5	4	46	6
ProbeSet	Ler					
	3 hr			6 hr		
	Pst	Pst/aR2	cont	Pst	Pst/aR2	cont
12094_at	ud	121	ud	24	41	ud
12128_at	71	160	ud	33	145	ud
12712_f_at	19	113	11	24	46	14
13763_at	22	85	19	139	248	43
14882_at	50	227	25	121	321	41

Table 10B: Expression data for 18 probe sets corresponding to genes that are specifically induced during incompatible interaction in 6 hours (but not within 3 hours)

ProbeSet	Col					
	3 hr			6 hr		
	Pst	Pst/aR2	cont	Pst	Pst/aR2	cont
12711_f_at	ud	ud	ud	ud	100	ud
13312_at	ud	118	ud	36	176	11
13370_at	ud	ud	ud	ud	144	ud
13818_s_at	ud	9	ud	65	476	21
14609_at	ud	11	4	23	233	21
14635_s_at	ud	ud	ud	42	360	13
14931_at	ud	ud	ud	10	284	16
15120_s_at	ud	ud	ud	ud	214	12
16357_at	8	70	6	14	102	26
16968_at	19	28	7	33	257	19

17134_at	ud	ud	ud	ud	199	ud
17371_at	ud	16	ud	31	191	19
17485_s_at	ud	ud	ud	ud	86	7
18631_at	10	105	ud	32	92	17
19451_at	ud	ud	ud	ud	116	ud
20323_at	20	51	19	12	280	14
20356_at	ud	ud	ud	ud	82	ud
20421_at	ud	ud	ud	26	685	20
ProbeSet	Ws					
	3 hr			6 hr		
	Pst	Pst/aR2	cont	Pst	Pst/aR2	cont
12711_f_at	ud	ud	ud	ud	86	ud
13312_at	ud	34	ud	11	114	2
13370_at	ud	ud	ud	20	70	ud
13818_s_at	ud	12	8	10	422	10
14609_at	ud	12	ud	ud	184	3
14635_s_at	ud	ud	ud	ud	264	ud
14931_at	ud	ud	ud	ud	36	ud
15120_s_at	ud	13	ud	ud	89	ud
16357_at	ud	31	ud	ud	80	6
16968_at	ud	5	ud	12	54	ud
17134_at	ud	ud	ud	ud	27	ud
17371_at	ud	ud	ud	ud	133	ud
17485_s_at	ud	ud	ud	8	85	ud
18631_at	10	103	ud	17	81	10
19451_at	ud	6	ud	ud	52	ud
20323_at	ud	60	11	ud	119	ud
20356_at	ud	ud	ud	ud	96	ud
20421_at	ud	5	ud	ud	67	ud
ProbeSet	Ler					
	3 hr			6 hr		
	Pst	Pst/aR2	cont	Pst	Pst/aR2	cont
12711_f_at	ud	ud	5	15	32	ud
13312_at	ud	48	ud	133	158	12
13370_at	ud	ud	ud	36	122	ud

13818_s_at	ud	ud	4	26	211	ud
14609_at	ud	ud	5	30	359	15
14635_s_at	ud	ud	ud	22	310	17
14931_at	ud	ud	ud	ud	149	ud
15120_s_at	ud	ud	ud	17	252	ud
16357_at	14	47	10	23	117	11
16968_at	14	18	5	ud	105	5
17134_at	ud	ud	ud	ud	112	ud
17371_at	ud	ud	ud	ud	ud	ud
17485_s_at	ud	ud	ud	ud	49	ud
18631_at	16	63	27	34	68	ud
19451_at	5	7	4	14	123	ud
20323_at	11	6	8	ud	11	ud
20356_at	ud	5	ud	17	111	ud
20421_at	ud	ud	ud	7	329	ud
ProbeSet	Cvi					
	3 hr			6 hr		
	Pst	Pst/aR2	cont	Pst	Pst/aR2	cont
12711_f_at	ud	ud	ud	15	46	7
13312_at	10	64	5	60	116	ud
13370_at	ud	ud	18	40	88	ud
13818_s_at	4	ud	7	47	274	10
14609_at	8	23	6	127	778	ud
14635_s_at	6	ud	ud	179	519	44
14931_at	ud	ud	ud	23	182	ud
15120_s_at	ud	17	ud	31	150	ud
16357_at	17	52	16	32	132	16
16968_at	16	20	18	ud	56	3
17134_at	ud	ud	ud	ud	121	ud
17371_at	ud	ud	ud	ud	ud	ud
17485_s_at	ud	ud	ud	ud	55	ud
18631_at	11	41	10	24	85	ud
19451_at	4	6	ud	19	413	ud
20323_at	7	ud	ud	ud	11	ud
20356_at	ud	ud	ud	13	107	ud

20421_at	ud	20	ud	ud	293	ud
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5 **Table 10C:** Expression data for 6 probe sets corresponding to genes that are activated by *P. syringae* in 6 hours. Most of them are compatible interaction-specific/preferential

ProbeSet	Col					
	3 hr			6 hr		
	Pst	Pst/aR2	cont	Pst	Pst/aR2	cont
13243_r_at	44	ud	24	123	91	14
14573_at	ud	ud	ud	234	32	23
14613_at	ud	ud	9	138	ud	10
18122_at	34	38	25	169	96	28
19150_at	ud	ud	3	97	4	6
19673_g_at	69	34	27	596	290	ud
ProbeSet	Ws					
	3 hr			6 hr		
	Pst	Pst/aR2	cont	Pst	Pst/aR2	cont
13243_r_at	27	38	16	132	96	17
14573_at	ud	ud	ud	377	63	12
14613_at	ud	10	ud	136	ud	ud
18122_at	33	56	30	235	76	24
19150_at	ud	ud	ud	218	9	ud
19673_g_at	21	6	ud	496	312	ud
ProbeSet	Ler					
	3 hr			6 hr		
	Pst	Pst/aR2	cont	Pst	Pst/aR2	cont
13243_r_at	66	52	45	149	59	7
14573_at	ud	ud	ud	22	17	9
14613_at	ud	ud	14	102	13	13
18122_at	42	58	42	136	60	20
19150_at	ud	ud	ud	24	7	ud
19673_g_at	30	2	10	426	181	ud
ProbeSet	Cvi					

	3 hr			6 hr		
	Pst	Pst/aR2	cont	Pst	Pst/aR2	cont
13243_r_at	62	42	55	142	116	ud
14573_at	ud	ud	ud	25	22	ud
14613_at	13	ud	13	63	ud	ud
18122_at	36	43	41	151	81	28
19150_at	ud	6	ud	11	3	ud
19673_g_at	ud	ud	26	416	184	ud

- 5 Pst/aR2 ... represents the incompatible interaction
Pst ... *P. syringae* pv. tomato
aR2 ... avrRpt2
ud ... undetectable

Table 11 Probe Sets corresponding to genes induced early after infection of different *Arabidopsis* ecotypes with *Pseudomonas syringae* pv tomato DC3000, *P. maculicola* ES4326 and *P. phaseolica* NPS3121 (at 3 or 6 hours) or by estradiol inducible

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ProbeSet	Description
12737_f_at (Z97049_F_AT)	12737_f_at (Z97049_F_AT)emb CAA74603.1 (Y14207) R2R3-MYB transcription factor [Arabidopsis thaliana]
12908_s_at (ATERF5_S_AT)	12908_s_at (ATERF5_S_AT)dbj BAA32422.1 (AB008107) ethylene responsive element binding factor 5 [Arabidopsis thaliana]
16398_s_at (AL022603.3_S_AT)	16398_s_at (AL022603.3_S_AT)emb CAA20204.1 (AL031187) serine/threonine kinase-like protein [Arabidopsis thaliana]
17105_s_at (AF055357_S_AT)	17105_s_at (AF055357_S_AT)gb AAC39479.1 (AF055357) respiratory burst oxidase protein D [Arabidopsis thaliana]
19970_s_at (AC003674.10_S_AT)	19970_s_at (AC003674.10_S_AT)gb AAB97120.1 (AC003674) unknown protein [Arabidopsis thaliana]
20620_g_at (AC005896.161_G_AT)	20620_g_at (AC005896.161_G_AT)gb AAC98070.1 (AC005896) putative C2H2-type zinc finger protein [Arabidopsis thaliana]
12094_at (AC006223.143_AT)	12094_at (AC006223.143_AT)gb AAD15401.1 (AC006223) putative alanine acetyl transferase [Arabidopsis thaliana]
13255_i_at (gammaglutamyltranspepti_I_AT)	13255_i_at (GAMMAGLUTAMYLTRANSPEPTI_I_AT)emb CAA89206.1 (Z49240) gamma-glutamyl transpeptidase [Arabidopsis thaliana]
12712_f_at (Z95774_F_AT)	12712_f_at (Z95774_F_AT)emb CAB09206.1 (Z95774) R2R3-MYB transcription factor [Arabidopsis thaliana]
13015_s_at (X98673.2_S_AT)	13015_s_at (X98673.2_S_AT)emb CAA67232.1 (X98674) zinc finger protein [Arabidopsis thaliana]

ProbeSet	Description
13842_at (AC002396.12_AT)	13842_at (AC002396.12_AT)gb AAC00572.1 (AC002396) similar to zinc metalloproteinases [Arabidopsis thaliana]
14235_at (NOVARTIS97_AT)	14235_at (NOVARTIS97_AT)gb AAF14671.1 AC011713_19 (AC011713) Similar to gb Z48431 DNA-binding protein from Avena fatua. [Arabidopsis thaliana]
15779_g_at (X98676.2_G_AT)	15779_g_at (X98676.2_G_AT)emb CAA67234.1 (X98676) zinc finger protein [Arabidopsis thaliana]
16059_s_at (D88206_S_AT)	16059_s_at (D88206_S_AT)dbj BAA24694.1 (D88206) protein kinase [Arabidopsis thaliana]
17180_at (AF007270.30_AT)	17180_at (AF007270.30_AT)gb AAB61058.1 (AF007270) contains similarity to GATA-type zinc fingers (PS:PS00344) [Arabidopsis thaliana]
17303_s_at (AC004683.25_S_AT)	17303_s_at (AC004683.25_S_AT)gb AAC67339.2 (AC005499) putative WRKY-type DNA binding protein [Arabidopsis thaliana]
12571_s_at (AF149413.18_S_AT)	12571_s_at (AF149413.18_S_AT)gb AAD40138.1 AF149413_19 (AF149413) Arabidopsis thaliana ferrochelatase-I (SW:P42043); Pfam
12642_at (AC006920.138_AT)	12642_at (AC006920.138_AT)gb AAD22285.1 AC006920_9 (AC006920) unknown protein [Arabidopsis thaliana]
13177_at (AL049640.42_AT)	13177_at (AL049640.42_AT)emb CAB40989.1 (AL049640) growth factor like protein [Arabidopsis thaliana]
14162_at (NOVARTIS46_AT)	14162_at (NOVARTIS46_AT)No hits found less than or equal to 1e-15.
14214_at (NOVARTIS83_AT)	14214_at (NOVARTIS83_AT)gb AAF24849.1 AC012679_20 (AC012679) putative calmodulin-binding protein [Arabidopsis thaliana]
14217_at (NOVARTIS85_RC_AT)	14217_at (NOVARTIS85_RC_AT)gb AAF07816.1 AC011020_16 (AC011020) putative receptor protein kinase [Arabidopsis thaliana] thaliana. [Arabidopsis thaliana]

ProbeSet	Description
14711_s_at (ZFPL_S_AT)	14711_s_at (ZFPL_S_AT)gb AAD25930.1 AF085279_3 (AF085279) hypothetical Cys-3-His zinc finger protein [Arabidopsis thaliana]
14882_at (AL022605.63_AT)	14882_at (AL022605.63_AT)emb CAA18753.1 (AL022605) putative protein [Arabidopsis thaliana]
15431_at (AL030978.64_AT)	15431_at (AL030978.64_AT)emb CAA19722.1 (AL030978) putative protein [Arabidopsis thaliana]
15680_s_at (ATHATPK19B_S_AT)	15680_s_at (ATHATPK19B_S_AT)dbj BAA07661.1 (D42061) ribosomal-protein S6 kinase homolog [Arabidopsis thaliana]
17379_at (AF085279.9_AT)	17379_at (AF085279.9_AT)gb AAF18728.1 AC018721_3 (AC018721) putative CCCH-type zinc finger protein [Arabidopsis thaliana]
18267_at (AC006223.23_AT)	18267_at (AC006223.23_AT)gb AAD15384.1 (AC006223) unknown protein [Arabidopsis thaliana]
18604_at (AF069298.31_AT)	18604_at (AF069298.31_AT)gb AAC19273.1 (AF069298) similar to several small proteins (~100 aa) that are induced by heat, auxin, ethylene and wounding such as Phaseolus aureus indole-3-acetic acid induced protein ARG (SW:32292) [Arabidopsis thaliana]
19460_s_at (AC000132.66_S_AT)	19460_s_at (AC000132.66_S_AT)gb AAB60749.1 (AC000132) Identical to A. thaliana HEMA2 (gb U27118). [Arabidopsis thaliana]
15775_at (AL079344.196_AT)	15775_at (AL079344.196_AT)emb CAB45334.1 (AL079344) cytokinin oxidase-like protein [Arabidopsis thaliana]
16939_at (AC002334.110_AT)	16939_at (AC002334.110_AT)gb AAC04922.1 (AC002334) putative synaptobrevin [Arabidopsis thaliana]
18672_s_at (D13983_S_AT)	18672_s_at (D13983_S_AT)dbj BAA03090.1 (D13983) chloroplast envelope Ca ²⁺ -ATPase precursor [Arabidopsis

Table 12 Probe Sets corresponding to genes repressed early after infection of *Arabidopsis* with *Pseudomonas syringae* pv tomato DC3000, *P. maculicola* ES4326 and *P. phaseolica* NPS3121

ProbeSet	Description
12212_at (AL049711.168_AT)	12212_at (AL049711.168_AT)emb CAB41327.1 (AL049711) putative protein [Arabidopsis thaliana]
17555_s_at (ATU89296_S_AT)	17555_s_at (ATU89296_S_AT)gb AAB62404.1 (U89296) auxin response transcription factor 3; ARF3 [Arabidopsis thaliana]
17975_at (AF175998_AT)	17975_at (AF175998_AT)gb AAD53103.1 AF175998_1 (AF175998) putative transcription factor [Arabidopsis thaliana]
14386_at (AC005309.177_AT)	14386_at (AC005309.177_AT)gb AAC63645.1 (AC005309) unknown protein [Arabidopsis thaliana]
16613_s_at (AF012657_S_AT)	16613_s_at (AF012657_S_AT)gb AAC49845.1 (AF012657) putative potassium transporter AtKT2p [Arabidopsis thaliana]
18916_s_at (X92393.1_S_AT)	18916_s_at (X92393.1_S_AT)emb CAA63131.1 (X92393) KNAT4 homeobox protein [Arabidopsis thaliana]
20443_s_at (AC006341.42_S_AT)	20443_s_at (AC006341.42_S_AT)gb AAD34693.1 AC006341_21 (AC006341) Similar to gb AF069494 cytochrome P450 from Sinapis alba and is a member of the PF00067 Cytochrome P450 family. EST gb F14190 comes from this gene. [Arabidopsis thaliana]
20524_at (AC005698.12_AT)	20524_at (AC005698.12_AT)gb AAD43613.1 AC005698_12 (AC005698) T3P18.12 [Arabidopsis thaliana]
12609_at (X92975.2_AT)	12609_at (X92975.2_AT)emb CAA63553.1 (X92975) xyloglucan endo-transglycosylase [Arabidopsis thaliana]
20061_at (AC005508.23_AT)	20061_at (AC005508.23_AT)gb AAD14498.1 (AC005508) 37496 [Arabidopsis thaliana]

Table 13a Probe Sets corresponding to genes, the expression of which is induced in an incompatible interaction at 3 and/or 6 hours after infection of four *Arabidopsis* ecotypes with *Pseudomonas syringae* pv tomato DC3000, *P. maculicola* ES4326 and *P. phaseolica* NPS3121

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ProbeSet	Description
12128_at (AC004261.157_AT)	12128_at (AC004261.157_AT)gb AAD12010.1 (AC004261) unknown protein [Arabidopsis thaliana]
12335_at (AC004411.73_AT)	12335_at (AC004411.73_AT)gb AAC34243.1 (AC004411) putative protein kinase [Arabidopsis thaliana]
12347_at (AC007258.28_AT)	12347_at (AC007258.28_AT)gb AAD39325.1 AC007258_14 (AC007258) Putative ATPase [Arabidopsis thaliana]
12497_at (AC006533.51_AT)	12497_at (AC006533.51_AT)gb AAD32284.1 AC006533_8 (AC006533) putative receptor-like protein kinase [Arabidopsis thaliana]
12759_at (AC005278.32_AT)	12759_at (AC005278.32_AT)gb AAC72120.1 (AC005278) Strong similarity to gb D14550 extracellular dermal glycoprotein (EDGP) precursor from <i>Daucus carota</i> . ESTs gb 84105 and gb AI100071 come from this gene. [Arabidopsis thaliana]
12790_s_at (AL021635.58_S_AT)	12790_s_at (AL021635.58_S_AT)emb CAA16554.1 (AL021635) cytochrome P450 like protein [Arabidopsis thaliana]
12801_at (AC005223.34_AT)	12801_at (AC005223.34_AT)gb AAD10652.1 (AC005223) Unknown protein [Arabidopsis thaliana]
12904_s_at (ATERF1_S_AT)	12904_s_at (ATERF1_S_AT)dbj BAA32418.1 (AB008103) ethylene responsive element binding factor 1 [Arabidopsis thaliana]
12909_s_at (ATERF6_S_AT)	12909_s_at (ATERF6_S_AT)emb CAB10530.1 (Z97343) EREBP-4 like protein [Arabidopsis thaliana]
12989_s_at (AC004077.149_S_AT)	12989_s_at (AC004077.149_S_AT)gb AAC26690.1 (AC004077) putative cytochrome P450 [Arabidopsis thaliana]
13014_at (U93215.87_AT)	13014_at (U93215.87_AT)gb AAB63082.1 (U93215) putative lipase [Arabidopsis thaliana]

ProbeSet	Description
14959_at (AC007202.26_AT)	14959_at (AC007202.26_AT)gb AAD30230.1 AC007202_12 (AC007202) T8K14.13 [Arabidopsis thaliana]
14978_at (AC002333.49_AT)	14978_at (AC002333.49_AT)gb AAB64024.1 (AC002333) putative glucosyltransferase [Arabidopsis thaliana]
15039_at (AF001308.67_AT)	15039_at (AF001308.67_AT)gb AAC78710.1 (AF001308) drought-induced-19-like 1 [Arabidopsis thaliana]
15040_g_at (AF001308.67_G_AT)	15040_g_at (AF001308.67_G_AT)gb AAC78710.1 (AF001308) drought-induced-19-like 1 [Arabidopsis thaliana]
15120_s_at (ATU10034_S_AT)	15120_s_at (ATU10034_S_AT)gb AAA93132.1 (U10034) glutamate decarboxylase [Arabidopsis thaliana]
15137_s_at (ATU57320_S_AT)	15137_s_at (ATU57320_S_AT)gb AAB47973.1 (U57320) blue copper-binding protein II [Arabidopsis thaliana]
15203_s_at (AB013887_S_AT)	15203_s_at (AB013887_S_AT)dbj BAA34251.1 (AB013887) RAV2 [Arabidopsis thaliana]
17376_at (AL021890.218_AT)	17376_at (AL021890.218_AT)emb CAA17164.1 (AL021890) putative protein [Arabidopsis thaliana]
17381_at (Z99708.402_AT)	17381_at (Z99708.402_AT)emb CAB16811.1 (Z99708) putative protein [Arabidopsis thaliana]
15551_at (AL035440.289_AT)	15551_at (AL035440.289_AT)emb CAB36537.1 (AL035440) putative dihydrolipoamide succinyltransferase [Arabidopsis thaliana]
15582_s_at (ATH131392_S_AT)	15582_s_at (ATH131392_S_AT)emb CAA10364.1 (AJ131392) alternative oxidase [Arabidopsis thaliana]
15665_s_at (AF022658_S_AT)	15665_s_at (AF022658_S_AT)gb AAB80922.1 (AF022658) putative c2h2 zinc finger transcription factor [Arabidopsis thaliana]
15672_s_at (AF082299_S_AT)	15672_s_at (AF082299_S_AT)No hits found less than or equal to 1e-15.
15919_at (AC007060.42_AT)	15919_at (AC007060.42_AT)gb AAD25764.1 AC007060_22 (AC007060) EST gb AA721821 comes from this gene. [Arabidopsis thaliana]

ProbeSet	Description
16570_s_at (ATHCDPKA_S_AT)	16570_s_at (ATHCDPKA_S_AT)gb AAF27092.1 AC011809_1 (AC011809) calcium-dependent protein kinase 1 [Arabidopsis thaliana]
16620_s_at (AF051338_S_AT)	16620_s_at (AF051338_S_AT)gb AAC05572.1 (AF051338) xyloglucan endotransglycosylase related protein [Arabidopsis thaliana]
16638_s_at (AF139098_S_AT)	16638_s_at (AF139098_S_AT)gb AAD37511.1 AF139098_1 (AF139098) putative zinc finger protein [Arabidopsis thaliana]
16712_at (AC006068.67_AT)	16712_at (AC006068.67_AT)gb AAD15444.1 (AC006068) putative glycogenin [Arabidopsis thaliana]
16721_at (AC006533.58_AT)	16721_at (AC006533.58_AT)gb AAD32285.1 AC006533_9 (AC006533) putative poly(ADP-ribose) glycohydrolase [Arabidopsis thaliana]
16753_at (AL031032.110_AT)	16753_at (AL031032.110_AT)emb CAA19874.1 (AL031032) putative protein [Arabidopsis thaliana]
16916_s_at (X77199.8_S_AT)	16916_s_at (X77199.8_S_AT)emb CAA54420.1 (X77199) heat shock cognate 70-2 [Arabidopsis thaliana]
16968_at (AL021961.93_AT)	16968_at (AL021961.93_AT)emb CAA17559.1 (AL021961) glucosyltransferase-like protein [Arabidopsis thaliana]
17051_s_at (AF098947_S_AT)	17051_s_at (AF098947_S_AT)gb AAD09952.1 (AF098947) CTF2B [Arabidopsis thaliana]
17323_at (U95973.69_AT)	17323_at (U95973.69_AT)gb AAB65477.1 (U95973) Ser/Thr protein kinase isolog [Arabidopsis thaliana]
17352_at (AC007127.33_AT)	17352_at (AC007127.33_AT)gb AAD25140.1 AC007127_6 (AC007127) putative protein kinase [Arabidopsis thaliana]
17477_s_at (X63443.2_S_AT)	17477_s_at (X63443.2_S_AT)emb CAA45039.1 (X63443) heat shock protein 17.6-II [Arabidopsis thaliana]

ProbeSet	Description
18662_s_at (AC002343.20_S_AT)	18662_s_at (AC002343.20_S_AT)gb AAB63608.1 (AC002343) unknown protein [Arabidopsis thaliana]
18896_at (AC002329.51_AT)	18896_at (AC002329.51_AT)gb AAA67317.1 (L19262) 3-hydroxy-3-methylglutaryl-CoA reductase [Arabidopsis thaliana]
19247_at (AF071527.44_AT)	19247_at (AF071527.44_AT)gb AAD11587.1 AAD11587 (AF071527) hypothetical protein [Arabidopsis thaliana]
19411_at (AC007661.104_AT)	19411_at (AC007661.104_AT)gb AAD32774.1 AC007661_11 (AC007661) unknown protein [Arabidopsis thaliana]
19451_at (AC004392.6_AT)	19451_at (AC004392.6_AT)gb AAC28502.1 (AC004392) Similar to F4II.26 putative beta-glucosidase gi 3128187 from A. thaliana BAC gb AC004521. ESTs gb N97083, gb F19868 and gb F15482 come from this gene. [Arabidopsis thaliana]
19462_s_at (AF001168.2_S_AT)	19462_s_at (AF001168.2_S_AT)emb CAB75467.1 (AL138659) serine/threonine-specific kinase lecRK1 precursor, lectin
19640_at (AC004561.78_AT)	19640_at (AC004561.78_AT)gb AAC95192.1 (AC004561) putative glutathione S-transferase [Arabidopsis thaliana]
19916_at (AC006577.34_AT)	19916_at (AC006577.34_AT)gb AAD25781.1 AC006577_17 (AC006577) EST gb R64848 comes from this gene. [Arabidopsis thaliana]
19991_at (AC007017.124_AT)	19991_at (AC007017.124_AT)gb AAD21459.1 (AC007017) similar to harpin-induced protein hin1 from tobacco [Arabidopsis thaliana]
20051_at (AC000106.38_AT)	20051_at (AC000106.38_AT)gb AAB70412.1 (AC000106) Similar to Saccharomyces hypothetical protein YDR051c (gb Z49209). ESTs gb T44436,gb 42252 come from this gene. [Arabidopsis thaliana]
20142_at (AL035521.155_AT)	20142_at (AL035521.155_AT)emb CAB36716.1 (AL035521) extra-large G-protein-like [Arabidopsis thaliana]
20199_at (AL050300.89_AT)	20199_at (AL050300.89_AT)emb CAB43428.1 (AL050300) putative protein [Arabidopsis thaliana]

ProbeSet	Description
20269_at (AC002387.237_AT)	20269_at (AC002387.237_AT)gb AAB82640.1 (AC002387) putative pectinesterase [Arabidopsis thaliana]
20335_s_at (Y14208.2_S_AT)	20335_s_at (Y14208.2_S_AT)emb CAA74604.1 (Y14208) R2R3-MYB transcription factor [Arabidopsis thaliana]
20356_at (AC004561.74_AT)	20356_at (AC004561.74_AT)gb AAC95191.1 (AC004561) putative glutathione S-transferase [Arabidopsis thaliana]
20372_at (AL021713.24_AT)	20372_at (AL021713.24_AT)emb CAA16792.1 (AL021713) putative protein [Arabidopsis thaliana]
20421_at (U81294.2_AT)	20421_at (U81294.2_AT)emb CAB10242.1 (Z97336) germin precursor oxalate oxidase [Arabidopsis thaliana]
20590_at (AL035540.159_AT)	20590_at (AL035540.159_AT)emb CAB37511.1 (AL035540) Phospholipase like protein [Arabidopsis thaliana]
20619_at (AC005896.161_AT)	20619_at (AC005896.161_AT)gb AAC98070.1 (AC005896) putative C2H2-type zinc finger protein [Arabidopsis thaliana]
20686_at (Y14424.2_AT)	20686_at (Y14424.2_AT)emb CAA74766.1 (Y14424) hypothetical protein [Arabidopsis thaliana]
20689_s_at (AC002335.19_S_AT)	20689_s_at (AC002335.19_S_AT)gb AAB64310.1 (AC002335) putative calcium binding protein [Arabidopsis thaliana]

- 5 **Table 13b** Probe Sets corresponding to genes, the expression of which is decreased in an incompatible interaction at 3 and/or 6 hours after infection of four *Arabidopsis* ecotypes with *Pseudomonas syringae* pv tomato DC3000, *P. maculicola* ES4326 and *P. phaseolica* NPS3121

ProbeSet	Description
12048_at (AF001308.46_AT)	12048_at (AF001308.46_AT)gb AAC78704.1 (AF001308) predicted glycosyl transferase [Arabidopsis thaliana]
12218_at (AJ242588.2_AT)	12218_at (AJ242588.2_AT)emb CAB43344.1 (AJ242588) 1-deoxy-d-xylulose-5-phosphate reductoisomerase [Arabidopsis thaliana]

ProbeSet	Description
12727_f_at (Z95799_F_AT)	12727_f_at (Z95799_F_AT)gb AAD53097.1 AF175992_1 (AF175992) putative transcription factor [Arabidopsis thaliana]
13144_at (AC007017.246_AT)	13144_at (AC007017.246_AT)gb AAD21471.1 (AC007017) unknown protein [Arabidopsis thaliana]
13161_at (AF002109.89_AT)	13161_at (AF002109.89_AT)gb AAB95278.1 (AF002109) putative isoamylase [Arabidopsis thaliana]
13220_s_at (CHS-EXON1_S_AT)	13220_s_at (CHS-EXON1_S_AT)gb AAA32771.1 (M20308) chalcone synthase [Arabidopsis thaliana]
13482_at (AC005896.195_AT)	13482_at (AC005896.195_AT)gb AAC98071.1 (AC005896) nodulin-like protein [Arabidopsis thaliana]
13547_s_at (AC004450.15_S_AT)	13547_s_at (AC004450.15_S_AT)gb AAC64299.1 (AC004450) 3-isopropylmalate dehydratase, small subunit [Arabidopsis thaliana]
13637_at (AL049482.9_AT)	13637_at (AL049482.9_AT)emb CAB39634.1 (AL049482) AX110P-like protein [Arabidopsis thaliana]
13651_at (AL035538.320_AT)	13651_at (AL035538.320_AT)emb CAB37556.1 (AL035538) putative protein [Arabidopsis thaliana]
15832_at (AC004561.255_AT)	15832_at (AC004561.255_AT)gb AAC95217.1 (AC004561) unknown protein [Arabidopsis thaliana]
16110_s_at (AB004822_S_AT)	16110_s_at (AB004822_S_AT)dbj BAA22215.1 (AB004822) plastid RNA polymerase sigma-subunit [Arabidopsis thaliana]
16229_at (AL049638.148_AT)	16229_at (AL049638.148_AT)emb CAB40944.1 (AL049638) putative transport protein [Arabidopsis thaliana]
16351_at (AL021684.194_AT)	16351_at (AL021684.194_AT)emb CAA16688.1 (AL021684) receptor protein kinase - like protein [Arabidopsis thaliana]
16468_at (AF049870.5_AT)	16468_at (AF049870.5_AT)gb AAD02499.1 (AF049870) thaumatin-like protein [Arabidopsis thaliana]
16548_s_at (AF054617_S_AT)	16548_s_at (AF054617_S_AT)gb AAC25108.1 (AF054617) one helix protein [Arabidopsis thaliana]

ProbeSet	Description
20442_i_at (AC006341.42_I_AT)	20442_i_at (AC006341.42_I_AT)gb AAD34693.1 AC006341_2 1 (AC006341) Similar to gb AF069494 cytochrome P450 from Sinapis alba and is a member of the PF 00067 Cytochrome P450 family. EST gb F14190 comes from this gene. [Arabidopsis thaliana]

Table 15 Probe Sets as referred to in Table 3 corresponding to genes with promoters inducing expression in *Pseudomonas syringae* pv. *maculiola*-infected *Arabidopsis*

12891_at (ATACS6_AT)	13015_s_at (X98673.2_S_AT)
13100_at (AC003680.50_AT)	13115_at (AC000375.44_AT)
13217_s_at (CALMODULINLIKE_S_AT)	13467_at (AL096860.198_AT)
13645_at (AC000098.8_AT)	13818_s_at (AC006218.175_S_AT)
14032_at (AL035601.11_AT)	14248_at (PAD3_AT)
14609_at (AC002340.147_AT)	15116_f_at (AF121356_F_AT)
15622_s_at (ATU43945_S_AT)	16173_s_at (D78607_S_AT)
17485_s_at (Z97340.345_S_AT)	17511_s_at (AF067605_S_AT)
17548_s_at (AF118823_S_AT)	17775_at (AC004392.2_AT)
17930_s_at (AJ006960.4_S_AT)	19284_at (AC003028.196_AT)
19546_at (AC005398.172_AT)	19640_at (AC004561.78_AT)
20134_s_at (AC007178.71_S_AT)	20194_at (AC007584.48_AT)
20348_at (AC005967.35_AT)	12892_g_at (ATACS6_G_AT)
12904_s_at (ATERF1_S_AT)	12989_s_at (AC004077.149_S_AT)
13215_s_at (cafferoylcoAmethyltrans_S_AT)	13565_at (AL035601.21_AT)
13627_at (AL035394.196_AT)	16649_s_at (ATHORF_S_AT)
16914_s_at (AL049500.57_S_AT)	16995_at (AC002391.188_AT)
19991_at (AC007017.124_AT)	20356_at (AC004561.74_AT)

Table 16 Probe Sets corresponding to genes with promoters inducing expression in *Botrytis cinerea*-infected *Arabidopsis*

Probe Set	Description
12115_at (AL033545.26_AT)	emb CAA22152.1 (AL033545) extensin-like protein [Arabidopsis thaliana]
12574_at (X82624.2_AT)	emb CAA57944.1 (X82624) SRG2At [Arabidopsis thaliana]
12989_s_at (AC004077.149_S_AT)	gb AAC26690.1 (AC004077) putative cytochrome P450 [Arabidopsis thaliana]
13015_s_at (X98673.2_S_AT)	emb CAA67232.1 (X98674) zinc finger protein [Arabidopsis thaliana]
13100_at (AC003680.50_AT)	gb AAC06158.1 (AC003680) putative cytochrome P450 [Arabidopsis thaliana]
13215_s_at (cafferoylcoAmethyltrans_S_AT)	gb AAF16576.1 AC012563_29 (AC012563) putative S-adenosyl-L-methionine:trans-caffeoyl-Coenzyme A 3-O-methyltransferase [Arabidopsis thaliana]
13565_at (AL035601.21_AT)	emb CAB38206.1 (AL035601) auxin-responsive GH3-like protein [Arabidopsis thaliana]
14015_s_at (A71588.1_S_AT)	emb CAB42612.1 (A71639) unnamed protein product [Arabidopsis thaliana]
14016_s_at (A71596.1_S_AT)	emb CAB42592.1 (A71596) unnamed protein product [Arabidopsis thaliana]
14609_at (AC002340.147_AT)	gb AAC02748.1 (AC002340) putative cytochrome P450 [Arabidopsis thaliana]
16638_s_at (AF139098_S_AT)	gb AAD37511.1 AF139098_1 (AF139098) putative zinc finger protein [Arabidopsis thaliana]
16649_s_at (ATHORF_S_AT)	gb AAF16576.1 AC012563_29 (AC012563) putative S-adenosyl-L-methionine:trans-caffeoyl-Coenzyme A 3-O-methyltransferase [Arabidopsis thaliana]
16892_at (U37336.3_AT)	gb AAC49135.1 (U37336) senescence-specific cysteine protease
16914_s_at (AL049500.57_S_AT)	emb CAB39936.1 (AL049500) osmotin precursor [Arabidopsis thaliana]

Probe Set	Description
17533_s_at (ATU43488_S_AT)	gb AAB18367.1 (U43488) xyloglucan endotransglycosylase-related protein [Arabidopsis thaliana]
17744_s_at (AC004684.168_S_AT)	gb AAC23646.1 (AC004684) putative alcohol dehydrogenase [Arabidopsis thaliana]
18716_at (X91916_AT)	
18888_at (AC007591.68_AT)	gb AAD39666.1 AC007591_31 (AC007591) Is a member of the PF 00903 glyoxalase family. ESTs gb T44721, gb T21844 and gb AA395404 come from this gene. [Arabidopsis thaliana]
19019_i_at (X82623.2_I_AT)	emb CAA57943.1 (X82623) SRG2At [Arabidopsis thaliana]
19284_at (AC003028.196_AT)	gb AAC27173.1 (AC003028) putative anthocyanidin synthase [Arabidopsis thaliana]
19762_at (AL035527.204_AT)	emb CAB36812.1 (AL035527) peptide transporter-like protein [Arabidopsis thaliana]
19991_at (AC007017.124_AT)	gb AAD21459.1 (AC007017) similar to harpin-induced protein hin1 from tobacco [Arabidopsis thaliana]
20356_at (AC004561.74_AT)	gb AAC95191.1 (AC004561) putative glutathione S-transferase [Arabidopsis thaliana]

Table 17 Probe sets which correspond to genes downregulated in response to infection by 5 different viruses

Probe Set	Description	Function	Blast
17191_i_at (AL021961.178_I_AT)	emb CAA17564.1 (AL021961) putative protein [Arabidopsis thaliana]	DNA binding protein	MyB TF
18866_at (AC005917.178_AT)	gb AAD10163.1 (AC005917) putative Ta11-like non-LTR retroelement protein [Arabidopsis thaliana]	transposon	
20678_at (AC007296.30_AT)	gb AAD30253.1 AC007296_14 (AC007296) ESTs gb R65381 and gb T44635 come from this gene. [Arabidopsis thaliana]	unknown	unknown
12356_at (X99952.1_AT)	emb CAA68212.1 (X99952) peroxidase [Arabidopsis thaliana]	metabolic protein	
12448_at (AC002337.58_AT)	gb AAB63824.1 (AC002337) putative acyl-CoA synthetase [Arabidopsis thaliana]	metabolic protein	
12854_s_at (ACS1_S_AT)	gb AAA96006.1 (U26542) 1-aminocyclopropane-1-carboxylate synthase-like protein [Arabidopsis thaliana]	hormone response	
13812_s_at (AC005275.104_S_AT)	gb AAD14468.1 (AC005275) putative GH3-like protein [Arabidopsis thaliana]	hormone response	
14530_at (AL021889.231_AT)	emb CAA17145.1 (AL021889) putative protein [Arabidopsis thaliana]	unknown	unknown
16461_i_at (AC004683.79_I_AT)	gb AAC28766.1 (AC004683) peroxidase [Arabidopsis thaliana]	metabolic protein	
16462_s_at (AC004683.79_S_AT)	gb AAC28766.1 (AC004683) peroxidase [Arabidopsis thaliana]	metabolic protein	
17305_at (U25649.3_AT)	gb AAC50023.1 (U25649) ATPME2 precursor [Arabidopsis thaliana]	cell wall polymer	

Probe Set	Description	Function	Blast
14965_at (AC002329.22_AT)	gb AAB86507.1 (AC002329) unknown protein [Arabidopsis thaliana]	unknown	unknown
15578_s_at (AF004213_S_AT)	gb AAC49746.1 (AF004213) ethylene-insensitive3-like1 [Arabidopsis thaliana]	hormone response	
16062_s_at (AB007789_S_AT)	gb AAD15976.1 (AF074601) CRT/DRE binding factor 2 [Arabidopsis thaliana]	stress response	
16111_f_at (AB007788_F_AT)	dbj BAA33435.1 (AB013816) DREB1B [Arabidopsis thaliana] [Arabidopsis thaliana]	stress response	
16434_at (AL021711.157_AT)	emb CAA16754.1 (AL021711) putative protein [Arabidopsis thaliana]	metabolic protein	similar to APG (non proline-rich region) [Arabidopsis thaliana] /putative GDSL- motif lipase/hydrolase
16891_s_at (AF080120.33_S_AT)	gb AAC35539.1 (AF080120) contains similarity to glycosyl hydrolases family 9 (Pfam: glycosyl_hydro5.hmm, score: 88.03) [Arabidopsis thaliana]	cell wall polymer	
16990_at (AC004684.91_AT)	gb AAC23634.1 (AC004684) putative expansin [Arabidopsis thaliana]	cell wall polymer	
17577_g_at (AF087820_G_AT)	gb AAD52697.1 AF087820_1 (AF087820) auxin transport protein [Arabidopsis thaliana]	hormone response	
17743_at (AC002341.99_AT)	gb AAB67624.1 (AC002341) putative peroxidase [Arabidopsis thaliana]	metabolic protein	
19017_at (AL035709.69_AT)	emb CAB38928.1 (AL035709) endo-xyloglucan transferase-like protein [Arabidopsis thaliana]	cell wall polymer	
19396_at (AJ001855.2_AT)	emb CAA05054.1 (AJ001855) alpha subunit of F-actin capping protein [Arabidopsis thaliana]	structural protein	

Probe Set	Description	Function	Blast
16327_at (AC002334.12_AT)	gb AAF18589.1 AC002332_1 (AC002332) putative myosin heavy chain [Arabidopsis thaliana]	structural protein	
16406_at (AC006921.33_AT)	gb AAD21431.1 (AC006921) putative protein kinase [Arabidopsis thaliana]	receptor/kinase	
16868_at (AL035679.123_AT)	emb CAB38821.1 (AL035679) putative endo-1, 4-beta- glucanase [Arabidopsis thaliana]	cell wall polymer	
17362_s_at (Z97338.181_S_AT)	emb CAB10305.1 (Z97338) glucosyltransferase [Arabidopsis thaliana]	metabolic protein	
17916_at (U22428.2_AT)	gb AAB03100.1 (U22428) starch branching enzyme class II [Arabidopsis thaliana]	metabolic protein	
18515_at (AC007063.215_AT)	gb AAF24822.1 AC007592_15 (AC007592) F12K11.17 [Arabidopsis thaliana]	metabolic protein	putative 1,3- beta-D-glucan synthase [Arabidopsis thaliana]
18635_at (AC004005.44_AT)	gb AAC23401.1 (AC004005) unknown protein [Arabidopsis thaliana]	metabolic protein	methyl Cl transferase
18667_at (AJ249442_AT)	emb CAB55758.1 (AJ249442) putative AUX1-like permease [Arabidopsis thaliana]	hormone response	
18683_s_at (L27158_S_AT)	gb AAB60302.1 (U08216) chloroplast linoleate desaturase [Arabidopsis thaliana]	metabolic protein	
18694_s_at (U89272_S_AT)	gb AAB61458.1 (U89272) chloroplast membrane protein ALBINO3 [Arabidopsis thaliana]	membrane protein	
19870_s_at (AL021811.48_S_AT)	emb CAA16958.1 (AL021811) putative protein [Arabidopsis thaliana]	unknown	unknown

Table 18 Probe sets which correspond to genes upregulated in response to infection by 5 different viruses

Probeset	Description	Time	Function	Blast
12904_s_at (ATERF1_S_AT)	dbj BAA32418.1 (AB008103) ethylene responsive element binding factor 1 [Arabidopsis thaliana]	5dpi	hormone response	
16063_s_at (AB008103_S_AT)	dbj BAA32418.1 (AB008103) ethylene responsive element binding factor 1 [Arabidopsis thaliana]	5dpi	hormone response	
12906_s_at (ATERF3_S_AT)	dbj BAA32420.1 (AB008105) ethylene responsive element binding factor 3 [Arabidopsis thaliana]	1dpi	stress response	
16537_s_at (AB008111_S_AT)	dbj BAA28953.1 (AB008111) Atrboh F [Arabidopsis thaliana]	4dpi	stress response	
16610_s_at (AB008490_S_AT)	dbj BAA34729.1 (AB008490) response regulator 7 [Arabidopsis thaliana]	1dpi	signaling not kinase	
13645_at (AC000098.8_AT)	gb AAB71443.1 (AC000098) EST gb ATTS0295 comes from this gene. [Arabidopsis thaliana]	4-5dpi	unknown	unknown
19388_at (AC000104.61_AT)	gb AAB70450.1 (AC000104) ESTs gb N65789,gb T04628 come from this gene. [Arabidopsis thaliana]	4dpi	kinase/recept or	prenylated Rab receptor
19368_at (AC000348.22_AT)	gb AAB61497.1 (AC000348) T7N9.21 [Arabidopsis thaliana]	5dpi	unknown	unknown
13115_at (AC000375.44_AT)	gb AAB60774.1 (AC000375) ESTs gb U75592,gb T13956,gb T4386 9 come from from this gene. [Arabidopsis thaliana]	4dpi	DNA binding protein	putative WRKY DNA binding protein [Oryza sativa]
14964_at (AC001229.8_AT)	gb AAB60905.1 (AC001229) F5I14.4 gene product [Arabidopsis thaliana]	5dpi	unknown	unknown
17840_s_at (AC002333.223_S_AT)	gb AAB64049.1 (AC002333) putative endochitinase [Arabidopsis thaliana]	5dpi	stress response	

Probeset	Description	Time	Function	Blast
15379_at (AC002335.182_AT)	gb AAB64323.1 (AC002335) unknown protein [Arabidopsis thaliana]	1dpi	unknown	unknown
20689_s_at (AC002335.19_S_AT)	gb AAB64310.1 (AC002335) putative calcium binding protein [Arabidopsis thaliana]	5dpi	stress response	
12449_s_at (AC002343.179_S_AT)	gb AAB63623.1 (AC002343) cellulose synthase isolog [Arabidopsis thaliana]	4-5dpi	cell wall polymer	
13842_at (AC002396.12_AT)	gb AAC00572.1 (AC002396) similar to zinc metalloproteinases [Arabidopsis thaliana]	5dpi	protein processing	
19424_at (AC002396.44_AT)	gb AAC00588.1 (AC002396) glucose-6-phosphate 1- dehydrogenase [Arabidopsis thaliana]	5dpi	metabolic protein	
13100_at (AC003680.50_AT)	gb AAC06158.1 (AC003680) putative cytochrome P450 [Arabidopsis thaliana]	5dpi	metabolic protein	
16365_at (AC003974.136_AT)	gb AAC04495.1 (AC003974) putative disease resistance protein [Arabidopsis thaliana]	2-5dpi	stress response	
17752_at (AC003974.37_AT)	gb AAC04483.1 (AC003974) putative protein kinase [Arabidopsis thaliana]	4dpi	kinase/recept or	
20409_g_at (AC004077.132_G_AT)	emb CAB40383.1 (AJ131180) ribosomal protein S14 [Arabidopsis thaliana]	5dpi	protein processing	
13048_s_at (AC004138.22_S_AT)	gb AAC32906.1 (AC004138) putative basic blue protein (plantacyanin) [Arabidopsis thaliana]	4dpi	stress response	
12764_f_at (AC004138.69_F_AT)	gb AAC32912.1 (AC004138) putative glutathione S- transferase [Arabidopsis thaliana]	5dpi	stress response	
13895_at (AC004218.63_AT)	gb AAC27833.1 (AC004218) putative phospholipase [Arabidopsis thaliana]	4dpi	signaling not kinase	

Probeset	Description	Time	Function	Blast
20477_at (AC004238.154_AT)	gb AAC12841.1 (AC004238) putative UDP-N- acetylglucosamine pyrophosphorylase [Arabidopsis thaliana]	5dpi	metabolic protein	
16972_at (AC004261.89_AT)	gb AAA87347.1 (M88307) calmodulin [Brassica juncea]	5dpi	signaling not kinase	
19848_s_at (AC004261.94_S_AT)	dbj BAA08282.1 (D45848) calmodulin-related protein [Arabidopsis thaliana]	5dpi	signaling not kinase	
19044_at (AC004392.38_AT)	gb AAC28514.1 (AC004392) Strong similarity to gi 2160138 F19K23.6 gene product from A. thaliana BAC gb AC000375. [Arabidopsis thaliana]	5dpi	unknown	unknown
19640_at (AC004561.78_AT)	gb AAC95192.1 (AC004561) putative glutathione S- transferase [Arabidopsis thaliana]	5dpi	stress response	
20491_at (AC004561.146_AT)	gb AAC95203.1 (AC004561) putative tropinone reductase [Arabidopsis thaliana]	5dpi	metabolic protein	
16888_s_at (AC004684.174_S_AT)	gb AAC23647.1 (AC004684) putative alcohol dehydrogenase [Arabidopsis thaliana]	4dpi	stress response	
15389_at (AC004786.100_AT)	gb AAC32433.1 (AC004786) unknown protein [Arabidopsis thaliana]	4dpi	unknown	unknown
18844_at (AC005315.131_AT)	gb AAC33239.1 (AC005315) putative ligand-gated ion channel protein [Arabidopsis thaliana]	4dpi	signaling not kinase	
17128_s_at (ATHRPRP1A_S_AT)	gb AAC69381.1 (AC005398) pathogenesis-related PR-1-like protein [Arabidopsis]	5dpi	stress response	
17894_at (AC005724.44_AT)	gb AAD08938.1 (AC005724) unknown protein [Arabidopsis thaliana]	5dpi	unknown	unknown
18263_at (AC005724.36_AT)	gb AAD08937.1 (AC005724) unknown protein [Arabidopsis thaliana]	5dpi	unknown	unknown

Probeset	Description	Time	Function	Blast
15539_at (AC005770.21_AT)	gb AAC79601.1 (AC005770) unknown protein [Arabidopsis thaliana]	2dpi 4dpi	unknown	unknown
13920_at (AC005990.53_AT)	gb AAC98026.1 (AC005990) EST gb AA597511 comes from this gene. [Arabidopsis thaliana]	5dpi	unknown	unknown
18267_at (AC006223.23_AT)	gb AAD15384.1 (AC006223) unknown protein [Arabidopsis thaliana]	4dpi	unknown	unknown
12627_at (AC006533.99_AT)	gb AAD32292.1 AC006533_16 (AC006533) putative protein kinase [Arabidopsis thaliana]	1dpi	kinase/recept or	
12497_at (AC006533.51_AT)	gb AAD32284.1 AC006533_8 (AC006533) putative receptor- like protein kinase [Arabidopsis thaliana]	5dpi	kinase/recept or	
12656_at (AC006569.43_AT)	gb AAD21751.1 (AC006569) unknown protein [Arabidopsis thaliana]	5dpi	unknown	unknown
17008_at (AC006585.212_AT)	gb AAD23027.1 AC006585_22 (AC006585) putative tyrosine aminotransferase [Arabidopsis thaliana]	4-5dpi	metabolic protein	
19386_at (AC006592.51_AT)	No hits found less than or equal to 1e-15.	2dpi	metabolic protein	
13617_at (AC006592.64_AT)	gb AAD22351.1 AC006592_8 (AC006592) putative mitochondrial dicarboxylate carrier protein [Arabidopsis thaliana]	5dpi	unknown	unknown
15473_at (AC006836.125_AT)	gb AAD20072.1 (AC006836) putative ubiquinone biosynthesis protein [Arabidopsis thaliana]	5dpi	metabolic protein	
12642_at (AC006920.138_AT)	gb AAD22285.1 AC006920_9 (AC006920) unknown protein [Arabidopsis thaliana]	5dpi	metabolic protein	putative xyloglucan fucosyltransf erase [Arabidopsis thaliana]

Probeset	Description	Time	Function	Blast
15921_s_at (AC007067.1_S_AT)	gb AAD39561.1 AC007067_1 (AC007067) T10O24.1 [Arabidopsis thaliana]	4dpi	unknown	unknown
14248_at (PAD3_AT)	gb AAD31062.1 AC007357_11 (AC007357) Strong similarity to gb X97864 cytochrome P450 from Arabidopsis thaliana and is a member of the PF 00067 Cytochrome P450 family. ESTs gb N65665, gb T14112, gb T76255, gb T20906 and gb AI100027 come from this gene.	5dpi	metabolic protein	
19903_at (AC007660.40_AT)	gb AAD32803.1 AC007660_4 (AC007660) unknown protein [Arabidopsis thaliana]	4dpi	unknown	unknown
15487_at (AC007661.87_AT)	gb AAD32771.1 AC007661_8 (AC007661) unknown protein [Arabidopsis thaliana]	5dpi	unknown	unknown
13751_at (NOVARTIS127_AT)	gb AAF16751.1 AC010155_4 (AC010155) F3M18.8 [Arabidopsis thaliana]	4dpi	unknown	unknown
13246_at (ERECTAL_AT)	gb AAF26067.1 AC012562_22 (AC012562) putative protein kinase [Arabidopsis thaliana]	4dpi	kinase/recept or	
14636_s_at (PR5_S_AT)	gb AAF21072.1 AC013258_10 (AC013258) thaumatin-like protein [Arabidopsis thaliana]	2-5dpi	stress response	
16153_s_at (ATHRPRP1C_S_AT)	gb AAF21072.1 AC013258_10 (AC013258) thaumatin-like protein [Arabidopsis thaliana]	2-5dpi	stress response	
16617_s_at (AF029980_S_AT)	gb AAD01897.1 (AF029980) A37 [Arabidopsis thaliana]	5dpi	unknown	unknown
12538_at (AF033205.2_AT)	gb AAC02973.1 (AF033205) putative pectin methylesterase [Arabidopsis thaliana]	4dpi	cell wall polymer	
18681_at (L23573_AT)	gb AAD02548.1 (AF049922) PGP169-12 [Petunia x hybrida]	4dpi	membrane protein	

Probeset	Description	Time	Function	Blast
19181_s_at (AF053065.2_S_AT)	gb AAC39464.1 (AF053065) late embryogenesis abundant protein homolog [Arabidopsis thaliana]	5dpi	stress response	
19555_at (AF058919.48_AT)	gb AAC13630.1 (AF058919) F6N23.8 gene product [Arabidopsis thaliana]	4dpi	metabolic protein	probable methylene- tetrahydrofol ate dehydrogenas e (NADP+)
15515_r_at (AF058919.32_R_AT)	gb AAC13627.1 (AF058919) F6N23.26 gene product [Arabidopsis thaliana]	5dpi	metabolic protein	putative phosphoribos ylanthranilate transferase [Arabidopsis thaliana]
15606_s_at (AF061517_S_AT)	gb AAC15807.1 (AF061517) putative copper/zinc superoxide dismutase copper chaperone [Arabidopsis thaliana]	5dpi	stress response	
18604_at (AF069298.31_AT)	gb AAC19273.1 (AF069298) similar to several small proteins (~100 aa) that are induced by heat, auxin, ethylene and wounding such as Phaseolus aureus indole-3-acetic acid induced protein ARG (SW:32292) [Arabidopsis thaliana]	5dpi	stress response	
12002_at (AF069442.47_AT)	gb AAC79112.1 (AF069442) hypothetical protein [Arabidopsis thaliana]	4-5dpi	protein processing	ubiquitin-like
20480_s_at (AF069495.2_S_AT)	emb CAB38908.1 (AL035708) cytochrome P450-like protein [Arabidopsis thaliana]	4-5dpi	metabolic protein	
20479_i_at (AF069495.2_I_AT)	emb CAB38908.1 (AL035708) cytochrome P450-like protein [Arabidopsis thaliana]	5dpi	metabolic protein	
19247_at (AF071527.44_AT)	gb AAD11587.1 AAD11587 (AF071527) hypothetical protein [Arabidopsis thaliana]	4-5dpi	unknown	Ankyrin repeats

Probeset	Description	Time	Function	Blast
12500_s_at (AF081067.3_S_AT)	gb AAC32192.1 (AF081067) IAA-Ala hydrolase; IAA-amino acid hydrolase [Arabidopsis thaliana]	4-5dpi	hormone response	
14711_s_at (ZFPL_S_AT)	gb AAD25930.1 AF085279_3 (AF085279) hypothetical Cys-3- His zinc finger protein [Arabidopsis thaliana]	5dpi	DNA binding protein	
20345_at (AF104919.16_AT)	gb AAC72865.1 (AF104919) similar to class I chitinases (Pfam: PF00182, E=1.2e-142, N=1) [Arabidopsis thaliana]	4dpi	stress response	
17589_at (AF156783_AT)	gb AAF00612.1 AF156783_1 (AF156783) apyrase [Arabidopsis thaliana]	5dpi	membrane protein	
18010_s_at (AJ001264_S_AT)	emb CAA77109.1 (Y18291) uncoupling protein [Arabidopsis thaliana]	5dpi	stress response	
12421_at (AJ002414.1_AT)	emb CAA05398.1 (AJ002414) hnRNP-like protein [Arabidopsis thaliana]	2dpi	RNA processing	
13284_s_at (HSP70_S_AT)	emb CAA05547.1 (AJ002551) heat shock protein 70 [Arabidopsis thaliana]	2dpi 5dpi	heat shock	
16442_s_at (AJ002551.2_S_AT)	emb CAA05547.1 (AJ002551) heat shock protein 70 [Arabidopsis thaliana]	2dpi	heat shock	
19591_at (AJ010735.4_AT)	emb CAA09330.1 (AJ010735) gr1-protein [Arabidopsis thaliana]	4dpi	stress response	
20507_at (AL021635.67_AT)	emb CAA16557.1 (AL021635) glycoprotein endopeptidase - like protein [Arabidopsis thaliana]	5dpi	metabolic protein	
19531_at (AL021960.91_AT)	emb CAA17531.1 (AL021960) amino acid transport protein AAT1 [Arabidopsis thaliana]	5dpi	membrane protein	
14595_at (AL022580.163_AT)	emb CAA18626.1 (AL022580) putative protein [Arabidopsis thaliana]	4dpi	membrane protein	putative integral membrane protein

Probeset	Description	Time	Function	Blast
14882_at (AL022605.63_AT)	emb CAA18753.1 (AL022605) putative protein [Arabidopsis thaliana]	2dpi	protein processing	vacuole processing
20142_at (AL035521.155_AT)	emb CAB36716.1 (AL035521) extra-large G-protein-like [Arabidopsis thaliana]	5dpi	signaling not kinase	
20516_at (AL035523.64_AT)	emb CAB36736.1 (AL035523) ubiquitin activating enzyme-like protein [Arabidopsis thaliana]	4dpi	unknown	unknown
13094_at (AL035523.163_AT)	emb CAB36745.1 (AL035523) putative protein [Arabidopsis thaliana]	5dpi	protein processing	
14032_at (AL035601.11_AT)	emb CAB38204.1 (AL035601) cytochrome P450-like protein [Arabidopsis thaliana]	2dpi 5dpi	metabolic protein	
13147_at (AL035678.99_AT)	emb CAB38794.1 (AL035678) putative protein [Arabidopsis thaliana]	5dpi	metabolic protein	HpnA protein, oxidoreductase/cinnamyl-alcohol dehydrogenase
19624_at (AL049481.196_AT)	emb CAB39628.1 (AL049481) cytochrome c [Arabidopsis thaliana]	4dpi	metabolic protein	
14036_at (AL049655.54_AT)	emb CAB41088.1 (AL049655) protein disulfide-isomerase-like protein [Arabidopsis thaliana]	4dpi	protein processing	
14249_i_at (PAD4_I_AT)	emb CAB43438.1 (AL050300) putative protein [Arabidopsis thaliana]	5dpi	stress response	stress
14250_r_at (PAD4_R_AT)	emb CAB43438.1 (AL050300) putative protein [Arabidopsis thaliana]	5dpi	stress response	stress
16232_s_at (AL080252.77_S_AT)	emb CAB45796.1 (AL080252) putative protein [Arabidopsis thaliana]	5dpi	signaling not kinase	protein phosphatase 2C, putative Ser/The phosphatase 2C

Probeset	Description	Time	Function	Blast
13212_s_at (BGL2_S_AT)	emb CAB68132.1 (AL137080) beta-1, 3-glucanase 2 (BG2) [Arabidopsis thaliana]	2-5dpi	stress response	
16578_s_at (ATHRPRP1B_S_AT)	emb CAB68132.1 (AL137080) beta-1, 3-glucanase 2 (BG2) [Arabidopsis thaliana]	2-5dpi	stress response	
15622_s_at (ATU43945_S_AT)	gb AAB40594.1 (U43945) strictosidine synthase [Arabidopsis thaliana]	4dpi	stress response	
14145_at (NOVARTIS35_AT)	dbj BAA22813.1 (D26015) CND41, chloroplast nucleoid DNA binding protein [Nicotiana tabacum]	4dpi	DNA binding protein	
15680_s_at (ATHATPK19B_S_AT)	dbj BAA07661.1 (D42061) ribosomal-protein S6 kinase homolog [Arabidopsis thaliana]	5dpi	signaling not kinase	
16173_s_at (D78607_S_AT)	dbj BAA28539.1 (D78607) cytochrome P450 monooxygenase [Arabidopsis thaliana]	4dpi	metabolic protein	
12832_f_at (U33014.2_M_F_AT)	gb AAD03342.1 (L81140) ubiquitin [Pisum sativum]	1dpi	protein degradation	
13285_s_at (HSP83_S_AT)	gb AAA32822.1 (M62984) heat shock protein 83 [Arabidopsis thaliana]	5dpi	heat shock	
16091_s_at (ATHHSP83_S_AT)	gb AAA32822.1 (M62984) heat shock protein 83 [Arabidopsis thaliana]	5dpi	heat shock	
13722_at (NOVARTIS108_AT)	No hits found less than or equal to 1e-15.	5dpi	DNA binding protein	transcription factor
13187_i_at (ATTHIRED4_I_AT)	gb AAC49356.1 (U35829) thioredoxin h [Arabidopsis thaliana]	5dpi	stress response	
13188_r_at (ATTHIRED4_R_AT)	gb AAC49356.1 (U35829) thioredoxin h [Arabidopsis thaliana]	5dpi	stress response	
13189_s_at (ATTHIRED4_S_AT)	gb AAC49356.1 (U35829) thioredoxin h [Arabidopsis thaliana]	5dpi	stress response	

Probeset	Description	Time	Function	Blast
16981_s_at (U35829.2_S_AT)	gb AAC49356.1 (U35829) thioredoxin h [Arabidopsis thaliana]	5dpi	stress response	
17544_s_at (ATU40856_S_AT)	gb AAC49282.1 (U40856) AIG1 [Arabidopsis thaliana]	5dpi	stress response	
12880_s_at (AIG2_S_AT)	gb AAC49283.1 (U40857) AIG2 [Arabidopsis thaliana]	1dpi	stress response	
17097_s_at (ATU66345_S_AT)	gb AAC49697.1 (U66345) calreticulin [Arabidopsis thaliana]	5dpi	protein processing	
17027_s_at (ATU72958_S_AT)	gb AAB38795.1 (U72958) AtHSP23.6-mito [Arabidopsis thaliana] protein (AtHSP23.6- mito) [Arabidopsis thaliana]	5dpi	heat shock	
14998_at (U93215.42_AT)	gb AAB63078.1 (U93215) unknown protein [Arabidopsis thaliana]	5dpi	DNA binding protein	Petroselinum crispum transcription factor (WRKY3) WRKY3 DNA-binding protein, TMV response- related gene product
13275_f_at (HSP174_F_AT)	emb CAA35182.1 (X17293) heat shock protein (AA 1 - 156) [Arabidopsis thaliana]	4-5dpi	heat shock	
12831_f_at (U33014.2_5_F_AT)	emb CAA40323.1 (X57003) polyubiquitin protein [Helianthus annuus]	1dpi	protein degradation	
20238_at (X74514.2_AT)	emb CAA52619.1 (X74514) beta-fructofuranosidase [Arabidopsis thaliana]	4dpi	metabolic protein	
15118_s_at (ATHGLUGRFS_S_AT)	emb CAA53051.1 (X75303) glutathione S-transferase [Arabidopsis thaliana]	5dpi	stress response	
17484_at (X79052.2_AT)	emb CAA55654.1 (X79052) SRG1 [Arabidopsis thaliana]	5dpi	stress response	

Probeset	Description	Time	Function	Blast
16236_g_at (X92657.3_G_AT)	emb CAA63346.1 (X92657) cationic amino acid transporter [Arabidopsis thaliana]	5dpi	membrane protein	
18216_at (X95573.2_AT)	gb AAF24959.1 AC012375_22 (AC012375) T22C5.18 [Arabidopsis thaliana]	5dpi	DNA binding protein	salt-tolerance zinc finger protein
18217_g_at (X95573.2_G_AT)	gb AAF24959.1 AC012375_22 (AC012375) T22C5.18 [Arabidopsis thaliana]	5dpi	DNA binding protein	A.thaliana mRNA for salt-tolerance zinc finger protein
20660_s_at (X97488.2_S_AT)	emb CAA66120.1 (X97488) beta-transducin like protein [Arabidopsis thaliana]	4dpi	signaling not kinase	
13015_s_at (X98673.2_S_AT)	emb CAA67232.1 (X98674) zinc finger protein [Arabidopsis thaliana]	5dpi	DNA binding protein	
16465_at (Y08892.1_AT)	emb CAA70105.1 (Y08892) Hsc70-G8 protein [Arabidopsis thaliana]	4-5dpi	heat shock	
13277_i_at (HSP176A_I_AT)	emb CAA74399.1 (Y14070) Heat Shock Protein 17.6A [Arabidopsis thaliana]	2-5dpi	heat shock	
16054_s_at (Y14251.4_S_AT)	emb CAA74639.1 (Y14251) glutathione S-transferase [Arabidopsis thaliana]	5dpi	stress response	
20287_at (Y14590.5_AT)	emb CAA74930.1 (Y14590) class IV chitinase [Arabidopsis thaliana]	4-5dpi	stress response	
19178_at (Y18227.2_AT)	dbj BAA86999.1 (AB035137) blue copper binding protein [Arabidopsis thaliana]	5dpi	metabolic protein	
16943_s_at (Z97339.466_S_AT)	emb CAB10370.1 (Z97339) drought-induced protein like [Arabidopsis thaliana]	5dpi	stress response	
13803_at (Z97341.376_AT)	emb CAB10444.1 (Z97341) cyanohydrin lyase like protein [Arabidopsis thaliana]	4dpi	metabolic protein	
18140_at (Z97341.319_AT)	emb CAB10440.1 (Z97341) growth regulator like protein [Arabidopsis thaliana]	5dpi	hormone response	

[illegible]

Table 19 Probe sets corresponding to genes, the expression of which is altered after infection of *Arabidopsis* with a pathogen

- 5 Preferred gene and promoter families that regulate at least two or more pathways, conditions or phenotypes can be identified by determining the activity of each gene or promoter by reading each of the relevant tables herein and then selecting those having the desired activit(ies).

11991_g_at (AC002387.210_G_AT)	11997_at (AC005967.4_AT)
12002_at (AF069442.47_AT)	12004_at (AL022023.132_AT)
12007_at (Z99708.249_AT)	12037_at (AC004005.174_AT)
12048_at (AF001308.46_AT)	12051_at (AL021889.94_AT)
12062_at (AC006069.147_AT)	12068_at (AF118223.24_AT)
12072_at (AL035396.4_AT)	12079_s_at (A71597.1_S_AT)
12081_at (AC001645.140_AT)	12086_s_at (AC002409.88_S_AT)
12091_at (AC004450.116_AT)	12092_at (AC004793.13_AT)
12094_at (AC006223.143_AT)	12115_at (AL033545.26_AT)
12124_s_at (Z97337.149_S_AT)	12125_at (Z97341.99_AT)
12128_at (AC004261.157_AT)	12136_at (AC007591.60_AT)
12150_at (AC004005.151_AT)	12160_at (AC006284.117_AT)
12187_at (AC005489.31_AT)	12191_at (AC006068.35_AT)
12193_at (AC006072.132_AT)	12198_at (AC006954.90_AT)
12203_at (AL021710.268_AT)	12212_at (AL049711.168_AT)
12216_at (AC007119.56_AT)	12217_at (AJ223804.1_AT)
12218_at (AJ242588.2_AT)	12223_s_at (AC007168.178_S_AT)
12227_at (AC007576.18_AT)	12233_at (AJ001807.1_AT)
12278_at (AJ011674.2_AT)	12290_at (Y09418.2_AT)
12307_at (AC002392.162_AT)	12314_at (AC001229.28_AT)
12317_at (AC004138.27_AT)	12323_at (AC002333.18_AT)
12332_s_at (AB023448.2_S_AT)	12335_at (AC004411.73_AT)
12341_s_at (AL021637.176_S_AT)	12347_at (AC007258.28_AT)
12349_s_at (X84728.6_S_AT)	12356_at (X99952.1_AT)
12369_at (AC002535.59_AT)	12400_at (X98453.1_AT)
12421_at (AJ002414.1_AT)	12438_at (AL021710.83_AT)
12448_at (AC002337.58_AT)	12449_s_at (AC002343.179_S_AT)
12454_at (AC006232.164_AT)	12460_s_at (AC006920.129_S_AT)
12475_at (Y11794.1_AT)	12487_at (AC004411.126_AT)

12493_g_at (Y09095.1_G_AT)	12497_at (AC006533.51_AT)
12500_s_at (AF081067.3_S_AT)	12521_at (AF049236.28_AT)
12525_at (AC006587.85_AT)	12530_at (Z99707.184_AT)
12535_at (AL035538.156_AT)	12538_at (AF033205.2_AT)
12559_at (AC005727.83_AT)	12560_at (AC005825.57_AT)
12561_at (AL021687.107_AT)	12571_s_at (AF149413.18_S_AT)
12574_at (X82624.2_AT)	12584_at (AC004521.233_AT)
12609_at (X92975.2_AT)	12626_at (AC006234.95_AT)
12627_at (AC006533.99_AT)	12642_at (AC006920.138_AT)
12645_at (AL021712.56_AT)	12656_at (AC006569.43_AT)
12698_at (AC000106.42_AT)	12711_f_at (Z95773_F_AT)
12712_f_at (Z95774_F_AT)	12727_f_at (Z95799_F_AT)
12736_f_at (Z97048_F_AT)	12737_f_at (Z97049_F_AT)
12744_at (AC001645.15_AT)	12759_at (AC005278.32_AT)
12760_g_at (AC005278.32_G_AT)	12764_f_at (AC004138.69_F_AT)
12772_at (AC005278.34_AT)	12776_at (AL021811.156_AT)
12790_s_at (AL021635.58_S_AT)	12797_s_at (AC007138.25_S_AT)
12801_at (AC005223.34_AT)	12802_at (AL022373.153_AT)
12831_f_at (U33014.2_5_F_AT)	12832_f_at (U33014.2_M_F_AT)
12851_s_at (ACCSYN1_S_AT)	12854_s_at (ACS1_S_AT)
12855_f_at (ADH_F_AT)	12879_s_at (AIG1_S_AT)
12880_s_at (AIG2_S_AT)	12883_s_at (APX_S_AT)
12889_s_at (ASA1_S_AT)	12891_at (ATACS6_AT)
12892_g_at (ATACS6_G_AT)	12904_s_at (ATERF1_S_AT)
12905_s_at (ATERF2_S_AT)	12906_s_at (ATERF3_S_AT)
12908_s_at (ATERF5_S_AT)	12909_s_at (ATERF6_S_AT)
12911_s_at (ATG6PDHE5_S_AT)	12921_s_at (ATHHMGCOAR_S_AT)
12930_s_at (ATLLS1_S_AT)	12951_at (AC005489.5_AT)
12958_at (AC002332.249_AT)	12962_at (AC004697.165_AT)
12965_at (AL021711.118_AT)	12966_s_at (AL023094.197_S_AT)
12989_s_at (AC004077.149_S_AT)	13003_s_at (AB021936.1_S_AT)
13005_at (AC004683.61_AT)	13014_at (U93215.87_AT)
13015_s_at (X98673.2_S_AT)	13025_at (AL050400.20_AT)
13040_at (AC002392.134_AT)	13048_s_at (AC004138.22_S_AT)
13070_at (AC006919.171_AT)	13094_at (AL035523.163_AT)
13100_at (AC003680.50_AT)	13110_at (AF074021.34_AT)

13115_at (AC000375.44_AT)	13119_at (AC007260.23_AT)
13128_at (AL049607.47_AT)	13134_s_at (AC002337.9_S_AT)
13137_at (AC007169.86_AT)	13144_at (AC007017.246_AT)
13147_at (AL035678.99_AT)	13152_s_at (AC005322.24_S_AT)
13154_s_at (AC002333.210_S_AT)	13157_at (AC002409.35_AT)
13161_at (AF002109.89_AT)	13163_s_at (AC005560.223_S_AT)
13176_at (AL031394.56_AT)	13177_at (AL049640.42_AT)
13187_i_at (ATTHIRED4_I_AT)	13188_r_at (ATTHIRED4_R_AT)
13189_s_at (ATTHIRED4_S_AT)	13190_s_at (ATTHIREDA_S_AT)
13211_s_at (BCHI_S_AT)	13212_s_at (BGL2_S_AT)
13215_s_at (cafferoylcoAmethyltrans_S_AT)	13217_s_at (calmodulinlike_S_AT)
13219_s_at (CHI4_S_AT)	13220_s_at (CHS-EXON1_S_AT)
13221_at (CHS-WHOLE-SEQ_AT)	13243_r_at (ELI32_R_AT)
13244_s_at (ELI32_S_AT)	13246_at (ERECTAL_AT)
13253_f_at (FPS1_F_AT)	13255_i_at (gammaglutamyltranspepti_I_AT)
13256_s_at (gammaglutamyltranspepti_S_AT)	13259_s_at (glutathioneperoxidase1_S_AT)
13261_s_at (glutathionereductase1_S_AT)	13263_s_at (GST1_RC_S_AT)
13266_s_at (GST4_S_AT)	13270_at (HSF21_AT)
13271_g_at (HSF21_G_AT)	13273_s_at (HSF4_S_AT)
13275_f_at (HSP174_F_AT)	13277_i_at (HSP176A_I_AT)
13279_s_at (HSP176II_S_AT)	13284_s_at (HSP70_S_AT)
13285_s_at (HSP83_S_AT)	13312_at (AC006223.75_AT)
13367_at (AC004680.97_AT)	13370_at (AC005322.4_AT)
13381_at (AC006580.8_AT)	13395_at (AL035528.202_AT)
13435_at (AF003102.3_AT)	13437_at (AF096371.8_AT)
13450_at (AL049657.33_AT)	13459_at (AF013294.21_AT)
13467_at (AL096860.198_AT)	13480_at (AC005223.15_AT)
13482_at (AC005896.195_AT)	13534_at (AF149413.36_AT)
13536_at (AL021636.47_AT)	13538_at (AL080254.75_AT)
13547_s_at (AC004450.15_S_AT)	13564_at (AC005312.113_AT)
13565_at (AL035601.21_AT)	13584_at (AC007127.23_AT)
13588_at (AL021961.24_AT)	13589_at (AC000132.24_AT)
13604_at (AC000104.20_AT)	13605_at (AL078470.75_AT)
13617_at (AC006592.64_AT)	13627_at (AL035394.196_AT)
13637_at (AL049482.9_AT)	13645_at (AC000098.8_AT)
13647_at (AF000657.22_AT)	13651_at (AL035538.320_AT)

14249_i_at (PAD4_I_AT)	14250_r_at (PAD4_R_AT)
14254_s_at (PAL1-MRNA_S_AT)	14256_f_at (PAL1-INTRON_F_AT)
14257_s_at (PAL2-MRNA_S_AT)	14320_at (AC005956.54_AT)
14381_at (AC002521.68_AT)	14386_at (AC005309.177_AT)
14408_at (AC002291.14_AT)	14428_s_at (AL023094.342_S_AT)
14431_at (AL035394.279_AT)	14448_at (AC002387.243_AT)
14450_at (AC002986.49_AT)	14459_at (AC006200.69_AT)
14460_at (AC006201.21_AT)	14461_at (AC006202.73_AT)
14468_at (AC007576.62_AT)	14475_at (AL021811.121_AT)
14487_at (Z97341.343_AT)	14498_at (AC004261.51_AT)
14530_at (AL021889.231_AT)	14573_at (AF069298.35_AT)
14584_at (AC007658.25_AT)	14591_at (AL035440.107_AT)
14595_at (AL022580.163_AT)	14605_at (AC006193.6_AT)
14608_at (AC007357.49_AT)	14609_at (AC002340.147_AT)
14613_at (AC004669.20_AT)	14614_at (AC004165.66_AT)
14620_s_at (PAT1_S_AT)	14635_s_at (PR.1_S_AT)
14636_s_at (PR5_S_AT)	14638_s_at (PRXCB_S_AT)
14640_s_at (PUTATIVEMLOHI_S_AT)	14643_s_at (RAR047_S_AT)
14660_s_at (THIOREDOXL_S_AT)	14663_s_at (trehalaseprecursor_RC_S_AT)
14667_s_at (TRPB_S_AT)	14672_s_at (TSA1_S_AT)
14673_s_at (TSB2_S_AT)	14675_s_at (VSP_S_AT)
14682_i_at (WT1012A_RC_I_AT)	14686_s_at (WT1073_S_AT)
14696_at (WT740_RC_AT)	14697_g_at (WT740_RC_G_AT)
14705_i_at (WT77_RC_I_AT)	14706_r_at (WT77_RC_R_AT)
14711_s_at (ZFPL_S_AT)	14735_s_at (AF008124_S_AT)
14750_s_at (AF096370.12_S_AT)	14763_at (X86958.1_AT)
14770_s_at (AC002338.167_S_AT)	14779_at (AC004680.71_AT)
14780_at (AC004683.103_AT)	14786_at (AC005397.115_AT)
14793_at (AC006202.10_AT)	14838_s_at (M96073.6_S_AT)
14882_at (AL022605.63_AT)	14884_at (AL031032.95_AT)
14895_s_at (Z97344.138_S_AT)	14900_at (AC000348.12_AT)
14923_at (AC006283.158_AT)	14924_at (AC006283.46_AT)
14928_at (AC006569.88_AT)	14931_at (AC006951.173_AT)
14959_at (AC007202.26_AT)	14964_at (AC001229.8_AT)
14965_at (AC002329.22_AT)	14972_at (AC005499.38_AT)
14978_at (AC002333.49_AT)	14998_at (U93215.42_AT)

15032_at (AC002294.8_AT)	15039_at (AF001308.67_AT)
15040_g_at (AF001308.67_G_AT)	15042_at (AL021961.3_AT)
15052_at (AC002332.103_AT)	15067_at (AC004683.36_AT)
15073_at (AC007069.93_AT)	15085_s_at (AL031018.274_S_AT)
15088_s_at (AC002311.37_S_AT)	15091_at (AC004683.97_AT)
15098_s_at (ATU26945_S_AT)	15116_f_at (AF121356_F_AT)
15118_s_at (ATHGLUGRFS_S_AT)	15120_s_at (ATU10034_S_AT)
15123_s_at (ATU40857_S_AT)	15124_s_at (ATU59508_S_AT)
15125_f_at (D85190_F_AT)	15129_s_at (AF030386_S_AT)
15132_s_at (AF121878_S_AT)	15137_s_at (ATU57320_S_AT)
15140_s_at (ATU93845_S_AT)	15141_s_at (D85191_S_AT)
15154_s_at (ATHMTGDAS_S_AT)	15161_s_at (ATU90522_S_AT)
15162_s_at (U01880_S_AT)	15175_s_at (ATU28215_S_AT)
15188_s_at (AF081202_S_AT)	15192_s_at (ATHERD1_S_AT)
15196_s_at (ATU43412_S_AT)	15197_s_at (ATU52851_S_AT)
15199_s_at (AB005804_S_AT)	15203_s_at (AB013887_S_AT)
15211_s_at (ATH243813_S_AT)	15216_s_at (ATU75191_S_AT)
15342_at (AC006593.101_AT)	15379_at (AC002335.182_AT)
15389_at (AC004786.100_AT)	15406_at (AC006931.179_AT)
15431_at (AL030978.64_AT)	15463_at (AL031326.226_AT)
15473_at (AC006836.125_AT)	15479_at (AL049483.205_AT)
15483_s_at (AC005819.20_S_AT)	15485_at (AC006233.109_AT)
15487_at (AC007661.87_AT)	15496_at (AC006282.167_AT)
15515_r_at (AF058919.32_R_AT)	15518_at (AC005322.28_AT)
15522_i_at (AL078637.213_I_AT)	15523_s_at (AL078637.213_S_AT)
15524_at (AC005508.25_AT)	15526_at (AC004122.16_AT)
15531_i_at (AL078637.191_I_AT)	15532_r_at (AL078637.191_R_AT)
15539_at (AC005770.21_AT)	15540_at (AC006585.205_AT)
15543_at (AF096371.10_AT)	15544_at (AL021633.110_AT)
15547_at (AC005970.122_AT)	15551_at (AL035440.289_AT)
15578_s_at (AF004213_S_AT)	15580_s_at (AF057043_S_AT)
15582_s_at (ATH131392_S_AT)	15594_s_at (ATU56635_S_AT)
15606_s_at (AF061517_S_AT)	15613_s_at (ATHHOMEOA_S_AT)
15614_s_at (ATHMERI5B_S_AT)	15617_s_at (ATHSAR1_S_AT)
15622_s_at (ATU43945_S_AT)	15625_s_at (ATU74610_S_AT)
15629_s_at (AB003280_S_AT)	15631_s_at (AB005805_S_AT)

15632_s_at (AB012570_S_AT)	15641_s_at (AF117063_S_AT)
15646_s_at (ATHSAT1G_S_AT)	15665_s_at (AF022658_S_AT)
15669_s_at (AF047834_S_AT)	15670_s_at (AF061638_S_AT)
15672_s_at (AF082299_S_AT)	15674_s_at (AF091844_S_AT)
15680_s_at (ATHATPK19B_S_AT)	15775_at (AL079344.196_AT)
15778_at (X98676.2_AT)	15779_g_at (X98676.2_G_AT)
15792_at (AC002341.106_AT)	15798_at (AC002521.173_AT)
15815_s_at (Z97342.366_S_AT)	15832_at (AC004561.255_AT)
15839_at (AC005662.203_AT)	15859_at (AC006587.164_AT)
15866_s_at (AC007133.59_S_AT)	15874_at (AL022223.106_AT)
15886_at (AL078637.204_AT)	15900_at (AC005311.74_AT)
15919_at (AC007060.42_AT)	15921_s_at (AC007067.1_S_AT)
15924_at (AC007138.61_AT)	15943_at (AC007202.16_AT)
15970_s_at (X71794.2_S_AT)	15978_at (X68592.6_AT)
15982_s_at (AC006260.78_S_AT)	16001_at (AF035385.2_AT)
16003_s_at (AL021749.64_S_AT)	16021_s_at (AL022224.182_S_AT)
16031_at (X94248.1_AT)	16043_at (AC005489.17_AT)
16048_at (X78586.2_AT)	16053_i_at (Y14251.4_I_AT)
16054_s_at (Y14251.4_S_AT)	16058_s_at (ATU94495_S_AT)
16059_s_at (D88206_S_AT)	16062_s_at (AB007789_S_AT)
16063_s_at (AB008103_S_AT)	16073_f_at (AF062908_F_AT)
16077_s_at (AF085230_S_AT)	16080_f_at (AF118822_F_AT)
16083_s_at (AF153283_S_AT)	16087_s_at (ATHATPK6A_S_AT)
16090_s_at (ATHFAD8A_S_AT)	16091_s_at (ATHHSP83_S_AT)
16092_s_at (ATHKAT1_S_AT)	16103_s_at (ATU60445_S_AT)
16105_s_at (ATU68017_S_AT)	16108_s_at (D78604_S_AT)
16110_s_at (AB004822_S_AT)	16111_f_at (AB007788_F_AT)
16130_s_at (AF078683_S_AT)	16133_s_at (AF089810_S_AT)
16134_s_at (AF132016_S_AT)	16151_s_at (ATHPRKINA_S_AT)
16153_s_at (ATHRPRP1C_S_AT)	16159_s_at (ATU37697_S_AT)
16161_s_at (ATU39072_S_AT)	16164_s_at (ATU47029_S_AT)
16173_s_at (D78607_S_AT)	16203_at (AC007519.53_AT)
16229_at (AL049638.148_AT)	16230_at (AL049655.78_AT)
16232_s_at (AL080252.77_S_AT)	16233_at (AL080254.83_AT)
16236_g_at (X92657.3_G_AT)	16241_at (AL022604.84_AT)
16272_at (AC006304.136_AT)	16288_at (AF024504.17_AT)

16298_at (AL021890.71_AT)	16299_at (AL024486.185_AT)
16301_s_at (AL031018.105_S_AT)	16306_at (AL049751.112_AT)
16327_at (AC002334.12_AT)	16329_s_at (AF013294.17_S_AT)
16335_at (AL079347.105_AT)	16340_at (AC004255.15_AT)
16351_at (AL021684.194_AT)	16357_at (AF149413.38_AT)
16363_at (AC004255.14_AT)	16365_at (AC003974.136_AT)
16383_at (AC006300.64_AT)	16391_at (AL050351.194_AT)
16398_s_at (AL022603.3_S_AT)	16405_at (AC005850.9_AT)
16406_at (AC006921.33_AT)	16409_at (AC004393.2_AT)
16434_at (AL021711.157_AT)	16440_s_at (AF002109.137_S_AT)
16442_s_at (AJ002551.2_S_AT)	16457_s_at (AC005397.17_S_AT)
16461_i_at (AC004683.79_I_AT)	16462_s_at (AC004683.79_S_AT)
16465_at (Y08892.1_AT)	16468_at (AF049870.5_AT)
16470_s_at (AF068299.4_S_AT)	16483_at (X68053_AT)
16496_s_at (AF030386.1_S_AT)	16510_at (AL034567.198_AT)
16522_at (X77500.2_AT)	16524_at (AC006577.38_AT)
16526_at (Z49227.1_AT)	16536_s_at (AB008107_S_AT)
16537_s_at (AB008111_S_AT)	16538_s_at (AB010259_S_AT)
16539_s_at (AB013301_S_AT)	16541_s_at (AB023423_S_AT)
16545_s_at (AF037229_S_AT)	16548_s_at (AF054617_S_AT)
16553_f_at (AF078821_F_AT)	16568_s_at (ATHATCDPK_S_AT)
16570_s_at (ATHCDPKA_S_AT)	16578_s_at (ATHRPRP1B_S_AT)
16589_s_at (ATU26937_S_AT)	16594_s_at (ATU39783_S_AT)
16603_s_at (ATU81293_S_AT)	16609_s_at (AB008104_S_AT)
16610_s_at (AB008490_S_AT)	16611_s_at (AB008782_S_AT)
16613_s_at (AF012657_S_AT)	16617_s_at (AF029980_S_AT)
16620_s_at (AF051338_S_AT)	16635_s_at (AF126057_S_AT)
16638_s_at (AF139098_S_AT)	16646_s_at (ATHDHS1_S_AT)
16649_s_at (ATHORF_S_AT)	16701_at (AC005312.61_AT)
16712_at (AC006068.67_AT)	16721_at (AC006533.58_AT)
16747_at (AL021713.3_AT)	16753_at (AL031032.110_AT)
16781_at (AC002392.100_AT)	16810_at (AC002339.46_AT)
16817_s_at (AL096882.91_S_AT)	16859_at (AL035523.135_AT)
16864_i_at (AF037367.4_I_AT)	16865_s_at (AF037367.4_S_AT)
16868_at (AL035679.123_AT)	16888_s_at (AC004684.174_S_AT)
16891_s_at (AF080120.33_S_AT)	16892_at (U37336.3_AT)

16902_at (AC007119.67_AT)	16903_g_at (AC007119.67_G_AT)
16908_at (AC002396.22_AT)	16914_s_at (AL049500.57_S_AT)
16916_s_at (X77199.8_S_AT)	16927_s_at (AF035384.2_S_AT)
16939_at (AC002334.110_AT)	16940_g_at (AC002334.110_G_AT)
16943_s_at (Z97339.466_S_AT)	16951_i_at (AC005662.30_I_AT)
16952_s_at (AC005662.30_S_AT)	16955_at (AL031326.215_AT)
16968_at (AL021961.93_AT)	16970_s_at (Y18291.5_S_AT)
16972_at (AC004261.89_AT)	16978_g_at (AF076641.2_G_AT)
16981_s_at (U35829.2_S_AT)	16989_at (AL030978.46_AT)
16990_at (AC004684.91_AT)	16995_at (AC002391.188_AT)
17007_at (AC005896.26_AT)	17008_at (AC006585.212_AT)
17009_at (AL021633.163_AT)	17018_s_at (ATU18929_S_AT)
17027_s_at (ATU72958_S_AT)	17039_s_at (D78602_S_AT)
17041_s_at (D89631_S_AT)	17051_s_at (AF098947_S_AT)
17066_s_at (ATHLIPOXY_S_AT)	17073_s_at (ATTS4391_S_AT)
17075_s_at (ATU09961_S_AT)	17083_s_at (ATU18770_S_AT)
17097_s_at (ATU66345_S_AT)	17104_s_at (D88541_S_AT)
17105_s_at (AF055357_S_AT)	17111_s_at (ATHACSC_S_AT)
17119_s_at (AF132212_S_AT)	17128_s_at (ATHRPRP1A_S_AT)
17134_at (AC000106.53_AT)	17180_at (AF007270.30_AT)
17187_at (AF128396.2_AT)	17191_i_at (AL021961.178_I_AT)
17300_at (X66017.2_AT)	17303_s_at (AC004683.25_S_AT)
17305_at (U25649.3_AT)	17323_at (U95973.69_AT)
17338_at (AC002535.97_AT)	17341_at (AL021713.89_AT)
17352_at (AC007127.33_AT)	17356_s_at (Z97338.190_S_AT)
17362_s_at (Z97338.181_S_AT)	17371_at (AF076243.44_AT)
17376_at (AL021890.218_AT)	17379_at (AF085279.9_AT)
17380_at (AL021961.39_AT)	17381_at (Z99708.402_AT)
17398_at (AC002535.143_AT)	17413_s_at (AJ006961.4_S_AT)
17451_at (AC002343.47_AT)	17452_g_at (AC002343.47_G_AT)
17458_at (AC006260.91_AT)	17464_at (AC000132.72_AT)
17477_s_at (X63443.2_S_AT)	17482_s_at (Z97343.441_S_AT)
17484_at (X79052.2_AT)	17485_s_at (Z97340.345_S_AT)
17487_s_at (U18993.2_S_AT)	17490_s_at (M90416.2_S_AT)
17494_s_at (ATU30478_S_AT)	17500_s_at (ATHCALLGA_S_AT)
17511_s_at (AF067605_S_AT)	17514_s_at (AF076277_S_AT)

18266_at (AC004684.33_AT)
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 18299_s_at (M23872.2_S_AT)
 18314_i_at (AL078579.83_I_AT)
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 18508_s_at (AC006532.89_S_AT)
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 18597_at (AL080282.74_AT)
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 18622_g_at (AJ005902.2_G_AT)
 18631_at (AC002510.112_AT)
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 18625_at (AC005278.22_AT)
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 18681_at (L23573_AT)
 18686_s_at (U18126_S_AT)
 18698_s_at (X17528_S_AT)
 18720_s_at (X92419_S_AT)
 18753_s_at (AF118222.28_S_AT)
 18803_at (AC005315.94_AT)
 18866_at (AC005917.178_AT)
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 18949_at (Z54136.1_AT)
 18963_at (AC004561.99_AT)
 18976_at (AC000106.31_AT)
 18984_at (AC003096.100_AT)
 19019_i_at (X82623.2_I_AT)
 19060_at (AC003671.34_AT)
 19110_s_at (X86947.2_S_AT)

19132_s_at (AL022603.298_S_AT)	19137_at (X74755.2_AT)
19140_at (AC005170.24_AT)	19150_at (AC006577.20_AT)
19161_at (AL078579.9_AT)	19171_at (AC002335.160_AT)
19178_at (Y18227.2_AT)	19181_s_at (AF053065.2_S_AT)
19182_at (AL031804.245_AT)	19207_at (AC006069.117_AT)
19219_at (AC007019.185_AT)	19230_at (AC003113.15_AT)
19247_at (AF071527.44_AT)	19257_s_at (AC000104.57_S_AT)
19284_at (AC003028.196_AT)	19288_at (AC005824.130_AT)
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20646_at (AC002291.20_AT)	20656_at (AL035396.46_AT)
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20715_at (AF079183.1_AT)	

Table 20a: cDNA-AFLP gene fragments with similarity to other known proteins

cDNA***	Known protein	Organism	Related accession number**	Blast score*
DESCA1	no significant similarity	-	-	-
DESCA2	ser/thr kinase	bean	AF078082	2e-12
DESCA3	endo-1,4-beta-glucanase	rape	AJ242807	4e-19
DESCA4	pdr 5-abc transporter	duckweed	Z70524	1e-27
DESCA5	transcriptional regulator	yeast	NP 014933	9e-1
DESCA6	kinase	Arabidopsis	T00502	7e-1
DESCA7	salicylate-induced glucosyltransferase IS5a	tobacco	T03747	2e-21
DESCA8	nbs-LRR	rice	AAF82158	5e-2
DESCA9	cytochrome p450 monooxygenase	tobacco	X96784	7e-31
DESCA10	MRP-like ABC transporter	Arabidopsis	U96399	8e-7
DESCA11	phosphoribosylanthranilate transferase	Arabidopsis	AAF18518	8e-17
DESCA12	hypersensitivity-related 201	tobacco	X95343	3e-23
DESCA13	integral membrane glycoprotein	puffer fish	AF013613	9e-1
7a tgaa	no significant similarity	-	-	-
10d tcg	hypothetical protein F3F9.18	Arabidopsis	AC013430	7e-15
11a tgca	no significant similarity	-	-	-
c.r. actin	actin	C. rubrum	X92353	7e-45

* NCBI BLASTX translated search (Altschul et al., 1997)

5 ** Accession numbers are listed in SEQ ID Nos 1967-1980

*** (DESCA sequences are listed in SEQ ID Nos 1954-1966)

Table 20b: Relative gene expression fold changes of cDNA-AFLP gene fragments with similarity to other known proteins at different time points during viral infections as determined by quantitative RT-PCR

cDNA	Gene expression fold changes				
	<i>C. amaranticolor</i>			<i>C. quinoa</i>	
	TMV ¹			TRV ²	
	4dai	7dai	11dai	4dai	4dai
DESCA1	200	180	6.1	278	not detectable
DESCA2	36	25	27	10	700
DESCA3	23	15	2.7	19	46
DESCA4	21	9.2	4.5	6.8	52
DESCA5	19	8.0	9.1	15	1100
DESCA6	8.4	9.6	12	2.1	not detectable
DESCA7	8.9	2.8	5.6	53	150
DESCA8	5.9	3.2	2.0	5.8	120
DESCA9	5.1	5.9	4.2	3.1	not detectable
DESCA10	5.6	1.9	0.95	4.1	not detectable
DESCA11	5.5	3.6	3.0	3.9	230
DESCA12	5.0	2.4	1.7	5.6	7.9
DESCA13	2.9	1.8	1.9	3.3	34
7a tgaa	1.5	1.4	1.7	not tested	not tested
10d tcg	2.2	0.75	0.25	not tested	not tested
11a tgca	1.6	0.54	0.18	not tested	not tested
c.r. actin	1.0	1.0	1.0	1.0	1.0

¹ Values are the fold increases in gene expression of TMV-MGfus infected compared to mock-inoculated plants.

² Values are the fold increases in gene expression of TRV infected compared to mock-inoculated plants.

³ Values are the fold increases in gene expression of TMV infected compared to mock-inoculated plants.

Table 22:

Correlation of Seq ID NOs to Reference Numbers

SEQ ID NO:	ProbeSet	Reference Number
---------------	----------	------------------

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2	11997_at	AC005967.4_AT
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4	12004_at	AL022023.132_AT
5	12007_at	Z99708.249_AT
6	12037_at	AC004005.174_AT
7	12048_at	AF001308.46_AT
8	12051_at	AL021889.94_AT
9	12062_at	AC006069.147_AT
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11	12072_at	AL035396.4_AT
12	12079_s_at	A71597.1_S_AT
13	12081_at	AC001645.140_AT
14	12086_s_at	AC002409.88_S_AT
15	12091_at	AC004450.116_AT
16	12092_at	AC004793.13_AT
17	12094_at	AC006223.143_AT
18	12115_at	AL033545.26_AT
19	12124_s_at	Z97337.149_S_AT
20	12125_at	Z97341.99_AT
21	12128_at	AC004261.157_AT
22	12136_at	AC007591.60_AT
23	12150_at	AC004005.151_AT
24	12160_at	AC006284.117_AT
25	12187_at	AC005489.31_AT
26	12191_at	AC006068.35_AT
27	12193_at	AC006072.132_AT
28	12198_at	AC006954.90_AT
29	12203_at	AL021710.268_AT
30	12212_at	AL049711.168_AT
31	12216_at	AC007119.56_AT
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105	12892_g_at	ATACS6_G_AT
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267	14197_at	NOVARTIS71_AT
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269	14217_at	NOVARTIS85_RC_AT
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271	14235_at	NOVARTIS97_AT
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322	14706_r_at	WT77_RC_R_AT

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813	19462_s_at	AF001168.2_S_AT
814	19464_at	AC005560.51_AT
815	19465_at	AL021768.96_AT
816	19494_at	AC007296.26_AT
817	19531_at	AL021960.91_AT
818	19546_at	AC005398.172_AT
819	19555_at	AF058919.48_AT
820	19591_at	AJ010735.4_AT
821	19614_at	AC003970.32_AT
822	19623_at	AF000657.40_AT
823	19624_at	AL049481.196_AT
824	19625_s_at	AC002311.26_S_AT
825	19635_at	AL049746.38_AT
826	19639_at	AL080252.22_AT
827	19640_at	AC004561.78_AT
828	19641_at	AC004561.66_AT

875	20142_at	AL035521.155_AT
876	20144_at	AL079350.68_AT
877	20165_at	AC002311.16_AT
878	20179_at	AL035538.229_AT
879	20189_at	AC005489.2_AT
880	20194_at	AC007584.48_AT
881	20199_at	AL050300.89_AT
882	20200_at	AL050400.67_AT
883	20215_s_at	AF117125.2_S_AT
884	20223_at	AL022347.145_AT
885	20238_at	X74514.2_AT
886	20239_g_at	X74514.2_G_AT
887	20245_s_at	AC005309.97_S_AT
888	20246_s_at	AF084037.3_S_AT
889	20247_at	AC004392.4_AT
890	20258_at	AF130252.1_AT
891	20262_at	AC002294.26_AT
892	20263_at	AB004798.1_AT
893	20269_at	AC002387.237_AT
894	20271_at	Z99707.27_AT
895	20285_s_at	AC003674.18_S_AT
896	20287_at	Y14590.5_AT
897	20288_g_at	Y14590.5_G_AT
898	20291_s_at	M92353.4_S_AT
899	20297_at	AC007153.27_AT
900	20323_at	AC004561.62_AT
901	20335_s_at	Y14208.2_S_AT
902	20345_at	AF104919.16_AT
903	20346_at	L031135.156_AT
904	20348_at	AC005967.35_AT
905	20356_at	AC004561.74_AT
906	20365_s_at	AC005850.19_S_AT
907	20370_at	AC004561.263_AT
908	20372_at	AL021713.24_AT
909	20382_s_at	AC002338.35_S_AT
910	20409_g_at	AC004077.132_G_AT
911	20420_at	AL024486.131_AT
912	20421_at	U81294.2_AT
913	20422_g_at	U81294.2_G_AT
914	20432_at	U43486.2_AT
915	20433_at	AC006232.147_AT
916	20442_i_at	AC006341.42_I_AT
917	20443_s_at	AC006341.42_S_AT
918	20450_at	AJ005930.2_AT
919	20461_at	20461_at
920	20462_at	U82399.2_AT

921	20477_at	AC004238.154_AT
922	20479_i_at	AF069495.2_I_AT
923	20480_s_at	AF069495.2_S_AT
924	20485_at	AC007660.131_AT
925	20491_at	AC004561.146_AT
926	20507_at	AL021635.67_AT
927	20511_at	AC007290.24_AT
928	20516_at	AL035523.64_AT
929	20517_at	Y17722.7_AT
930	20524_at	AC005698.12_AT
931	20529_at	Z97341.125_AT
932	20551_at	AC006081.211_AT
933	20572_s_at	AC005560.229_S_AT
934	20577_at	AL078464.72_AT
935	20584_at	AC004450.75_AT
936	20586_i_at	AC005824.195_I_AT
937	20587_s_at	AC005824.195_S_AT
938	20589_at	AF081066.3_AT
939	20590_at	AL035540.159_AT
940	20591_at	AL080252.115_AT
941	20619_at	AC005896.161_AT
942	20620_g_at	AC005896.161_G_AT
943	20646_at	AC002291.20_AT
944	20656_at	AL035396.46_AT
945	20658_s_at	2AL050400.70_S_AT
946	20660_s_at	X97488.2_S_AT
947	20669_s_at	AC002388.6_S_AT
948	20675_at	AC006234.204_AT
949	20678_at	AC007296.30_AT
950	20685_at	AL049751.46_AT
951	20686_at	Y14424.2_AT
952	20689_s_at	AC002335.19_S_AT
953	20715_at	AF079183.1_AT
1001	12891_at	
1002	13217_s_at	
1003	14248_at	
1004	15116_f_at	
1005	15622_s_at	
1006	16173_s_at	
1007	17511_s_at	
1008	17548_s_at	
1009	13115_at	
1010	13645_at	
1011	14032_at	
1012	17485_s_at	
1013	17930_s_at	

1014	19640_at
1015	20194_at
1016	20348_at
1017	13467_at
1018	17775_at
1019	19546_at
1020	20134_s_at
1021	13818_s_at
1022	12892_g_at
1023	12904_s_at
1024	13627_at
1025	16995_at
1026	17533_s_at
1027	18716_at
1028	18888_at
1029	12115_at
1030	12574_at
1031	14015_s_at
1032	14016_s_at
1033	17744_s_at
1034	19019_i_at
1035	19762_at
1036	13100_at
1037	14609_at
1038	13015_s_at
1039	19284_at
1040	13215_s_at
1041	16649_s_at
1042	13565_at
1043	16914_s_at
1044	19991_at
1045	20356_at
1046	12989_s_at
1047	14635_s_at
1048	17128_s_at
1049	20619_at
1050	20620_g_at
1051	20421_at
1052	20422_g_at
1053	20142_at
1054	12908_s_at
1055	16536_s_at
1056	13370_at
1057	17134_at
1058	19672_at
1059	19673_g_at

1060 19150_at
1061 12710
1062 12711_f_at
1063 18166
1064 19451_at
1065 13763_at
1066 14214_at
1067 14931_at
1068 13818_s_at
1069 14635_s_at
1070 17128_s_at
1071 20356_at
1072 20323_at
1073 18122_at
1074 14609_at
1075 14613_at
1076 12094_at
1077 13312_at
1078 19970_s_at
1079 12128_at
1080 18631_at
1081 14573_at
1082 17371_at
1083 20421_at
1084 20422_g_at
1085 17485_s_at
1086 16398_s_at
1087 16968_at
1088 13243_r_at
1089 13244_s_at
1090 14882_at
1091 15120_s_at
1092 16357_at
1093 17180_at
1094 12908_s_at
1095 16536_s_at

Table 23

Correlation of Seq ID NOs to the Rice Orthologs and their Promoters

5	3	

	rice homolog:	promoter:
	2808	4884
	3066	5142
10	3820	5896
	4655	6731
	6	
15	-----	
	rice homolog:	promoter:
	2757	4833
	3013	5089
	3393	5469
20	3899	5975
	7	

	rice homolog:	promoter:
25	3227	5303
	3579	5655
	3851	5927
	3890	5966
	4516	6592
30	8	

	rice homolog:	promoter:
	3086	5162
	3341	5417
35	3762	5838
	3767	5843
	4285	6361
	4487	6563
	4488	6564
40	4489	6565
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45	rice homolog:	promoter:
	3629	5705
	3914	5990

[illegible]

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4311 6387

[illegible]

5	rice homolog:	promoter:
	3718	5794
	4345	6421

10 -----
rice homolog: promoter:
4493 6569

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	rice homolog:	promoter:
	3479	5555
	4208	6284
	4236	6312

rice homolog: promoter:
3891 5967

rice homolog: promoter:
4645 6721

rice homolog: promoter:
4210 6286

	rice homolog:	promoter:
40	2864	4940
	2964	5040
	4218	6294
	4307	6383
	4458	6534

	rice homolog:	promoter:
	3035	5111
	3157	5233
	3379	5455
5	3626	5702
	3990	6066

55

	rice homolog:	promoter:
10	2687	4763
	2869	4945
	2984	5060
	3054	5130
15	3180	5256
	3561	5637
	4306	6382
	4326	6402
	4460	6536
20	4476	6552
	4521	6597
	4603	6679

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	rice homolog:	promoter:
25	4005	6081

59

	rice homolog:	promoter:
30	2922	4998
	3833	5909
	3967	6043
35	4202	6278

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	rice homolog:	promoter:
40	2706	4782
	4125	6201
	4720	6796

65

	rice homolog:	promoter:
45		

2815	4891
4112	6188
4288	6364

5 67

rice homolog:	promoter:
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	2716	4792
	2928	5004
10	2940	5016
	3182	5258
	3333	5409
	3351	5427
	3386	5462
15	3387	5463
	3445	5521
	3530	5606
	3581	5657
	3727	5803
20	3825	5901
	3915	5991
	4120	6196
	4170	6246
	4267	6343
25	4280	6356
	4350	6426
	4479	6555
	4713	6789

30 68

rice homolog:	promoter:
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	2764	4840
	3072	5148
35	3192	5268
	3290	5366
	3546	5622
	3553	5629
	3658	5734
40	3747	5823
	3972	6048
	4543	6619

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rice homolog:	promoter:
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Variable	Mean	SD	Min	Max	Skewness	Kurtosis	Shapiro-Wilk	Normality
Age	35.5	10.5	20	65	0.1	3.0	0.95	0.95
Gender	1.5	0.5	1	2	0.0	3.0	0.95	0.95
Marital Status	1.5	0.5	1	2	0.0	3.0	0.95	0.95
Education	12.5	2.0	9	16	0.1	3.0	0.95	0.95
Income	1500	500	500	3000	0.2	3.0	0.95	0.95
Occupation	1.5	0.5	1	2	0.0	3.0	0.95	0.95
Health Status	1.5	0.5	1	2	0.0	3.0	0.95	0.95
Stress Level	2.5	1.0	1	4	0.1	3.0	0.95	0.95
Life Satisfaction	3.5	1.0	1	5	0.1	3.0	0.95	0.95
Resilience	3.5	1.0	1	5	0.1	3.0	0.95	0.95
Emotional Stability	3.5	1.0	1	5	0.1	3.0	0.95	0.95
Life Satisfaction	3.5	1.0	1	5	0.1	3.0	0.95	0.95
Resilience	3.5	1.0	1	5	0.1	3.0	0.95	0.95
Emotional Stability	3.5	1.0	1	5	0.1	3.0	0.95	0.95
Life Satisfaction	3.5	1.0	1	5	0.1	3.0	0.95	0.95
Resilience	3.5	1.0	1	5	0.1	3.0	0.95	0.95
Emotional Stability	3.5	1.0	1	5	0.1	3.0	0.95	0.95
Life Satisfaction	3.5	1.0	1	5	0.1	3.0	0.95	0.95
Resilience	3.5	1.0	1	5	0.1	3.0	0.95	0.95
Emotional Stability	3.5	1.0	1	5	0.1	3.0	0.95	0.95
Life Satisfaction	3.5	1.0	1	5	0.1	3.0	0.95	0.95
Resilience	3.5	1.0	1	5	0.1	3.0	0.95	0.95
Emotional Stability	3.5	1.0	1	5	0.1	3.0	0.95	0.95
Life Satisfaction	3.5	1.0	1	5	0.1	3.0	0.95	0.95
Resilience	3.5	1.0	1	5	0.1	3.0	0.95	0.95
Emotional Stability	3.5	1.0	1	5	0.1	3.0	0.95	0.95
Life Satisfaction	3.5	1.0	1	5	0.1	3.0	0.95	0.95
Resilience	3.5	1.0	1	5	0.1	3.0	0.95	0.95
Emotional Stability	3.5	1.0	1	5	0.1	3.0	0.95	0.95
Life Satisfaction	3.5	1.0	1	5	0.1	3.0	0.95	0.95
Resilience	3.5	1.0	1	5	0.1	3.0	0.95	0.95
Emotional Stability	3.5	1.0	1	5	0.1	3.0	0.95	0.95
Life Satisfaction	3.5	1.0	1	5	0.1	3.0	0.95	0.95
Resilience	3.5	1.0	1	5	0.1	3.0	0.95	0.95
Emotional Stability	3.5	1.0	1	5	0.1	3.0	0.95	0.95
Life Satisfaction	3.5	1.0	1	5	0.1	3.0	0.95	0.95
Resilience	3.5	1.0	1	5	0.1	3.0	0.95	0.95
Emotional Stability	3.5	1.0	1	5	0.1	3.0	0.95	0.95
Life Satisfaction	3.5	1.0	1	5	0.1	3.0	0.95	0.95
Resilience	3.5	1.0	1	5	0.1	3.0	0.95	0.95
Emotional Stability	3.5	1.0	1	5	0.1	3.0	0.95	0.95
Life Satisfaction	3.5	1.0	1	5	0.1	3.0	0.95	0.95
Resilience	3.5	1.0	1	5	0.1	3.0	0.95	0.95
Emotional Stability	3.5	1.0	1	5	0.1	3.0	0.95	0.95
Life Satisfaction	3.5	1.0	1	5	0.1	3.0	0.95	0.95
Resilience	3.5	1.0	1	5	0.1	3.0	0.95	0.95
Emotional Stability	3.5	1.0	1	5	0.1	3.0		

rice homolog:	promoter:
3245	5321
4329	6405
4412	6488

rice homolog:	promoter:
2862	4938
3012	5088
3506	5582

rice homolog:	promoter:
2920	4996
3417	5493
3742	5818
3927	6003
4061	6137

78	

rice homolog:	promoter:
2705	4781
2737	4813
2738	4814
4654	6730
4681	6757

rice homolog:	promoter:
3163	5239
3525	5601
3965	6041
4114	6190

45 rice homolog: promoter:
3138 5214

93

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102

	rice homolog:	promoter:
	3563	5639
	3683	5759
5	4108	6184
	4168	6244
	4232	6308
	110	
10	-----	
	rice homolog:	promoter:
	2876	4952
	3099	5175
	3367	5443
15	3610	5686
	4363	6439
	4618	6694
	4656	6732
20	111	

	rice homolog:	promoter:
	2747	4823
	2766	4842
25	2955	5031
	3450	5526
	3988	6064
	112	
30	-----	
	rice homolog:	promoter:
	2779	4855
	3345	5421
	3799	5875
35	3801	5877
	4216	6292
	113	

40	rice homolog:	promoter:
	3371	5447
	3372	5448
	3373	5449
	4022	6098
45	4319	6395

rice homolog:	promoter:
2707	4783
2871	4947
3261	5337
3452	5528
4513	6589

rice homolog:	promoter:
2833	4909
2939	5015
3200	5276
3571	5647
4031	6107

rice homolog:	promoter:
2944	5020
3186	5262
3631	5707
3633	5709
3697	5773
3726	5802
4009	6085
4597	6673

rice homolog:	promoter:
3169	5245
3637	5713
3638	5714
3639	5715
3656	5732

rice homolog: 4692 promoter: 6768

	rice homolog:	promoter:
	3041	5117
	3179	5255
	3291	5367
5	4269	6345
	4633	6709
	124	

10	rice homolog:	promoter:
	3388	5464
	3410	5486
	3469	5545
	4316	6392
15	4449	6525
	126	

20	rice homolog:	promoter:
	3215	5291
	3557	5633
	3575	5651
	3847	5923
	4044	6120
25	4400	6476
	4444	6520
	4496	6572
	4593	6669
	4629	6705
30	127	

	rice homolog:	promoter:
	2981	5057
35	3199	5275
	3467	5543
	3963	6039
	4053	6129
40	128	

	rice homolog:	promoter:
	3267	5343
	4182	6258
45	4530	6606

130

	rice homolog:	promoter:
	2890	4966
5	3293	5369
	3312	5388
	3326	5402
	3812	5888
	3889	5965
10	4134	6210
	4254	6330

133

	rice homolog:	promoter:
	2799	4875
	3008	5084
	3208	5284
	3706	5782
20	3765	5841

134

	rice homolog:	promoter:
25	3005	5081
	3145	5221
	3146	5222
	3328	5404
	3511	5587
30	4572	6648
	4584	6660

135

	rice homolog:	promoter:
35	2832	4908
	3073	5149
	3257	5333
	3352	5428
40	3378	5454
	3555	5631
	3761	5837
	3869	5945
	4609	6685

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137

	rice homolog:	promoter:
	4146	6222
	4398	6474
	4399	6475
5	152	

	rice homolog:	promoter:
	4368	6444
10	4483	6559
	4550	6627
	4551	6628
	4616	6692
15	158	

	rice homolog:	promoter:
	3023	5099
	3880	5956
20	4237	6313
	4492	6568
	159	

25	rice homolog:	promoter:
	2720	4796
	3115	5191
	3383	5459
	3844	5920
30	3989	6065
	4157	6233
	4627	6703
	162	
35	-----	
	rice homolog:	promoter:
	2813	4889
	2927	5003
	3346	5422
40	3423	5499
	3682	5758
	3781	5857
	3830	5906
	4225	6301
45	4475	6551
	4622	6698

	rice homolog:	promoter:
5	3232	5308
	3491	5567
	4590	6666
	4625	6701
10	165	

	rice homolog:	promoter:
	3271	5347
	3322	5398
15	3406	5482
	3681	5757
	3973	6049
	4231	6307
	4324	6400
20	166	

	rice homolog:	promoter:
	2767	4843
25	2781	4857
	3347	5423
	4093	6169
	4130	6206
30	171	

	rice homolog:	promoter:
	2733	4809
	2761	4837
35	3049	5125
	3402	5478
	3945	6021
	172	
40	-----	
	rice homolog:	promoter:
	3389	5465
	3509	5585
	3603	5679
45	3664	5740
	3665	5741

rice homolog: 4608 promoter: 6684

rice homolog:	promoter:
3754	5830
3835	5911
4015	6091
4198	6274
4420	6496

rice homolog:	promoter:
2684	4760
4394	6470

rice homolog:	promoter:
3158	5234
3635	5711
4557	6633
4558	6634

rice homolog:	promoter:
2696	4772
3850	5926
4549	6625

rice homolog:	promoter:
3110	5186
3304	5380
3518	5594
3594	5670
3853	5929

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	rice homolog:	promoter:
	2730	4806
	2893	4969
5	3087	5163
	3176	5252
	4234	6310
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10	188	
<hr/>		
	rice homolog:	promoter:
	3068	5144
	3082	5158
	3644	5720
15	4344	6420
	4427	6503
	4468	6544
	4636	6712
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20	189	
<hr/>		
	rice homolog:	promoter:
	2778	4854
	3514	5590
25	4662	6738
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	190	
<hr/>		
	rice homolog:	promoter:
30	3020	5096
	3088	5164
	3605	5681
	3606	5682
	3992	6068
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35	199	
<hr/>		
	rice homolog:	promoter:
	2873	4949
40	2942	5018
	3492	5568
	3671	5747
	3856	5932
	4030	6106
45	4100	6176
	4253	6329

4680 6756

202

5	rice homolog:	promoter:
	2711	4787
	3015	5091
	3774	5850
	3906	5982
10	3943	6019

203

	rice homolog:	promoter:
15	3135	5211
	3318	5394
	3443	5519
	3523	5599
	3911	5987
20	3924	6000
	4596	6672

204

25	rice homolog:	promoter:
	2851	4927
	2852	4928
	3151	5227
	3152	5228
30	4186	6262

205

35	rice homolog:	promoter:
	3078	5154
	3984	6060
	4085	6161

206

40	rice homolog:	promoter:
	3051	5127
	3075	5151
	3117	5193
45	3527	5603
	3756	5832

[illegible]

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	2662	4738
	2695	4771
	3457	5533
	3504	5580
5	3842	5918
	4580	6656
	4583	6659
	218	
10	-----	
	rice homolog:	promoter:
	3338	5414
	3951	6027
	4051	6127
15	219	

	rice homolog:	promoter:
	2789	4865
20	2801	4877
	2802	4878
	2803	4879
	3703	5779
	4222	6298
25	220	

	rice homolog:	promoter:
	2885	4961
30	3394	5470
	3395	5471
	3396	5472
	3499	5575
35	221	

	rice homolog:	promoter:
	2918	4994
	3225	5301
40	4453	6529
	4534	6610
	4553	6630
	225	
45	-----	
	rice homolog:	promoter:

	3634	5710
	3673	5749
	3920	5996
	4440	6516
5	4668	6744

229

	rice homolog:	promoter:
10	2731	4807
	3466	5542
	3897	5973
	4395	6471
	4664	6740

15

237

	rice homolog:	promoter:
	2847	4923
20	3126	5202
	3237	5313
	3508	5584
	3704	5780
	3930	6006
25	4006	6082

239

	rice homolog:	promoter:
30	2924	5000
	4707	6783

240

	rice homolog:	promoter:
35	3211	5287
	3751	5827

247

40	rice homolog:	promoter:
	3971	6047

250

45	rice homolog:	promoter:
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	2971	5047
	3696	5772
	3719	5795
	4035	6111
5	4273	6349
	4675	6751

252

10	rice homolog:	promoter:
	2909	4985
	3738	5814
	3831	5907
	3904	5980
15	4039	6115
	4219	6295
	4246	6322
	4467	6543
	4495	6571

20

254

	rice homolog:	promoter:
	2771	4847
25	2874	4950
	3413	5489
	3510	5586
	4143	6219

30 255

	rice homolog:	promoter:
	2664	4740
	2740	4816
35	2792	4868
	3171	5247
	3368	5444
	3425	5501
	3788	5864
40	4183	6259
	4206	6282
	4439	6515

256

45

	rice homolog:	promoter:
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	2798	4874
	3109	5185
	3566	5642
	3901	5977
5	4190	6266
	4501	6577
	4579	6655
	4601	6677
10	258	

	rice homolog:	promoter:
	2952	5028
	3283	5359
15	4001	6077
	4040	6116
	4397	6473
	260	
20	-----	
	rice homolog:	promoter:
	3438	5514
	3886	5962
	4070	6146
25	4215	6291
	4703	6779
	263	

30	rice homolog:	promoter:
	2752	4828
	3098	5174
	3276	5352
	3625	5701
35	4309	6385
	265	

	rice homolog:	promoter:
40	2701	4777
	2861	4937
	3164	5240
	4187	6263
	4270	6346
45	267	

	rice homolog:	promoter:
	2866	4942
	2941	5017
5	3002	5078
	4330	6406

270

	rice homolog:	promoter:
10	2875	4951
	3001	5077
	3061	5137
	3282	5358
15	3590	5666
	3608	5684
	3618	5694
	3817	5893
	3969	6045
20	4211	6287
	4265	6341
	4333	6409
	4377	6453

25

	rice homolog:	promoter:
	3979	6055
	4570	6646
30	4571	6647

274

	rice homolog:	promoter:
35	3426	5502
	3534	5610

275

	rice homolog:	promoter:
40	2951	5027
	3268	5344
	3909	5985
	4277	6353
45	4490	6566

285

	rice homolog:	promoter:
	3336	5412
5	3987	6063
	4431	6507

286

	rice homolog:	promoter:
10	3430	5506

287

	rice homolog:	promoter:
15	2703	4779
	3028	5104
	3329	5405
	3595	5671
20	3667	5743
	3895	5971
	4598	6674
	4602	6678
	4688	6764

25

288

	rice homolog:	promoter:
	2820	4896
30	2977	5053
	2991	5067
	3007	5083
	3057	5133
	3097	5173
35	3155	5231
	3170	5246
	3464	5540
	3528	5604
	3532	5608
40	3872	5948
	3953	6029
	3966	6042
	4025	6101
	4161	6237
45	4544	6620

289

	rice homolog:	promoter:
	2668	4744
5	2746	4822
	3147	5223
	3284	5360
	3285	5361
	3878	5954
10	4373	6449
	4457	6533

290

	rice homolog:	promoter:
15	2780	4856
	2896	4972
	3569	5645
	4486	6562
20	4731	6807

295

	rice homolog:	promoter:
25	2785	4861
	2807	4883
	2921	4997
	2957	5033
	3281	5357
30	3303	5379
	3477	5553
	3792	5868
	3925	6001
	3946	6022
35	4175	6251

296

	rice homolog:	promoter:
40	2689	4765
	2995	5071
	2996	5072
	3133	5209
	4058	6134
45	4185	6261
	4695	6771

TABLE 1		TABLE 2		TABLE 3		TABLE 4		TABLE 5		TABLE 6		TABLE 7		TABLE 8		TABLE 9		TABLE 10		TABLE 11		TABLE 12		TABLE 13		TABLE 14		TABLE 15		TABLE 16		TABLE 17		TABLE 18		TABLE 19		TABLE 20		TABLE 21		TABLE 22		TABLE 23		TABLE 24		TABLE 25		TABLE 26		TABLE 27		TABLE 28		TABLE 29		TABLE 30		TABLE 31		TABLE 32		TABLE 33		TABLE 34		TABLE 35		TABLE 36		TABLE 37		TABLE 38		TABLE 39		TABLE 40		TABLE 41		TABLE 42		TABLE 43		TABLE 44		TABLE 45		TABLE 46		TABLE 47		TABLE 48		TABLE 49		TABLE 50		TABLE 51		TABLE 52		TABLE 53		TABLE 54		TABLE 55		TABLE 56		TABLE 57		TABLE 58		TABLE 59		TABLE 60		TABLE 61		TABLE 62		TABLE 63		TABLE 64		TABLE 65		TABLE 66		TABLE 67		TABLE 68		TABLE 69		TABLE 70		TABLE 71		TABLE 72		TABLE 73		TABLE 74		TABLE 75		TABLE 76		TABLE 77		TABLE 78		TABLE 79		TABLE 80		TABLE 81		TABLE 82		TABLE 83		TABLE 84		TABLE 85		TABLE 86		TABLE 87		TABLE 88		TABLE 89		TABLE 90		TABLE 91		TABLE 92		TABLE 93		TABLE 94		TABLE 95		TABLE 96		TABLE 97		TABLE 98		TABLE 99		TABLE 100		TABLE 101		TABLE 102		TABLE 103		TABLE 104		TABLE 105		TABLE 106		TABLE 107		TABLE 108		TABLE 109		TABLE 110		TABLE 111		TABLE 112		TABLE 113		TABLE 114		TABLE 115		TABLE 116		TABLE 117		TABLE 118		TABLE 119		TABLE 120		TABLE 121		TABLE 122		TABLE 123		TABLE 124		TABLE 125		TABLE 126		TABLE 127		TABLE 128		TABLE 129		TABLE 130		TABLE 131		TABLE 132		TABLE 133		TABLE 134		TABLE 135		TABLE 136		TABLE 137		TABLE 138		TABLE 139		TABLE 140		TABLE 141		TABLE 142		TABLE 143		TABLE 144		TABLE 145		TABLE 146		TABLE 147		TABLE 148		TABLE 149		TABLE 150		TABLE 151		TABLE 152		TABLE 153		TABLE 154		TABLE 155		TABLE 156		TABLE 157		TABLE 158		TABLE 159		TABLE 160		TABLE 161		TABLE 162		TABLE 163		TABLE 164		TABLE 165		TABLE 166		TABLE 167		TABLE 168		TABLE 169		TABLE 170		TABLE 171		TABLE 172		TABLE 173		TABLE 174		TABLE 175		TABLE 176		TABLE 177		TABLE 178		TABLE 179		TABLE 180		TABLE 181		TABLE 182		TABLE 183		TABLE 184		TABLE 185		TABLE 186		TABLE 187		TABLE 188		TABLE 189		TABLE 190		TABLE 191		TABLE 192		TABLE 193		TABLE 194		TABLE 195		TABLE 196		TABLE 197		TABLE 198		TABLE 199		TABLE 200		TABLE 201		TABLE 202		TABLE 203		TABLE 204		TABLE 205		TABLE 206		TABLE 207		TABLE 208		TABLE 209		TABLE 210		TABLE 211		TABLE 212		TABLE 213		TABLE 214		TABLE 215		TABLE 216		TABLE 217		TABLE 218		TABLE 219		TABLE 220		TABLE 221		TABLE 222		TABLE 223		TABLE 224		TABLE 225		TABLE 226		TABLE 227		TABLE 228		TABLE 229		TABLE 230		TABLE 231		TABLE 232		TABLE 233		TABLE 234		TABLE 235		TABLE 236		TABLE 237		TABLE 238		TABLE 239		TABLE 240		TABLE 241		TABLE 242		TABLE 243		TABLE 244		TABLE 245		TABLE 246		TABLE 247		TABLE 248		TABLE 249		TABLE 250		TABLE 251		TABLE 252		TABLE 253		TABLE 254		TABLE 255		TABLE 256		TABLE 257		TABLE 258		TABLE 259		TABLE 260		TABLE 261		TABLE 262		TABLE 263		TABLE 264		TABLE 265		TABLE 266		TABLE 267		TABLE 268		TABLE 269		TABLE 270		TABLE 271		TABLE 272		TABLE 273		TABLE 274		TABLE 275		TABLE 276		TABLE 277		TABLE 278		TABLE 279		TABLE 280		TABLE 281		TABLE 282		TABLE 283		TABLE 284		TABLE 285		TABLE 286		TABLE 287		TABLE 288		TABLE 289		TABLE 290		TABLE 291		TABLE 292		TABLE 293		TABLE 294		TABLE 295		TABLE 296		TABLE 297		TABLE 298		TABLE 299		TABLE	
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302

45 rice homolog: promoter:
2836 4912

3236 5312

304

5	rice homolog:	promoter:
	2960	5036
	3111	5187
	3252	5328
	3884	5960
10	3885	5961

305

	rice homolog:	promoter:
15	2899	4975
	3074	5150
	3431	5507
	3713	5789
	4008	6084

20 312

	rice homolog:	promoter:
	2721	4797
25	3256	5332
	3385	5461
	3539	5615
	3541	5617
	4145	6221

30 314

	rice homolog:	promoter:
	2839	4915
35	3240	5316
	3485	5561
	3643	5719
	3848	5924
	3957	6033
40	4406	6482
	4514	6590

316

45	rice homolog:	promoter:
	3119	5195

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Variable	Mean	SD	Min	Max	Median	Q1	Q3	Mode	Skewness	Kurtosis	Shapiro-Wilk	Normality
Age	35.2	12.5	18	65	32	28	38	35	0.15	2.1	0.98	Normal
Gender	0.5	0.5	0	1	0.5	0.5	0.5	0.5	0.0	0.0	0.99	Normal
Education	12.5	1.5	9	16	12	11.5	13	12	0.1	1.5	0.95	Normal
Income	2500	1500	500	6000	2000	1500	3000	2500	0.2	2.5	0.92	Normal
Marital Status	0.7	0.5	0	1	0.7	0.7	0.7	0.7	0.0	0.0	0.99	Normal
Occupation	1.5	1.0	1	5	2	1.5	3	2	0.1	1.8	0.96	Normal
Health Status	0.8	0.4	0	1	0.8	0.8	0.8	0.8	0.0	0.0	0.99	Normal
Stress Level	3.5	1.5	1	6	3	2.5	4	3	0.1	1.5	0.95	Normal
Life Satisfaction	4.5	1.0	3	6	4.5	4.0	5.0	4.5	0.0	0.5	0.99	Normal
Resilience	5.5	1.5	3	7	5	4.5	6	5	0.1	1.8	0.96	Normal
Optimism	6.5	1.0	5	7	6.5	6.0	7.0	6.5	0.0	0.5	0.99	Normal
Emotional Stability	5.0	1.5	3	7	5	4.5	6	5	0.1	1.8	0.96	Normal
Self-Esteem	6.0	1.0	5	7	6.0	5.5	6.5	6.0	0.0	0.5	0.99	Normal
Life Satisfaction	4.5	1.0	3	6	4.5	4.0	5.0	4.5	0.0	0.5	0.99	Normal
Resilience	5.5	1.5	3	7	5	4.5	6	5	0.1	1.8	0.96	Normal
Optimism	6.5	1.0	5	7	6.5	6.0	7.0	6.5	0.0	0.5	0.99	Normal
Emotional Stability	5.0	1.5	3	7	5	4.5	6	5	0.1	1.8	0.96	Normal
Self-Esteem	6.0	1.0	5	7	6.0	5.5	6.5	6.0	0.0	0.5	0.99	Normal

15	333	
	rice homolog:	promoter:
	2796	4872
	2958	5034
20	3191	5267
	3365	5441
	3687	5763
	3932	6008
	4342	6418
25	4360	6436

	341	

	rice homolog:	promoter:
40	3248	5324
	3942	6018

45 rice homolog: promoter:
 4299 6375

348

	rice homolog:	promoter:
5	3000	5076
	3137	5213
	3866	5942
	4038	6114
	4327	6403
10	4425	6501

360

	rice homolog:	promoter:
15	2989	5065
	2990	5066
	3090	5166
	3100	5176
	3436	5512
20	3515	5591
	3522	5598
	3636	5712
	3883	5959
	3977	6053
25	4028	6104
	4199	6275
	4201	6277
	4223	6299
	4317	6393
30	4354	6430
	4408	6484
	4450	6526
	4509	6585

35 365

	rice homolog:	promoter:
	3678	5754
	3941	6017
40	4547	6623
	4577	6653
	4684	6760
	4714	6790

45 366

	rice homolog:	promoter:
	2691	4767
	3614	5690
	3711	5787
5	3763	5839
	3975	6051
	369	

10	rice homolog:	promoter:
	2708	4784
	3125	5201
	3144	5220
	3190	5266
15	3370	5446
	3432	5508
	4067	6143
	4355	6431
	4410	6486
20	4546	6622
	4587	6663
	370	

25	rice homolog:	promoter:
	4056	6132
	372	

30	rice homolog:	promoter:
	3414	5490
	3471	5547
	4247	6323
	4482	6558
35	4650	6726
	374	

40	rice homolog:	promoter:
	2776	4852
	3497	5573
	3645	5721
	3728	5804
	3837	5913
45	378	

	rice homolog:	promoter:
	3808	5884
	4045	6121
5	4308	6384
	4525	6601

380

10	rice homolog:	promoter:
	3207	5283
	3773	5849
	4701	6777
	4715	6791
15	4716	6792

381

20	rice homolog:	promoter:
	4034	6110

382

25	rice homolog:	promoter:
	4405	6481
	4537	6613

385

30	rice homolog:	promoter:
	3490	5566
	4065	6141
	4104	6180
	4454	6530
35	4456	6532
	4730	6806

389

40	rice homolog:	promoter:
	2750	4826
	3529	5605
	3620	5696
	4575	6651
45	4694	6770
	4723	6799

391

	rice homolog:	promoter:
5	2671	4747
	3862	5938
	3863	5939
	3955	6031
	3956	6032
10	4133	6209

393

	rice homolog:	promoter:
15	3010	5086
	3802	5878
	3839	5915
	3923	5999
	4421	6497
20	4556	6632
	4614	6690

394

	rice homolog:	promoter:
25	3069	5145
	3159	5235
	3870	5946
	4147	6223
30	4512	6588

398

	rice homolog:	promoter:
35	2976	5052
	3680	5756

404

	rice homolog:	promoter:
40	4217	6293

405

	rice homolog:	promoter:
45	4116	6192

[illegible]

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3968 6044

437

5 rice homolog: promoter:
2855 4931
2937 5013
4341 6417
4640 6716

10

438

15 rice homolog: promoter:
2818 4894
2863 4939
3344 5420
3454 5530
3613 5689
4683 6759

20

439

25 rice homolog: promoter:
2819 4895
2905 4981
2935 5011
3949 6025
3958 6034
4413 6489
30 4417 6493
4465 6541

441

35 rice homolog: promoter:
3330 5406
3708 5784
3836 5912
3898 5974
40 4419 6495

448

45 rice homolog: promoter:
2715 4791
2773 4849

<hr/>		
	rice homolog:	promoter:
	2739	4815
	2772	4848
5	3168	5244
	3382	5458
	3451	5527
	3865	5941
	3974	6050
10	3982	6058
	4364	6440
	476	
<hr/>		
15	rice homolog:	promoter:
	2829	4905
	3343	5419
	3593	5669
	3741	5817
20	3829	5905
	482	
<hr/>		
25	rice homolog:	promoter:
	2853	4929
	4062	6138
	4106	6182
	4127	6203
30	484	
<hr/>		
	rice homolog:	promoter:
	2702	4778
	3302	5378
35	3327	5403
	3701	5777
	4502	6578
	487	
40	<hr/>	
	rice homolog:	promoter:
	3143	5219
	3677	5753
	4075	6151
45	4443	6519
	4710	6786

Variable	Mean	SD	Min	Max
Age	34.5	10.2	21	55
Gender	0.5	0.5	0	1
Marital status	0.6	0.5	0	1
Education	12.5	1.5	9	16
Income	15.2	5.8	10	25
Health status	0.7	0.4	0	1
Smoking status	0.3	0.5	0	1
Alcohol consumption	0.2	0.4	0	1
Exercise frequency	0.4	0.5	0	1
Stress level	0.6	0.5	0	1
Sleep quality	0.5	0.5	0	1
Work satisfaction	0.4	0.5	0	1
Life satisfaction	0.5	0.5	0	1
Depression score	10.5	5.2	0	20
Anxiety score	12.3	6.1	0	25
Quality of life score	18.7	7.4	0	30

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	rice homolog:	promoter:
	3857	5933
	4611	6687
5	505	

	rice homolog:	promoter:
	3165	5241
	3242	5318
10	3749	5825
	4383	6459
	4718	6794
	507	
15		

	rice homolog:	promoter:
	2763	4839
	3026	5102
	3409	5485
20	3468	5544
	3983	6059
	509	

25	rice homolog:	promoter:
	2759	4835
	3418	5494
	3912	5988
	4079	6155
30	4470	6546
	517	

	rice homolog:	promoter:
35	2672	4748
	2690	4766
	2727	4803
	2846	4922
	3278	5354
40	3337	5413
	3526	5602
	3730	5806
	3929	6005
	4052	6128
45	4081	6157
	4089	6165

4314 6390
4628 6704

525

5

rice homolog: promoter:
4162 6238

526

10

rice homolog: promoter:
2840 4916
2994 5070
3003 5079

15

4020 6096
4653 6729

528

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rice homolog: promoter:
3004 5080
3433 5509
3674 5750
3789 5865
25 4638 6714

533

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rice homolog: promoter:
3044 5120
3241 5317
3646 5722
3961 6037
4518 6594

35

535

40

rice homolog: promoter:
3859 5935
4328 6404

536

45

rice homolog: promoter:
3286 5362
3545 5621

	3659	5735
	4117	6193
	4149	6225
5	539	

	rice homolog:	promoter:
	3641	5717
	4248	6324
10	4286	6362
	540	

	rice homolog:	promoter:
15	3093	5169
	3127	5203
	3325	5401
	541	
20	-----	
	rice homolog:	promoter:
	2888	4964
	3037	5113
25	543	

	rice homolog:	promoter:
	3116	5192
	3434	5510
30	3435	5511
	4087	6163
	4088	6164
	546	
35	-----	
	rice homolog:	promoter:
	2791	4867
	2933	5009
	3735	5811
40	3970	6046
	4154	6230
	4213	6289
	4292	6368
	4401	6477
45	549	

	rice homolog:	promoter:
	3369	5445
	3420	5496
5	3421	5497
	3441	5517
	3559	5635
	4069	6145
	4300	6376
10	4301	6377
	4561	6637

550

	rice homolog:	promoter:
15	3141	5217
	3361	5437
	3377	5453
	3939	6015
20	3960	6036
	4091	6167

551

	rice homolog:	promoter:
25	3340	5416
	3363	5439
	4142	6218
	4159	6235
30	4436	6512

552

	rice homolog:	promoter:
35	3805	5881
	3993	6069
	4016	6092
	4077	6153
	4136	6212

40

553

	rice homolog:	promoter:
	2666	4742
45	2945	5021
	3101	5177

3224	5300
4459	6535

556

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rice homolog:	promoter:
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2929	5005
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3810	5886
------	------

3811	5887
------	------

10	4046	6122
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4548	6624
------	------

559

15

rice homolog:	promoter:
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2734	4810
------	------

3611	5687
------	------

3737	5813
------	------

4179	6255
------	------

20	4647	6723
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560

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rice homolog:	promoter:
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3598	5674
------	------

3599	5675
------	------

3600	5676
------	------

3712	5788
------	------

4388	6464
------	------

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566

rice homolog:	promoter:
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2953	5029
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35	2954	5030
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3615	5691
------	------

4386	6462
------	------

4387	6463
------	------

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569

rice homolog:	promoter:
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2786	4862
------	------

3019	5095
------	------

45	3233	5309
----	------	------

3307	5383
------	------

	4469	6545
	572	
5	rice homolog:	promoter:
	2674	4750
	4099	6175
	4366	6442
10	577	
	rice homolog:	promoter:
	2825	4901
	3006	5082
15	3136	5212
	3822	5898
	4010	6086
	581	
20	rice homolog:	promoter:
	2765	4841
	3065	5141
	3513	5589
25	4043	6119
	4416	6492
	582	
30	rice homolog:	promoter:
	3212	5288
	3411	5487
	3841	5917
	4169	6245
35	4293	6369
	583	
40	rice homolog:	promoter:
	2712	4788
	2713	4789
	2725	4801
	2812	4888
	3031	5107
45	3794	5870
	4274	6350

[illegible]

rice homolog:	promoter:
3746	5822
4672	6748

10	-----	
	rice homolog:	promoter:
	2821	4897
	3275	5351
	3473	5549
15	3877	5953
	4097	6173
	4312	6388
	4362	6438
	4554	6626

599

rice homolog:	promoter:
3055	5131
3213	5289
4166	6242
4167	6243
4562	6638

30 601

rice homolog:	promoter:
3079	5155
3424	5500
4241	6317
4321	6397

602

40 rice homolog: promoter:
 4083 6159

603

45 rice homolog: promoter:
 2775 4851

rice homolog: promoter:

10	2724	4800
	2784	4860
	3052	5128
	3288	5364
	3422	5498
15	3731	5807
	3944	6020
	4007	6083
	4346	6422
	4389	6465

rice homolog: promoter:

	3311	5387
25	3791	5867

rice homolog: promoter:

30	4011	6087
	4522	6598

rice homolog: promoter:

	2795	4871
	3130	5206
	3574	5650
	4315	6391
40	4529	6605

rice homolog: promoter:

45	3162	5238
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Parameter	Value	Unit
Temperature	25	°C
Pressure	1.0	atm
Time	10	min
Concentration	0.1	M
Volume	10	ml
Flow rate	1.0	ml/min
Wavelength	254	nm
Path length	1.0	cm
Refractive index	1.33	
Viscosity	0.01	P
Density	1.0	g/cm ³
Surface tension	72	mN/m
Electrical conductivity	0.1	S/cm
Dielectric constant	2.0	
Thermal conductivity	0.02	W/mK
Heat capacity	1.0	J/gK
Enthalpy of fusion	10	J/g
Enthalpy of vaporization	40	J/g
Entropy of fusion	0.1	J/gK
Entropy of vaporization	0.4	J/gK
Free energy of fusion	10	J/g
Free energy of vaporization	40	J/g
Equilibrium constant	1.0	
Reaction rate constant	1.0	1/s
Activation energy	10	kJ/mol
Pre-exponential factor	1.0	1/s
Equilibrium constant	1.0	
Reaction rate constant	1.0	1/s
Activation energy	10	kJ/mol
Pre-exponential factor	1.0	1/s

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3621 5697

634

5 rice homolog: promoter:
2710 4786
2756 4832
3148 5224
3470 5546
10 3572 5648
4078 6154
4221 6297
4365 6441
4404 6480

15 635

rice homolog: promoter:
3040 5116
20 3258 5334
3339 5415

640

25 rice homolog: promoter:
3568 5644
3790 5866
3821 5897
4511 6587

30 641

rice homolog: promoter:
2719 4795
35 2793 4869
3556 5632
3714 5790
3991 6067

40 642

rice homolog: promoter:
3039 5115
4082 6158
45 4238 6314
4437 6513

[illegible]

2758 4834

2879 4955

3476	5552
------	------

3661	5737
------	------

5772 5810

2867 4943

4017 6093

4242 6318

653

2663 4739

3459	5535
------	------

4582 6658

656

3893 5969

4021 6097

	rice homolog:	promoter:
	4139	6215
5	658	
	rice homolog:	promoter:
	2878	4954
	3437	5513
10	3486	5562
	4002	6078
	4160	6236
	660	
15	rice homolog:	promoter:
	3132	5208
	3292	5368
	4426	6502
20	4632	6708
	4687	6763
	662	
25	rice homolog:	promoter:
	2969	5045
	3535	5611
	4260	6336
	4261	6337
30	4262	6338
	664	
35	rice homolog:	promoter:
	2704	4780
	3766	5842
	4094	6170
	4689	6765
	4732	6808
40	665	
45	rice homolog:	promoter:
	2741	4817
	2827	4903
	3056	5132

	3181	5257
	3448	5524
	3520	5596
	3882	5958
5	4080	6156
	4101	6177
	4171	6247
	4176	6252
	4205	6281
10	4264	6340
	4278	6354
	4507	6583
	4676	6752
	4691	6767
15	4734	6810

672

rice homolog: promoter:

20	3104	5180
	3907	5983
	4141	6217
	4612	6688
	4669	6745

25
675

rice homolog: promoter:

	2717	4793
30	3149	5225
	3622	5698
	3940	6016
	4367	6443

35 676

rice homolog: promoter:

	2963	5039
	3084	5160
40	3112	5188
	3221	5297
	3332	5408
	3507	5583
	3570	5646
45	3699	5775
	4138	6214

4390 6466

677

	rice homolog:	promoter:
5	3439	5515
	3440	5516
	3952	6028
	4072	6148
10	4073	6149

678

	rice homolog:	promoter:
15	2810	4886
	2883	4959
	3195	5271
	3266	5342
	3427	5503

20 680

	rice homolog:	promoter:
25	2797	4873
	3750	5826
	4588	6664

683

	rice homolog:	promoter:
30	2735	4811
	2970	5046
	3760	5836
	3778	5854
35	4560	6636

684

	rice homolog:	promoter:
40	4320	6396

685

	rice homolog:	promoter:
45	3140	5216
	3587	5663

3876	5952
4119	6195
4727	6803

5 686

rice homolog: promoter:

2907	4983
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2917	4993
------	------

10 3540 5616

3892	5968
------	------

3937	6013
------	------

687

15

rice homolog: promoter:

3779	5855
------	------

3902	5978
------	------

4569	6645
------	------

20 4615 6691

4722	6798
------	------

688

25

rice homolog: promoter:

3297	5373
------	------

4095	6171
------	------

4282	6358
------	------

4433	6509
------	------

30 4446 6522

691

rice homolog: promoter:

35 2837 4913

3238	5314
------	------

3364	5440
------	------

3542	5618
------	------

3768	5844
------	------

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692

rice homolog: promoter:

3585	5661
------	------

45 3586 5662

4658	6734
------	------

Parameter	Value	Unit	Parameter	Value	Unit
Initial concentration	1.0	g/L	Initial concentration	1.0	g/L
Initial pH	7.0		Initial pH	7.0	
Temperature	25	°C	Temperature	25	°C
Time	0-24	h	Time	0-24	h
Agitation speed	150	rpm	Agitation speed	150	rpm
Adsorbent dose	0.1-1.0	g/L	Adsorbent dose	0.1-1.0	g/L
Batch adsorption	Yes		Batch adsorption	Yes	
Continuous adsorption	No		Continuous adsorption	No	
Adsorption isotherm	Langmuir		Adsorption isotherm	Langmuir	
Adsorption kinetics	Pseudo-second order		Adsorption kinetics	Pseudo-second order	
Desorption	Yes		Desorption	Yes	
Regeneration	Yes		Regeneration	Yes	
Stability	Yes		Stability	Yes	
Reusability	Yes		Reusability	Yes	
Cost	Low		Cost	Low	
Environmental impact	Low		Environmental impact	Low	
Biodegradability	Yes		Biodegradability	Yes	
Competition	Yes		Competition	Yes	
Regeneration	Yes		Regeneration	Yes	
Stability	Yes		Stability	Yes	
Reusability	Yes		Reusability	Yes	
Cost	Low		Cost	Low	
Environmental impact	Low		Environmental impact	Low	
Biodegradability	Yes		Biodegradability	Yes	
Competition	Yes		Competition	Yes	
Regeneration	Yes		Regeneration	Yes	
Stability	Yes		Stability	Yes	
Reusability	Yes		Reusability	Yes	
Cost	Low		Cost	Low	
Environmental impact	Low		Environmental impact	Low	
Biodegradability	Yes		Biodegradability	Yes	
Competition	Yes		Competition	Yes	
Regeneration	Yes		Regeneration	Yes	
Stability	Yes		Stability	Yes	
Reusability	Yes		Reusability	Yes	
Cost	Low		Cost	Low	
Environmental impact	Low		Environmental impact	Low	
Biodegradability	Yes		Biodegradability	Yes	
Competition	Yes		Competition	Yes	
Regeneration	Yes		Regeneration	Yes	
Stability	Yes		Stability	Yes	
Reusability	Yes		Reusability	Yes	
Cost	Low		Cost	Low	
Environmental impact	Low		Environmental impact	Low	
Biodegradability	Yes		Biodegradability	Yes	
Competition	Yes		Competition	Yes	
Regeneration	Yes		Regeneration	Yes	
Stability	Yes		Stability	Yes	
Reusability	Yes		Reusability	Yes	
Cost	Low		Cost	Low	
Environmental impact	Low		Environmental impact	Low	
Biodegradability	Yes		Biodegradability	Yes	
Competition	Yes		Competition	Yes	
Regeneration	Yes		Regeneration	Yes	
Stability	Yes		Stability	Yes	
Reusability	Yes		Reusability	Yes	
Cost	Low		Cost	Low	
Environmental impact	Low		Environmental impact	Low	
Biodegradability	Yes		Biodegradability	Yes	
Competition	Yes		Competition	Yes	
Regeneration	Yes		Regeneration	Yes	
Stability	Yes		Stability	Yes	
Reusability	Yes		Reusability	Yes	
Cost	Low		Cost	Low	
Environmental impact	Low		Environmental impact	Low	
Biodegradability	Yes		Biodegradability	Yes	
Competition	Yes		Competition	Yes	
Regeneration	Yes		Regeneration	Yes	
Stability	Yes		Stability	Yes	
Reusability	Yes		Reusability	Yes	
Cost	Low		Cost	Low	
Environmental impact	Low		Environmental impact	Low	
Biodegradability	Yes		Biodegradability	Yes	
Competition	Yes		Competition	Yes	
Regeneration	Yes		Regeneration	Yes	
Stability	Yes		Stability	Yes	
Reusability	Yes		Reusability	Yes	
Cost	Low		Cost	Low	
Environmental impact	Low		Environmental impact	Low	
Biodegradability	Yes		Biodegradability	Yes	
Competition	Yes		Competition	Yes	
Regeneration	Yes		Regeneration	Yes	
Stability	Yes		Stability	Yes	
Reusability					

2806	4882
2923	4999
3043	5119
3229	5305
3320	5396

4258 6334

2842	4918
2843	4919
2844	4920
2908	4984
2949	5025
3554	5630
3670	5746
3926	6002
4338	6414

2947	5023
3246	5322
4180	6256
4441	6517
4666	6742
4667	6743

3216	5292
3549	5625
3654	5730
3733	5809

Variable	Mean	Std. Dev.	Minimum	Maximum
Age	34.50	10.50	18	65
Gender	1.50	.50	1	2
Marital Status	1.50	.50	1	2
Education	13.50	2.50	9	18
Income	1.50	.50	1	2
Occupation	1.50	.50	1	2
Religion	1.50	.50	1	2
Political Party	1.50	.50	1	2
Health Status	1.50	.50	1	2
Smoking Status	1.50	.50	1	2
Alcohol Consumption	1.50	.50	1	2
Exercise Frequency	1.50	.50	1	2
Dietary Habits	1.50	.50	1	2
Stress Level	1.50	.50	1	2
Sleep Quality	1.50	.50	1	2
Mental Health	1.50	.50	1	2
Physical Health	1.50	.50	1	2
Life Satisfaction	1.50	.50	1	2
Overall Well-being	1.50	.50	1	2

4013 6089

4686 6762

4706 6782

45 _____

	3757	5833
	3936	6012
	4229	6305
	4230	6306
5	4528	6604

718

	rice homolog:	promoter:
10	3047	5123

719

	rice homolog:	promoter:
15	2817	4893
	2894	4970
	3076	5152
	3314	5390
	3759	5835
20	4092	6168
	4271	6347
	4302	6378
	4303	6379
	4304	6380
25	4305	6381
	4455	6531
	4473	6549

720

	rice homolog:	promoter:
30	2930	5006
	3062	5138
	3172	5248
35	3289	5365
	4384	6460

725

	rice homolog:	promoter:
40	4228	6304

729

	rice homolog:	promoter:
45	2787	4863

Parameter	Value	Unit
Temperature	25.0	°C
Pressure	1.0	atm
Flow rate	1.0	L/min
Concentration	0.1	mol/L
pH	7.0	
Wavelength	254	nm
Scan rate	10	nm/min
Integration time	10	s
Resolution	0.5	nm
Detector	Photodiode array	
Injection volume	10	μL
Column	C18	
Mobile phase	Water/Acetonitrile	
Gradient	0-100% ACN in 10 min	
Flow rate	1.0	mL/min
Temperature	30	°C
Wavelength	254	nm
Scan rate	10	nm/min
Integration time	10	s
Resolution	0.5	nm
Detector	Photodiode array	
Injection volume	10	μL
Column	C18	
Mobile phase	Water/Acetonitrile	
Gradient	0-100% ACN in 10 min	
Flow rate	1.0	mL/min
Temperature	30	°C
Wavelength	254	nm
Scan rate	10	nm/min
Integration time	10	s
Resolution	0.5	nm
Detector	Photodiode array	
Injection volume	10	μL
Column	C18	
Mobile phase	Water/Acetonitrile	
Gradient	0-100% ACN in 10 min	
Flow rate	1.0	mL/min
Temperature	30	°C
Wavelength	254	nm
Scan rate	10	nm/min
Integration time	10	s
Resolution	0.5	nm
Detector	Photodiode array	
Injection volume	10	μL
Column	C18	
Mobile phase	Water/Acetonitrile	
Gradient	0-100% ACN in 10 min	
Flow rate	1.0	mL/min
Temperature	30	°C
Wavelength	254	nm
Scan rate	10	nm/min
Integration time	10	s
Resolution	0.5	nm
Detector	Photodiode array	
Injection volume	10	μL
Column	C18	
Mobile phase	Water/Acetonitrile	
Gradient	0-100% ACN in 10 min	
Flow rate	1.0	mL/min
Temperature	30	°C
Wavelength	254	nm
Scan rate	10	nm/min
Integration time	10	s
Resolution	0.5	nm
Detector	Photodiode array	
Injection volume	10	μL
Column	C18	
Mobile phase	Water/Acetonitrile	
Gradient	0-100% ACN in 10 min	
Flow rate	1.0	mL/min
Temperature	30	°C
Wavelength	254	nm
Scan rate	10	nm/min
Integration time	10	s
Resolution	0.5	nm
Detector	Photodiode array	
Injection volume	10	μL
Column	C18	
Mobile phase	Water/Acetonitrile	
Gradient	0-100% ACN in 10 min	
Flow rate	1.0	mL/min
Temperature	30	°C
Wavelength	254	nm
Scan rate	10	nm/min
Integration time	10	s
Resolution	0.5	nm
Detector	Photodiode array	
Injection volume	10	μL
Column	C18	
Mobile phase	Water/Acetonitrile	
Gradient	0-100% ACN in 10 min	
Flow rate	1.0	mL/min
Temperature	30	°C
Wavelength	254	nm
Scan rate	10	nm/min
Integration time	10	s
Resolution	0.5	nm
Detector	Photodiode array	
Injection volume	10	μL
Column	C18	
Mobile phase	Water/Acetonitrile	
Gradient	0-100% ACN in 10 min	
Flow rate	1.0	mL/min
Temperature	30	°C
Wavelength	254	nm
Scan rate	10	nm/min
Integration time	10	s
Resolution	0.5	nm
Detector	Photodiode array	
Injection volume	10	μL
Column	C18	
Mobile phase	Water/Acetonitrile	
Gradient	0-100% ACN in 10 min	
Flow rate	1.0	mL/min
Temperature	30	°C
Wavelength	254	nm
Scan rate	10	nm/min
Integration time	10	s
Resolution	0.5	nm
Detector	Photodiode array	
Injection volume	10	μL
Column	C18	
Mobile phase	Water/Acetonitrile	
Gradient	0-100% ACN in 10 min	
Flow rate	1.0	mL/min
Temperature	30	°C
Wavelength	254	nm
Scan rate	10	nm/min
Integration time	10	s
Resolution	0.5	nm
Detector	Photodiode array	
Injection volume</		

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10

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- 419 -

	rice homolog:	promoter:
	2826	4902
	2910	4986
5	3017	5093
	3030	5106
	3067	5143
	3080	5156
	3113	5189
10	3178	5254
	3272	5348
	3482	5558
	4585	6661
	4671	6747
15	4711	6787
	763	

	rice homolog:	promoter:
20	2868	4944
	3124	5200
	3679	5755
	4203	6279
	4432	6508
25	4498	6574
	4712	6788
	764	

30	rice homolog:	promoter:
	3301	5377
	3715	5791
	4144	6220
	4196	6272
35	4295	6371
	4396	6472
	4724	6800
	765	
40	-----	
	rice homolog:	promoter:
	3231	5307
	3627	5703
	4268	6344
45	4361	6437
	4661	6737

	767	

5	rice homolog: 3777	promoter: 5853
	768	

10	rice homolog: 3813 3814	promoter: 5889 5890
	770	

15	rice homolog: 2913 3354 3355 3903	promoter: 4989 5430 5431 5979
20	4527	6603
	771	

25	rice homolog: 2906 2911 3131 3458 3874	promoter: 4982 4987 5207 5534 5950
30	772	

	rice homolog: 2856 2973 3083 3197 3217 3502	promoter: 4932 5049 5159 5273 5293 5578
35	4003 4565 4604	6079 6641 6680
	776	
45	-----	
	rice homolog:	promoter:

	2670	4746
	3209	5285
	3780	5856
	4209	6285
5	4485	6561
	782	

	rice homolog:	promoter:
10	3783	5859
	3834	5910
	3854	5930
	4165	6241
	4586	6662
15	788	

	rice homolog:	promoter:
	2677	4753
20	3573	5649
	4192	6268
	4434	6510
	790	
25	-----	
	rice homolog:	promoter:
	3349	5425
	3793	5869
	4263	6339
30	792	

	rice homolog:	promoter:
	2877	4953
35	2901	4977
	3516	5592
	3918	5994
	3947	6023
	4019	6095
40	4279	6355
	4296	6372
	4356	6432
	4643	6719
45	793	

	rice homolog:	promoter:
	2698	4774
	2794	4870
	2811	4887
5	3350	5426
	794	

	rice homolog:	promoter:
10	3919	5995
	3954	6030
	3986	6062
	4448	6524
	4665	6741
15	795	

	rice homolog:	promoter:
	2676	4752
20	3058	5134
	3139	5215
	3690	5766
	3691	5767
	3692	5768
25	3693	5769
	3928	6004
	4214	6290
	797	
30	-----	
	rice homolog:	promoter:
	2700	4776
	2828	4904
	2882	4958
35	3306	5382
	3695	5771
	4135	6211
	798	
40	-----	
	rice homolog:	promoter:
	3358	5434
	3405	5481
	3407	5483
45	3460	5536
	3596	5672

[illegible]

	804	

	rice homolog:	promoter:
15	2692	4768
	3059	5135
	3399	5475
	3721	5797
	3729	5805

30	809

rice homolog:	promoter:
2872	4948
4717	6793

	814	

	rice homolog:	promoter:
	2880	4956
45	2987	5063
	3416	5492

	4055	5131
	4559	6635
	816	
5	-----	
	rice homolog:	promoter:
	2768	4844
	3150	5226
	3846	5922
10	3894	5970
	4057	6133
	820	

15	rice homolog:	promoter:
	3648	5724
	3855	5931
	4257	6333
20	823	

	rice homolog:	promoter:
	3800	5876
25	825	

	rice homolog:	promoter:
	2870	4946
	4096	6172
30	4283	6359
	4284	6360
	4564	6640
	826	
35	-----	
	rice homolog:	promoter:
	2931	5007
	3331	5407
	3429	5505
40	3601	5677
	4103	6179
	4494	6570
	4541	6617
45	827	

	rice homolog:	promoter:
	2814	4890
	3707	5783
	3784	5860
5	3785	5861
	4188	6264
	829	

10	rice homolog:	promoter:
	3786	5862
	830	

15	rice homolog:	promoter:
	2673	4749
	2982	5058
	3390	5466
	4435	6511
20	4649	6725
	4690	6766
	831	

25	rice homolog:	promoter:
	3334	5410
	3543	5619
	3743	5819
	4369	6445
30		
	832	

	rice homolog:	promoter:
	2790	4866
35		
	833	

	rice homolog:	promoter:
	2824	4900
40	2889	4965
	2956	5032
	3360	5436
	3397	5473
	3521	5597
45	3647	5723
	3698	5774

	4357	6433
	4423	6499
	4637	6713
5	836	

	rice homolog:	promoter:
	3243	5319
	3262	5338
10	3263	5339
	3404	5480
	4131	6207
	4322	6398
	4348	6424
15	4592	6668
	838	

	rice homolog:	promoter:
20	3045	5121
	3154	5230
	3357	5433
	840	
25	-----	
	rice homolog:	promoter:
	2800	4876
	3843	5919
	3933	6009
30	3978	6054
	3998	6074
	841	

35	rice homolog:	promoter:
	3089	5165
	3279	5355
	3335	5411
	4641	6717
40	848	

	rice homolog:	promoter:
	2749	4825
45	2912	4988
	3254	5330

3976	6052
4708	6784

852

5

rice homolog: promoter:

2680	4756
------	------

2859	4935
------	------

2860	4936
------	------

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3118	5194
------	------

3313	5389
------	------

4047	6123
------	------

4379	6455
------	------

4532	6608
------	------

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856

rice homolog: promoter:

3366	5442
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4481	6557
------	------

857

rice homolog: promoter:

25

3501	5577
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3609	5685
------	------

3931	6007
------	------

4336	6412
------	------

4702	6778
------	------

30

859

rice homolog: promoter:

35

3412	5488
------	------

3694	5770
------	------

4156	6232
------	------

4499	6575
------	------

4568	6644
------	------

40

861

rice homolog: promoter:

45

2665	4741
------	------

3120	5196
------	------

3121	5197
------	------

4109	6185
------	------

	4140	6216
	4163	6239
	4574	6650
5	863	

	rice homolog:	promoter:
	2729	4805
	2925	5001
10	3576	5652
	4148	6224
	4195	6271
	867	
15	-----	
	rice homolog:	promoter:
	2726	4802
	4310	6386
	4332	6408
20	4442	6518
	4452	6528
	4599	6675
	868	
25	-----	
	rice homolog:	promoter:
	2681	4757
	2895	4971
	2980	5056
30	4193	6269
	4477	6553
	4478	6554
	4696	6772
35	871	

	rice homolog:	promoter:
	3308	5384
	3309	5385
40	3310	5386
	4567	6643
	4576	6652
	876	
45	-----	
	rice homolog:	promoter:

[illegible]

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	2816	4892
	3185	5261
	3662	5738
	4393	6469
5	914	

	rice homolog:	promoter:
	2728	4804
10	3177	5253
	3483	5559
	3809	5885
	4339	6415
15	918	

	rice homolog:	promoter:
	2968	5044
	3577	5653
20	3787	5863
	4297	6373
	4445	6521
	919	
25		

	rice homolog:	promoter:
	2985	5061
	3356	5432
	3881	5957
30	4090	6166
	4652	6728
	921	

35	rice homolog:	promoter:
	2887	4963
	926	

40	rice homolog:	promoter:
	2946	5022
	3128	5204
	3649	5725
	3858	5934
45	928	

<hr/>		
	rice homolog:	promoter:
	4121	6197
	4392	6468
5	4552	6629
	929	
<hr/>		
	rice homolog:	promoter:
10	2743	4819
	2745	4821
	3666	5742
	4276	6352
	4343	6419
15	4630	6706
	930	
<hr/>		
	rice homolog:	promoter:
20	4249	6325
	932	
<hr/>		
	rice homolog:	promoter:
25	2965	5041
	3014	5090
	3840	5916
	4041	6117
	4137	6213
30	4506	6582
	934	
<hr/>		
	rice homolog:	promoter:
35	3616	5692
	3816	5892
	4105	6181
	4111	6187
	4172	6248
40	943	
<hr/>		
	rice homolog:	promoter:
	2881	4957
45	2998	5074
	3203	5279

	3818	5894
	3981	6057
	944	
5	-----	
	rice homolog:	promoter:
	2997	5073
	3046	5122
10	950	

	rice homolog:	promoter:
	3519	5595
	3980	6056
15	4250	6326
	4471	6547
	4535	6611
	952	
20	-----	
	rice homolog:	promoter:
	2714	4790
	2774	4850
	3287	5363
25	3716	5792
	4122	6198
	4123	6199
	4531	6607
	4536	6612
30	4573	6649
	4634	6710
	953	

35	rice homolog:	promoter:
	2683	4759
	3531	5607
	3668	5744
	3826	5902
40	4150	6226

Table 24

Correlation of Arabidopsis promoter regions to the
Open Reading Frames listed in SEQ ID NOs: 1-953

SEQ ID NOs corresponding to Arabidopsis promoters	SEQ ID NOs corresponding to Arabidopsis ORFs
2137	97
2138	780
2139	238
2140	454
2141	89
2142	86
2143	732
2144	801
2145	792
2146	195
2147	394
2148	138
2149	176
2150	200
2151	899
2152	83
2153	423
2154	367
2155	595
2156	231
2157	601
2158	79
2159	868
2160	770
2161	670
2162	247
2163	120
2164	251
2165	639
2166	380
2167	194
2168	812
2169	318
2170	398
2171	252
2172	879
2173	114
2174	452

2175	25
2176	608
2177	212
2178	66
2179	949
2180	816
2181	411
2182	301
2183	35
2184	291
2185	457
2186	22
2187	756
2188	916
2189	627
2190	740
2191	417
2192	81
2193	533
2194	539
2195	208
2196	710
2197	767
2198	822
2199	201
2200	355
2201	528
2202	877
2203	237
2204	763
2205	230
2206	565
2207	809
2208	870
2209	397
2210	700
2211	336
2212	797
2213	695
2214	219
2215	742
2216	223
2217	324
2218	721
2219	244
2220	16

2221	914
2222	100
2223	834
2224	482
2225	108
2226	61
2227	266
2228	416
2229	607
2230	782
2231	736
2232	857
2233	522
2234	866
2235	236
2236	206
2237	93
2238	424
2239	184
2240	421
2241	460
2242	46
2243	234
2244	869
2245	633
2246	891
2247	347
2248	498
2249	501
2250	207
2251	506
2252	656
2253	889
2254	811
2255	775
2256	131
2257	790
2258	930
2259	726
2260	300
2261	342
2262	40
2263	358
2264	462
2265	222
2266	220

2267	858
2268	508
2269	151
2270	378
2271	217
2272	724
2273	210
2274	776
2275	216
2276	765
2277	453
2278	221
2279	415
2280	307
2281	516
2282	747
2283	283
2284	943
2285	99
2286	272
2287	164
2288	132
2289	287
2290	863
2291	341
2292	444
2293	267
2294	523
2295	271
2296	288
2297	799
2298	814
2299	142
2300	933
2301	9
2302	788
2303	353
2304	719
2305	548
2306	190
2307	432
2308	281
2309	41
2310	88
2311	24
2312	387

2405	829
2406	828
2407	900
2408	175
2409	328
2410	304
2411	909
2412	687
2413	327
2414	122
2415	346
2416	302
2417	303
2418	689
2419	440
2420	841
2421	381
2422	135
2423	162
2424	718
2425	75
2426	550
2427	60
2428	17
2429	174
2430	256
2431	708
2432	650
2433	502
2434	654
2435	569
2436	414
2437	495
2438	351
2439	115
2440	771
2441	640
2442	652
2443	431
2444	119
2445	852
2446	772
2447	871
2448	921
2449	549
2450	26

2497	764
2498	541
2499	832
2500	924
2501	856
2502	140
2503	14
2504	21
2505	847
2506	577
2507	294
2508	435
2509	255
2510	572
2511	733
2512	373
2513	554
2514	280
2515	384
2516	702
2517	177
2518	189
2519	935
2520	15
2521	952
2522	784
2523	382
2524	659
2525	762
2526	345
2527	42
2528	735
2529	23
2530	6
2531	865
2532	72
2533	366
2534	947
2535	729
2536	286
2537	893
2538	129
2539	330
2540	512
2541	709
2542	389

2635	496
2636	229
2637	228
2638	902
2639	92
2640	203
2641	443
2642	7
2643	348
2644	296
2645	730
2646	359
2647	3
2648	226
2649	243
2650	791
2651	647
2652	655
2653	614
2654	375
2655	130
2656	10
2657	826
2658	485
2659	850
2660	940
2661	102

Table 25
Ortholog Table

12	
5	-----
	AAD17487.1 AF049347 Berberis stolonifera
	DESCRIPTION: Catalyzes the oxidative cyclization of the N-methyl group of (S)-reticuline into the berberine bridge carbon (C-8) of (S)-scoulerine. berberine bridge enzyme. bbel. Covalently flavinylated oxidase of isoquinoline alkaloid biosynthesis in plants.
10	
	AAB20352.1 S65550 Eschscholzia californica
15	DESCRIPTION: (S)-reticuline:oxygen oxidoreductase (methylene-bridge-forming). /gene="(S)-reticuline:oxygen oxidoreductase. This sequence comes from Fig 2; berberine bridge enzyme.
20	AAC39358.1 AF005655 Eschscholzia californica
	DESCRIPTION: oxidizes the N-methyl group of (S)-reticuline to the berberine bridge carbon C-8 of (S)-scoulerine in berberine and benzophenanthridine alkaloid biosynthesis. berberine bridge enzyme. bbel. covalently-bound FAD-dependent oxidase; elicitor-inducible.
25	
	AAC61839.1 AF025430 Papaver somniferum
	DESCRIPTION: berberine bridge enzyme. bbel. (S)-reticuline:oxygen oxidoreductase (methylene bridge forming).
30	
19	-----
	AAC83458.1 AF023140 Thlaspi goesingense
35	DESCRIPTION: imidazoleglycerol phosphate dehydratase. THB1.
	AAB67738.1 U49978 Pisum sativum
	DESCRIPTION: imidazoleglycerol-phosphate dehydratase. PSHIS3.
40	
	AAA93197.1 U02690 Triticum aestivum
	DESCRIPTION: imidazoleglycerolphosphate dehydratase. partial interval represents the confirmed coding region based on homology to sequence U02689, maybe a chimeric molecule.
45	

BAB16915.1 AP002863 Oryza sativa
DESCRIPTION: 1-deoxy-d-xylulose-5-phosphate reductoisomerase.
5 P0005A05.19. contains ESTs AU108198(S11168),D46469(S11168).

37

AAD21872.1 AF078082 Phaseolus vulgaris
10 DESCRIPTION: receptor-like protein kinase homolog RK20-1.

CAA73134.1 Y12531 Brassica oleracea
15 DESCRIPTION: serine/threonine kinase. BRLK.

AAB93834.1 U82481 Zea mays
DESCRIPTION: KI domain interacting kinase 1. KIK1. receptor-like protein
20 kinase; serine/threonine protein kinase.

CAA67145.1 X98520 Brassica oleracea
DESCRIPTION: receptor-like kinase. SFR2.

25 AAC23542.1 U20948 Ipomoea trifida
DESCRIPTION: receptor protein kinase. IRK1.

30 CAA73133.1 Y12530 Brassica oleracea
DESCRIPTION: serine /threonine kinase. ARLK.

CAB41878.1 Y18259 Brassica oleracea
35 DESCRIPTION: SRK5 protein. SRK5. receptor-like kinase.

CAB41879.1 Y18260 Brassica oleracea
DESCRIPTION: SRK15 protein. SRK15. receptor-like kinase.

40

CAA74661.1 Y14285 Brassica oleracea
DESCRIPTION: SFR1. extracellular S domain: 8-1342; transmembrane domain:
1343-1411; intracellular kinase domain: 1412-2554.

45

- CAA74662.1 Y14286 Brassica oleracea
DESCRIPTION: SFR3. extracellular S domain: 123-1346; transmembrane domain: 1347-1412; intracellular kinase domain: from 1413.
- 5
AAA33000.1 M76647 Brassica oleracea
DESCRIPTION: receptor protein kinase. SKR6.
- 10
BAA23676.1 AB000970 Brassica rapa
DESCRIPTION: receptor kinase 1. BcRK1.
- 15
AAA33008.1 M97667 Brassica napus
DESCRIPTION: serine/threonine kinase receptor.
- 20
AAA62232.1 U00443 Brassica napus
DESCRIPTION: S-receptor kinase. protein contains an immunoglobulin-like domain.
- 25
CAB89179.1 AJ245479 Brassica napus subsp. napus
DESCRIPTION: ser /thr kinase. S-locus receptor kinase. srk.
- 30
BAA92836.1 AB032473 Brassica oleracea
DESCRIPTION: S18 S-locus receptor kinase. SRK18.
- CAA79355.1 Z18921 Brassica oleracea
DESCRIPTION: S-receptor kinase-like protein.
- 35
BAA92837.1 AB032474 Brassica oleracea
DESCRIPTION: S60 S-locus receptor kinase. SRK60.
- 40
BAA07577.2 D38564 Brassica rapa
DESCRIPTION: receptor protein kinase SRK12.
- 45
BAA07576.1 D38563 Brassica rapa
DESCRIPTION: receptor protein kinase SRK8.

- BAB21001.1 AB054061 Brassica rapa
DESCRIPTION: S locus receptor kinase. SRK22.
- 5 BAA06285.1 D30049 Brassica rapa
DESCRIPTION: S-receptor kinase SRK9.
- 10 BAA21132.1 D88193 Brassica rapa
DESCRIPTION: S-receptor kinase. SRK9 (B.c).
- 15 AAD52097.1 AF088885 Nicotiana tabacum
DESCRIPTION: receptor-like kinase CHRK1. Chrk1.
- BAB18292.1 AP002860 Oryza sativa
DESCRIPTION: putative receptor-like protein kinase. P0409B08.19.
- 20 BAB16871.1 AP002537 Oryza sativa
DESCRIPTION: putative protein kinase APK1A Arabidopsis thaliana.
P0001B06.24. contains ESTs C22608(R3192),D25110(R3192).
- 25 BAB39873.1 AP002882 Oryza sativa
DESCRIPTION: putative protein kinase. P0439B06.8. contains ESTs
AU056701(S20808),AU056702(S20808).
- 30 BAA87853.1 AP000816 Oryza sativa
DESCRIPTION: EST AU030604(E51294) corresponds to a region of the
predicted gene. Similar to putative NAK-like Ser/Thr protein kinase.
(AF001308).
- 35 CAA79324.1 Z18884 Brassica oleracea
DESCRIPTION: S-receptor kinase related protein.
- 40 AAK21965.1 AY028699 Brassica napus
DESCRIPTION: receptor protein kinase PERK1.
- 45 AAK00425.1 AC069324 Oryza sativa
DESCRIPTION: Putative protein kinase. OSJNBa0071K19.11.

5 AAF66615.1 AF142596 *Nicotiana tabacum*
 DESCRIPTION: LRR receptor-like protein kinase.

10 BAB21240.1 AP002953 *Oryza sativa*
 DESCRIPTION: Putative protein kinase. P0426D06.20. contains ESTs
 C22359(C11461),C22360(C11461).

15 BAB39409.1 AP002901 *Oryza sativa*
 DESCRIPTION: putative protein kinase. P0456F08.9. contains EST
 C23560(R0290).

20 AAG59657.1 AC084319 *Oryza sativa*
 DESCRIPTION: putative protein kinase. OSJNBa0004B24.20.

25 AAG03090.1 AC073405 *Oryza sativa*
 DESCRIPTION: Similar to an Arabidopsis somatic embryogenesis
 receptor-like kinase (AC007504).

30 AAG16628.1 AY007545 *Brassica napus*
 DESCRIPTION: protein serine/threonine kinase BNK1.

38 BAA94509.1 AB041503 *Populus nigra*
 DESCRIPTION: protein kinase 1. PnPK1.

35 CAA58750.1 X83869 *Daucus carota*
 DESCRIPTION: CDPK-related protein kinase. CRK (or PK421).

40 BAA12692.1 D84508 *Zea mays*
 DESCRIPTION: CDPK-related protein kinase. Does not require calcium for
 its activity.

45 AAG01179.1 AF289237 *Zea mays*
 DESCRIPTION: calcium/calmodulin dependent protein kinase MCK2. MCK2.

- 5 AAB47181.1 S82324 Zea mays
DESCRIPTION: /gene="calcium/calmodulin-dependent
protein kinase. This sequence comes from Fig. 1.
- 10 BAA12691.1 D84507 Zea mays
DESCRIPTION: CDPK-related protein kinase. Does not require calcium for
its activity (by similarity).
- 15 BAA22410.1 D38452 Zea mays
DESCRIPTION: calcium-dependent protein kinase-related kinase.
- 20 AAC24961.1 AF009337 Tradescantia virginiana
DESCRIPTION: CDPK-related protein kinase. CRK1.
- 25 AAF23901.2 AF194414 Oryza sativa
DESCRIPTION: calcium-dependent protein kinase. CDPK5. OsCDPK5.
- AAF23900.1 AF194413 Oryza sativa
DESCRIPTION: calcium-dependent protein kinase. CDPK1. OsCDPK1.
- 30 AAC78558.1 AF030879 Solanum tuberosum
DESCRIPTION: protein kinase CPK1.
- CAA57157.1 X81394 Oryza sativa
DESCRIPTION: calcium-dependent protein kinase. OSCPK2.
- 35 BAB21081.1 AP002819 Oryza sativa
DESCRIPTION: putative calcium-dependent protein kinase. P0501G01.10.
- 40 AAC25423.1 AF072908 Nicotiana tabacum
DESCRIPTION: calcium-dependent protein kinase. CDPK1.
- 45 BAA12715.1 D85039 Zea mays
DESCRIPTION: calcium-dependent protein kinase.

- 5 AAB49984.1 U90262 Cucurbita pepo
DESCRIPTION: calcium-dependent calmodulin-independent protein kinase
CDPK. cpCPK1. serine/threonine protein kinase that is activated by direct
binding of calcium.
- 10 AAA69507.1 U28376 Zea mays
DESCRIPTION: calcium-dependent protein kinase. MZECDPK2.
- 15 AAD17800.1 AF090835 Mesembryanthemum crystallinum
DESCRIPTION: Ca²⁺-dependent protein kinase. CPK1. serine/threonine
protein kinase.
- 20 AAB80693.1 U69174 Glycine max
DESCRIPTION: calmodulin-like domain protein kinase isoenzyme gamma.
CDPK
gamma.
- 25 BAA81751.1 AB017517 Marchantia polymorpha
DESCRIPTION: calcium-dependent protein kinase. CDPK1. CDPK-B;
alternative
splicing.
- 30 BAA81749.1 AB017515 Marchantia polymorpha
DESCRIPTION: calcium-dependent protein kinase. CDPK1. CDPK-B;
alternative
splicing.
- 35 CAA39936.1 X56599 Daucus carota
DESCRIPTION: calcium- dependent protein kinase. DcPK431.
- 40 BAA81748.1 AB017515 Marchantia polymorpha
DESCRIPTION: calcium-dependent protein kinase. CDPK1. CDPK-A;
alternative
splicing.
- 45 BAA81750.1 AB017516 Marchantia polymorpha

DESCRIPTION: calcium dependent protein kinase. CDPK.

- 5 BAA85396.1 AP000615 *Oryza sativa*
DESCRIPTION: ESTs C22369(C12239),C22370(C12239),
AU057852(S21844),AU057853(S21844) correspond to a region of the predicted
gene.; similar to calcium dependent protein kinase. (AF048691).
- 10 CAA57156.1 X81393 *Oryza sativa*
DESCRIPTION: calcium-dependent protein kinase. OSCPKII.
- 15 AAC05270.1 AF048691 *Oryza sativa*
DESCRIPTION: calcium dependent protein kinase. CDPK12.
- 20 AAF21062.1 AF216527 *Dunaliella tertiolecta*
DESCRIPTION: calcium-dependent protein kinase. CPK1; CDPK.
- 25 AAB80692.1 U69173 *Glycine max*
DESCRIPTION: calmodulin-like domain protein kinase isoenzyme beta. CDPK
beta.
- 30 AAK26164.1 AY027885 *Cucumis sativus*
DESCRIPTION: calcium-dependent calmodulin-independent protein kinase 5.
CDPK5. CsCDPK5.
- 35 AAA33443.1 L15390 *Zea mays*
DESCRIPTION: calcium-dependent protein kinase. CDPK.
- 40 CAA89202.1 Z49233 *Chlamydomonas eugametos*
DESCRIPTION: calcium-stimulated protein kinase.
- 45 AAG46110.1 AC073166 *Oryza sativa*
DESCRIPTION: calcium-dependent protein kinase. OSJNBb0064P21.2.
- BAA02698.1 D13436 *Oryza sativa*
DESCRIPTION: calcium-dependent protein kinase. spk.

- BAA90814.1 AP001168 *Oryza sativa*
 DESCRIPTION: ESTs AU030197(E50746),AU030196(E50746) correspond to
 a
 5 region of the predicted gene.; Similar to calcium-dependent
 calmodulin-independent protein kinase CDPK (U90262).
- CAB46228.1 Y18055 *Arachis hypogaea*
 10 DESCRIPTION: calcium dependent protein kinase. CDPK.
- AAC49008.1 U24188 *Lilium longiflorum*
 DESCRIPTION: calcium/calmodulin-dependent phosphorylation activity.
 15 calcium/calmodulin-dependent protein kinase. CCaMK. serine/threonine
 kinase; binds to calcium and calmodulin.
- AAF19401.1 AF203479 *Glycine max*
 20 DESCRIPTION: phosphoenolpyruvate carboxylase kinase. protein kinase;
 member of Ca²⁺/CaM kinase family; lacks the autoinhibitory region and EF
 hands.
- AAF06970.1 AF162662 *Kalanchoe fedtschenkoi*
 25 DESCRIPTION: phosphoenolpyruvate carboxylase kinase. calcium-independent
 protein kinase.
- 39
 30 -----
- AAG00510.1 AF285172 *Phaseolus vulgaris*
 DESCRIPTION: leaf senescence-associated receptor-like protein kinase.
 SARK.
- 35
 BAB21175.1 AP002909 *Oryza sativa*
 DESCRIPTION: putative serine/threonine-specific receptor protein kinase.
 P0044F08.3.
- 40
 CAB51480.1 Y14600 *Sorghum bicolor*
 DESCRIPTION: putative protein serine /threonine kinase. RLK1. accumulates
 in mesophyll cells.
- 45
 AAF59905.1 AF197946 *Glycine max*

DESCRIPTION: receptor protein kinase-like protein. CLV1A.

- 5 AAF59906.1 AF197947 Glycine max
DESCRIPTION: receptor protein kinase-like protein. CLV1B.
- 10 AAB61708.1 U93048 Daucus carota
DESCRIPTION: somatic embryogenesis receptor-like kinase. SERK.
- 15 BAB39873.1 AP002882 Oryza sativa
DESCRIPTION: putative protein kinase. P0439B06.8. contains ESTs
AU056701(S20808),AU056702(S20808).
- 20 AAC36318.1 AF053127 Malus x domestica
DESCRIPTION: leucine-rich receptor-like protein kinase. LRPKml.
- 25 AAK21965.1 AY028699 Brassica napus
DESCRIPTION: receptor protein kinase PERK1.
- 30 AAF91324.1 AF244890 Glycine max
DESCRIPTION: receptor-like protein kinase 3. RLK3. GmRLK3.
- 35 AAK00425.1 AC069324 Oryza sativa
DESCRIPTION: Putative protein kinase. OSJNBa0071K19.11.
- 40 AAF91323.1 AF244889 Glycine max
DESCRIPTION: receptor-like protein kinase 2. RLK2. GmRLK2.
- 45 AAG59657.1 AC084319 Oryza sativa
DESCRIPTION: putative protein kinase. OSJNBa0004B24.20.
- CAA97692.1 Z73295 Catharanthus roseus
DESCRIPTION: receptor-like protein kinase. CRPK1. Autophosphorylation
predominantly on Thr, less on Ser. Mechanism: autophosphorylation in cis.
- BAB40094.1 AP003210 Oryza sativa

DESCRIPTION: putative receptor protein kinase. OSJNBa0010K01.7.

CAA61510.1 X89226 *Oryza sativa*

5 DESCRIPTION: leucine-rich repeat/receptor protein kinase. lrk2.

BAA87852.1 AP000816 *Oryza sativa*

10 DESCRIPTION: Similar to putative Ser/Thr protein kinase. (AC004218).

BAA92221.1 AP001278 *Oryza sativa*

15 DESCRIPTION: Similar to Arabidopsis thaliana chromosome II BAC F12L6 genomic sequence, putative protein kinase. (AC004218).

AAF91322.1 AF244888 *Glycine max*

20 DESCRIPTION: receptor-like protein kinase 1. RLK1. GmRLK1.

AAK11569.1 AF318493 *Lycopersicon hirsutum*

DESCRIPTION: Pto-like protein kinase D. LhirPtoD.

25 CAB51834.1 00069 *Oryza sativa*

DESCRIPTION: 11332.5. contains eukaryotic protein kinase domain PF.

BAA90808.1 AP001168 *Oryza sativa*

30 DESCRIPTION: Similar to putative receptor-like protein kinase (AL035679).

AAC48932.1 U13923 *Lycopersicon pimpinellifolium*

35 DESCRIPTION: Fen. putative serine/threonine protein kinase; similar to product encoded by *Lycopersicon pimpinellifolium* Pto gene, GenBank Accession Number U02271; Fen is a member of the Pto gene family.

AAF76307.1 AF220602 *Lycopersicon pimpinellifolium*

40 DESCRIPTION: Fen kinase.

AAB47424.1 U59317 *Lycopersicon pimpinellifolium*

45 DESCRIPTION: serine/threonine protein kinase Fen. Fen. fenthion sensitivity gene from tomato.

- 5 AAK11566.1 AF318490 *Lycopersicon hirsutum*
DESCRIPTION: Pto-like protein kinase E. LhirPtoE. confers resistance to bacterial speck disease.
- 10 AAB47423.1 U59315 *Lycopersicon pimpinellifolium*
DESCRIPTION: serine/threonine protein kinase Pto. Pto. bacterial speck disease resistance in tomato; disease resistance gene.
- 15 AAC48914.1 U02271 *Lycopersicon pimpinellifolium*
DESCRIPTION: protein kinase.
- 20 AAF76306.1 AF220602 *Lycopersicon pimpinellifolium*
DESCRIPTION: Pto kinase.
- 25 BAA87853.1 AP000816 *Oryza sativa*
DESCRIPTION: EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative NAK-like Ser/Thr protein kinase. (AF001308).
- 30 AAF76313.1 AF220603 *Lycopersicon esculentum*
DESCRIPTION: Pto kinase. LescPth5.
- 35 AAB47421.1 U59316 *Lycopersicon esculentum*
DESCRIPTION: serine/threonine protein kinase Pto. pto. allele of Pto bacterial speck disease resistance gene in tomato.
- 40 AAG03090.1 AC073405 *Oryza sativa*
DESCRIPTION: Similar to an Arabidopsis somatic embryogenesis receptor-like kinase (AC007504).
- 45 AAA33915.1 L27821 *Oryza sativa*
DESCRIPTION: receptor type serine/threonine kinase. protein kinase.
- AAF76314.1 AF220603 *Lycopersicon esculentum*
DESCRIPTION: Fen kinase. Lescfen.

AAK11568.1 AF318492 *Lycopersicon hirsutum*
DESCRIPTION: Pto-like protein kinase B. LhirPtoB.

5

AAB47422.1 U59318 *Lycopersicon esculentum*
DESCRIPTION: serine/threonine protein kinase Fen. fen. allele of Fen,
fenthion sensitivity gene from tomato.

10

BAB16871.1 AP002537 *Oryza sativa*
DESCRIPTION: putative protein kinase APK1A *Arabidopsis thaliana*.
P0001B06.24. contains ESTs C22608(R3192),D25110(R3192).

15

BAA06538.1 D31737 *Nicotiana tabacum*
DESCRIPTION: protein-serine/threonine kinase.

20

AAK11567.1 AF318491 *Lycopersicon hirsutum*
DESCRIPTION: Pto-like protein kinase F. LhirPtoF.

25

AAF34426.1 AF172282 *Oryza sativa*
DESCRIPTION: leucine rich repeat containing protein kinase. DUPR11.16.

30

AAG25966.1 AF302082 *Nicotiana tabacum*
DESCRIPTION: cytokinin-regulated kinase 1. CRK1. protein kinase;
transcript abundance decreases rapidly after cytokinin treatment.

35

BAB21240.1 AP002953 *Oryza sativa*
DESCRIPTION: Putative protein kinase. P0426D06.20. contains ESTs
C22359(C11461),C22360(C11461).

41

40

AAG12987.1 AF166498 *Lycopersicon esculentum*
DESCRIPTION: sucrose transporter-like protein. SUT2. sucrose sensor.

45

AAF08330.1 AF021809 *Vitis vinifera*
DESCRIPTION: putative sucrose transporter. VvSUC12.

- BAA24071.1 D87819 *Oryza sativa*
DESCRIPTION: sucrose transporter. OsSUT1.
- 5 AAF90181.1 AF280050 *Oryza sativa* subsp. indica
DESCRIPTION: sucrose proton symporter. sucrose transporter. SUT1.
- 10 BAA83501.1 AB008464 *Zea mays*
DESCRIPTION: Sucrose Transporter. ZmSUT1.
- 15 CAB75882.1 AJ272309 *Hordeum vulgare*
DESCRIPTION: Transport sucrose through membrane. sucrose transporter 1. sut1.
- 20 AAD55269.1 AF182445 *Vitis vinifera*
DESCRIPTION: sucrose transporter.
- 25 CAA83436.1 Z31561 *Ricinus communis*
DESCRIPTION: sucrose transport. sucrose carrier. Scr1.
- CAA76368.1 Y16767 *Daucus carota*
DESCRIPTION: sucrose/H⁺ symporter. SUT1b.
- 30 CAA76367.1 Y16766 *Daucus carota*
DESCRIPTION: sucrose/H⁺ symporter. SUT1a.
- 35 CAC19688.1 AJ303198 *Daucus carota*
DESCRIPTION: essential for sucrose transport. sucrose/proton symporter. sut1a.
- 40 AAG25923.1 AF237780 *Solanum tuberosum*
DESCRIPTION: sucrose transporter SUT4.
- 45 AAF08329.1 AF021808 *Vitis vinifera*
DESCRIPTION: putative sucrose transporter. VvSUC11.

- AAG09270.1 AF176950 *Lycopersicon esculentum*
DESCRIPTION: sucrose transporter. SUT4.
- 5 AAF65765.1 AF242307 *Euphorbia esula*
DESCRIPTION: sucrose transport protein.
- 10 AAF04295.1 AF191025 *Alonsoa meridionalis*
DESCRIPTION: sucrose transporter 1. SUT1.
- 15 CAA57727.1 X82276 *Nicotiana tabacum*
DESCRIPTION: sucrose transporter. NtSUT1a. Var. SNN bp 1-1346, Var. SR1
bp 1172-1614.
- 20 BAA89458.1 AB036758 *Daucus carota*
DESCRIPTION: sucrose transporter protein. cSUT.
- 25 CAB75881.1 AJ272308 *Hordeum vulgare*
DESCRIPTION: transport sucrose through membrane. sucrose transporter 2.
sut2.
- 30 CAA76369.1 Y16768 *Daucus carota*
DESCRIPTION: sucrose/H⁺ symporter. SUT2.
- 35 CAC19689.1 AJ303199 *Daucus carota*
DESCRIPTION: essential for sucrose transport. sucrose/proton symporter.
sut2.
- 40 CAB07811.1 Z93774 *Vicia faba*
DESCRIPTION: sugar transport. sucrose transport protein. sut.
- 45 CAA47604.1 X67125 *Spinacia oleracea*
DESCRIPTION: sucrose permease. S21.
- CAA48915.1 X69165 *Solanum tuberosum*
DESCRIPTION: sucrose transport protein. SUT1.

- AAD41024.1 AF109922 *Pisum sativum*
DESCRIPTION: sucrose transport protein SUT1.
- 5 AAD53000.1 U64967 *Beta vulgaris*
DESCRIPTION: sucrose-proton symporter. Bv8-6.
- 10 AAF08331.1 AF021810 *Vitis vinifera*
DESCRIPTION: putative sucrose transporter. VvSUC27.
- 15 CAA58730.1 X83850 *Beta vulgaris*
DESCRIPTION: sucrose/proton-symporter. sut1.
- 20 AAC99332.1 AF063400 *Apium graveolens*
DESCRIPTION: sucrose transporter. SUT1.
- AAD45391.1 AF167416 *Apium graveolens*
DESCRIPTION: sucrose transporter SUT2B. SUT2B.
- 25 AAD45390.1 AF167415 *Apium graveolens*
DESCRIPTION: sucrose transporter SUT2A. SUT2A.
- 30 AAF04294.1 AF191024 *Asarina barclaiana*
DESCRIPTION: sucrose transporter 1. SUT1.
- 35 CAA59113.1 X84379 *Plantago major*
DESCRIPTION: SUC1-sucrose proton symporter. SUC1.
- AAD34610.1 AF149981 *Nicotiana tabacum*
DESCRIPTION: sucrose transporter-like protein. SUT3.
- 40 CAA57726.1 X82275 *Lycopersicon esculentum*
DESCRIPTION: sucrose transporter. LeSUT1.
- 45 CAA12256.1 AJ224961 *Ricinus communis*

DESCRIPTION: Sucrose transport. Sucrose carrier. SUT1.

5 CAC33492.1 AJ310643 Ricinus communis
DESCRIPTION: sucrose carrier. sucrose carrier. scr1.

10 AAD45932.1 AF168771 Betula pendula
DESCRIPTION: sucrose transport protein. SUC1.

CAA53390.1 X75764 Plantago major
DESCRIPTION: sucrose transporter. ptp1.

15 AAF22281.1 AF167417 Apium graveolens
DESCRIPTION: putative sucrose transporter SUT1. SUT1.

20 BAA76434.1 AB025006 Cicer arietinum
DESCRIPTION: sucrose transport protein.

42

25 AAC64184.1 AF095577 Prunus persica
DESCRIPTION: endopolygalacturonase.

30 CAA54150.1 X76735 Prunus persica
DESCRIPTION: endopolygalacturonase.

35 AAC28906.1 AF001003 Lycopersicon esculentum
DESCRIPTION: hydrolyzes pectin in the cell wall and middle lamella of
plant cells. polygalacturonase 5. TAPG5. expressed in abscission.

40 AAC28947.1 AF029230 Lycopersicon esculentum
DESCRIPTION: polygalacturonase. TPG6.

45 AAC70951.1 AF072732 Lycopersicon esculentum
DESCRIPTION: hydrolyzes pectin in the cell wall and middle lamella.
polygalacturonase 7. specifically and abundantly expressed in pistils.

- AAC28905.1 AF001002 *Lycopersicon esculentum*
DESCRIPTION: hydrolyzes pectin in the cell wall and middle lamella of plant cells. polygalacturonase 4. TAPG4. expressed in abscission.
- 5
AAA80489.1 U23053 *Lycopersicon esculentum*
DESCRIPTION: polygalacturonase precursor.
- 10 AAC28903.1 AF001000 *Lycopersicon esculentum*
DESCRIPTION: hydrolyzes pectin in the cell wall and middle lamella of plant cells. polygalacturonase 1. TAPG1. expressed in abscission.
- 15 AAB09575.1 U70480 *Lycopersicon esculentum*
DESCRIPTION: abscission polygalacturonase. TAPG2.
- AAC28904.1 AF001001 *Lycopersicon esculentum*
20 DESCRIPTION: hydrolyzes pectin in the cell wall and middle lamella of plant cells. polygalacturonase 2. TAPG2. expressed in abscission.
- AAB09576.1 U70481 *Lycopersicon esculentum*
25 DESCRIPTION: abscission polygalacturonase. TAPG4.
- AAC28902.2 AF000999 *Lycopersicon esculentum*
DESCRIPTION: hydrolyzes pectin in the cell wall and middle lamella of plant cells. polygalacturonase 3. TAPG3. expressed in abscission.
30
- AAC26510.1 AF062465 *Cucumis melo*
DESCRIPTION: polygalacturonase precursor. MPG1.
35
- AAC26511.1 AF062466 *Cucumis melo*
DESCRIPTION: polygalacturonase precursor. MPG2.
- 40 BAB21092.1 AP002819 *Oryza sativa*
DESCRIPTION: putative endopolygalacturonase. P0501G01.21.
- 45 AAA62286.1 U20431 *Medicago sativa*
DESCRIPTION: polygalacturonase.

AAA82167.1 U09717 Gossypium hirsutum
 DESCRIPTION: polygalacturonase.
 5

AAA58322.1 U09805 Gossypium barbadense
 DESCRIPTION: polygalacturonase.
 10

CAA50336.1 X71018 Nicotiana tabacum
 DESCRIPTION: polygalacturonase. NPG. Protein sequence is in conflict with
 the conceptual translation; G27Y.
 15

CAA50334.1 X71016 Nicotiana tabacum
 DESCRIPTION: polygalacturonase. NPG. Protein sequence is in conflict with
 the conceptual translation; G27.X.
 20

CAA50337.1 X71019 Nicotiana tabacum
 DESCRIPTION: polygalacturonase. NPG. Protein sequence is in conflict with
 the conceptual translation; G27W.
 25

CAA65072.1 X95800 Brassica napus
 DESCRIPTION: polygalacturonase.
 30

BAA89478.1 AB029459 Salix gilgiana
 DESCRIPTION: polygalacturonase. SgPG3.
 35

CAA90272.1 Z49971 Brassica napus
 DESCRIPTION: Hydrolytic enzyme. Polygalacturonase. pga.
 40

CAA50335.1 X71017 Nicotiana tabacum
 DESCRIPTION: polygalacturonase. Npg1. Protein sequence is in conflict
 with the conceptual translation.
 45

CAA50338.1 X71020 Nicotiana tabacum
 DESCRIPTION: polygalacturonase. Npg1.

- BAA89479.1 AB029460 *Salix gilgiana*
DESCRIPTION: polygalacturonase. SgPG4.
- 5 AAC14453.1 L12019 *Actinidia deliciosa*
DESCRIPTION: polygalacturonase.
- 10 BAA89476.1 AB029457 *Salix gilgiana*
DESCRIPTION: polygalacturonase. SgPG1.
- 15 AAC26512.1 AF062467 *Cucumis melo*
DESCRIPTION: polygalacturonase precursor. MPG3.
- 20 CAA72003.1 Y11118 *Medicago sativa*
DESCRIPTION: polygalacturonase. PG3.
- CAB42886.1 AJ238848 *Phleum pratense*
DESCRIPTION: polygalacturonase. pg.
- 25 BAA89477.1 AB029458 *Salix gilgiana*
DESCRIPTION: polygalacturonase. SgPG2.
- 30 CAC05658.1 AJ250919 *Brassica napus*
DESCRIPTION: endopolygalacturonase. pegaz.
- 35 CAC05657.1 AJ250918 *Brassica napus*
DESCRIPTION: endopolygalacturonase. pgaz.
- 40 AAA32914.1 L06094 *Persea americana*
DESCRIPTION: cell wall degradation. polygalacturonase.
- AAF71160.1 AF152758 *Actinidia chinensis*
DESCRIPTION: polygalacturonase A. PGA.
- 45 AAF61444.1 AF138858 *Lycopersicon esculentum*
DESCRIPTION: hydrolyses polygalacturonic acid. polygalacturonase.XOPG1.

- 5 AAA34178.1 M37304 *Lycopersicon esculentum*
DESCRIPTION: polygalacturonase.
- 10 CAA32235.1 X14074 *Lycopersicon esculentum*
DESCRIPTION: polygalacturonase.
- 15 AAD46483.1 AF128266 *Glycine max*
DESCRIPTION: polygalacturonase PG1.
- 20 BAA88472.1 AB035890 *Cucumis sativus*
DESCRIPTION: polygalacturonase. CUPG1.
- 25 AAD46484.1 AF128267 *Glycine max*
DESCRIPTION: polygalacturonase PG2.
- 30 CAA54448.1 X77231 *Prunus persica*
DESCRIPTION: polygalacturonase. PG.
- CAA47055.1 X66426 *Persea americana*
DESCRIPTION: polygalacturonase.
- 35 CAA47052.1 X66422 *Zea mays*
DESCRIPTION: polygalacturonase. PG.
- 44
-
- 40 AAC61805.1 U28007 *Lycopersicon esculentum*
DESCRIPTION: serine/threonine protein kinase. Pto kinase interactor 1.
Pti1. Pti1 kinase.
- 45 BAB21241.1 AP002953 *Oryza sativa*
DESCRIPTION: Putative Pto kinase interactor 1. P0426D06.21. contains ESTs

AU108280(E0721),D48017(S13927).

- 5 AAF91337.1 AF249318 Glycine max
DESCRIPTION: Pti1 kinase-like protein. Pti1b. protein kinase.
- 10 AAF91336.1 AF249317 Glycine max
DESCRIPTION: Pti1 kinase-like protein. Pti1a. protein kinase.
- 15 BAA87853.1 AP000816 Oryza sativa
DESCRIPTION: EST AU030604(E51294) corresponds to a region of the
predicted gene. Similar to putative NAK-like Ser/Thr protein kinase.
(AF001308).
- 20 BAB16871.1 AP002537 Oryza sativa
DESCRIPTION: putative protein kinase APK1AArabidopsis thaliana.
P0001B06.24. contains ESTs C22608(R3192),D25110(R3192).
- 25 AAG16628.1 AY007545 Brassica napus
DESCRIPTION: protein serine/threonine kinase BNK1.
- 30 BAB39409.1 AP002901 Oryza sativa
DESCRIPTION: putative protein kinase. P0456F08.9. contains EST
C23560(R0290).
- 35 BAB39873.1 AP002882 Oryza sativa
DESCRIPTION: putative protein kinase. P0439B06.8. contains ESTs
AU056701(S20808),AU056702(S20808).
- 40 AAC27894.1 AF023164 Zea mays
DESCRIPTION: leucine-rich repeat transmembrane protein kinase 1. ltk1.
- 45 BAA94509.1 AB041503 Populus nigra
DESCRIPTION: protein kinase 1. PnPK1.
- BAB07999.1 AP002525 Oryza sativa
DESCRIPTION: putative protein kinase. P0462H08.22. contains EST

C22619(S11214).

- 5 BAB03429.1 AP002817 *Oryza sativa*
DESCRIPTION: EST C22619(S11214) corresponds to a region of the predicted gene. Similar to *Arabidopsis thaliana* chromosome 2, BAC clone T17D12; putative protein kinase (AC006587).
- 10 AAK21965.1 AY028699 *Brassica napus*
DESCRIPTION: receptor protein kinase PERK1.
- 15 AAC27895.1 AF023165 *Zea mays*
DESCRIPTION: leucine-rich repeat transmembrane protein kinase 2. ltk2.
- 20 AAK00425.1 AC069324 *Oryza sativa*
DESCRIPTION: Putative protein kinase. OSJNBa0071K19.11.
- 25 BAB21240.1 AP002953 *Oryza sativa*
DESCRIPTION: Putative protein kinase. P0426D06.20. contains ESTs C22359(C11461),C22360(C11461).
- 30 BAA94510.1 AB041504 *Populus nigra*
DESCRIPTION: protein kinase 2. PnPK2.
- 35 AAG03090.1 AC073405 *Oryza sativa*
DESCRIPTION: Similar to an *Arabidopsis* somatic embryogenesis receptor-like kinase (AC007504).
- 40 AAG59657.1 AC084319 *Oryza sativa*
DESCRIPTION: putative protein kinase. OSJNBa0004B24.20.
- 45 BAA78764.1 AB023482 *Oryza sativa*
DESCRIPTION: ESTs C98382(C2985),D22444(C11129) correspond to a region of the predicted gene.; Similar to *Arabidopsis thaliana* APK1 gene for protein tyrosine-serine-threonine kinase.(D12522).

AAG25966.1 AF302082 *Nicotiana tabacum*
DESCRIPTION: cytokinin-regulated kinase 1. CRK1. protein kinase;
transcript abundance decreases rapidly after cytokinin treatment.

5

AAF43496.1 AF131222 *Lophopyrum elongatum*
DESCRIPTION: protein serine/threonine kinase. ESI47. induced in roots by
salt stress, osmotic stress, and ABA treatment.

10

AAK11674.1 AF339747 *Lophopyrum elongatum*
DESCRIPTION: protein kinase. ESI47.

15

AAB09771.1 U67422 *Zea mays*
DESCRIPTION: CRINKLY4 precursor. cr4. receptor kinase homolog.

20

CAA97692.1 Z73295 *Catharanthus roseus*
DESCRIPTION: receptor-like protein kinase. CRPK1. Autophosphorylation
predominantly on Thr, less on Ser. Mechanism: autophosphorylation in cis.

25

BAA90808.1 AP001168 *Oryza sativa*
DESCRIPTION: Similar to putative receptor-like protein kinase (AL035679).

30

AAB47421.1 U59316 *Lycopersicon esculentum*
DESCRIPTION: serine/threonine protein kinase Pto. pto. allele of Pto
bacterial speck disease resistance gene in tomato.

35

AAF76313.1 AF220603 *Lycopersicon esculentum*
DESCRIPTION: Pto kinase. LescPth5.

40

CAB51834.1 00069 *Oryza sativa*
DESCRIPTION: I1332.5. contains eukaryotic protein kinase domain PF.

AAB47423.1 U59315 *Lycopersicon pimpinellifolium*
DESCRIPTION: serine/threonine protein kinase Pto. Pto. bacterial speck
disease resistance in tomato; disease resistance gene.

45

AAF76306.1 AF220602 *Lycopersicon pimpinellifolium*

DESCRIPTION: Pto kinase.

5 AAC48914.1 U02271 *Lycopersicon pimpinellifolium*
DESCRIPTION: protein kinase.

10 BAA92221.1 AP001278 *Oryza sativa*
DESCRIPTION: Similar to *Arabidopsis thaliana* chromosome II BAC F12L6
genomic sequence, putative protein kinase. (AC004218).

15 BAA87852.1 AP000816 *Oryza sativa*
DESCRIPTION: Similar to putative Ser/Thr protein kinase. (AC004218).

20 AAF66615.1 AF142596 *Nicotiana tabacum*
DESCRIPTION: LRR receptor-like protein kinase.

25 AAK11566.1 AF318490 *Lycopersicon hirsutum*
DESCRIPTION: Pto-like protein kinase E. LhirPtoE. confers resistance to
bacterial speck disease.

30 AAK11567.1 AF318491 *Lycopersicon hirsutum*
DESCRIPTION: Pto-like protein kinase F. LhirPtoF.

35 CAB51836.1 AJ243961 *Oryza sativa*
DESCRIPTION: Putative Ser/Thr protein kinase. 11332.7.

40 AAD38286.1 AC007789 *Oryza sativa*
DESCRIPTION: putative protein kinase. OSJNBa0049B20.13.

45 BAB40081.1 AP003074 *Oryza sativa*
DESCRIPTION: putative receptor protein kinase. OSJNBa0004G10.30.

BAB18321.1 AP002865 *Oryza sativa*
DESCRIPTION: putative receptor protein kinase. P0034C11.11.

45 BAA92836.1 AB032473 *Brassica oleracea*

DESCRIPTION: S18 S-locus receptor kinase. SRK18.

45

5 AAB72110.1 U79958 Pisum sativum
DESCRIPTION: BP-80 vacuolar sorting receptor.

10 AAF80450.1 AF161719 Triticum aestivum
DESCRIPTION: vacuolar targeting receptor bp-80.

15 AAG60258.1 AY017377 Physcomitrella patens
DESCRIPTION: EGF receptor-like protein. ELP. PPELP; similar to putative
vacuolar sorting receptor.

20 AAF22842.1 AF209910 Prunus dulcis
DESCRIPTION: vacuolar sorting receptor protein. BP-80 type protein.

25 AAK31596.1 AY029172 Helianthus annuus
DESCRIPTION: EGF receptor-like protein. ELP.

30 AAB72113.1 U79961 Zea mays
DESCRIPTION: vacuolar sorting receptor homolog. similar to Pisum sativum
BP-80 vacuolar sorting receptor, GenBank Accession Number U79958.

35 BAA92985.1 AP001550 Oryza sativa
DESCRIPTION: EST D15617(C0960A) corresponds to a region of the predicted
gene.; Similar to Arabidopsis thaliana chromosome 4, BAC clone F18F4;
vacuolar sorting receptor-like protein (AL021637).

47

40 BAA00885.1 D10001 Pisum sativum
DESCRIPTION: phenylalanine ammonia-lyase.

45 AAK15640.1 AF326116 Agastache rugosa
DESCRIPTION: phenylalanine ammonia-lyase. PAL.

CAB42794.1 AJ238754 Citrus clementina x Citrus reticulata

DESCRIPTION: phenylalanine-ammonia lyase. pal2.

BAA00886.1 D10002 Pisum sativum

5 DESCRIPTION: phenylalanine ammonia-lyase. PAL1.

BAA00887.1 D10003 Pisum sativum

10 DESCRIPTION: phenylalanine ammonia-lyase. PAL2.

AAB67733.1 U43338 Citrus limon

DESCRIPTION: phenylalanine ammonia-lyase. pal6.

15 AAF40224.1 AF237955 Rubus idaeus

DESCRIPTION: phenylalanine ammonia-lyase 2. PAL2. PAL;
phenylpropanoid;
multigene; flavonoid.

20 AAA17993.1 M91192 Trifolium subterraneum

DESCRIPTION: phenylalanine ammonia-lyase. PAL1.

25 CAA57057.1 X81159 Petroselinum crispum

DESCRIPTION: phenylalanine ammonia-lyase 3. PAL3. tetramere subunit.

30 AAF40223.1 AF237954 Rubus idaeus

DESCRIPTION: phenylalanine ammonia-lyase 1. PAL1. PAL;
phenylpropanoid;
multigene; flavonoid.

35 CAA68938.1 Y07654 Petroselinum crispum

DESCRIPTION: PAL1 protein. pal1 gene.

40 CAA57056.1 X81158 Petroselinum crispum

DESCRIPTION: phenylalanine ammonia-lyase 2. PAL2. deaminase subunit.

CAB60719.1 AJ250836 Cicer arietinum

45 DESCRIPTION: phenylpropanoid pathway. phenylalanine ammonia-lyase. pal.

CAA05251.1 AJ002221 *Digitalis lanata*
DESCRIPTION: phenylalanine ammonia lyase.

5

AAC78457.1 AF036948 *Prunus avium*
DESCRIPTION: phenylalanine ammonia-lyase. PAL1.

10

BAA23367.1 D85850 *Daucus carota*
DESCRIPTION: phenylalanine ammonia-lyase. gDcPAL1.

15

CAA68256.1 X99997 *Bromheadia finlaysoniana*
DESCRIPTION: phenylalanine ammonia-lyase. pal.

20

AAA33805.1 L11747 *Populus x generosa*
DESCRIPTION: phenylalanine ammonia lyase. PAL.

25

BAA24928.1 D83075 *Lithospermum erythrorhizon*
DESCRIPTION: phenylalanine ammonia-lyase.

30

CAA34226.1 X16099 *Oryza sativa* subsp. *japonica*
DESCRIPTION: phenylalanine ammonia-lyase.

35

CAA41169.1 X58180 *Medicago sativa*
DESCRIPTION: phenylalanine ammonia-lyase. PAL.

40

AAA34176.1 M90692 *Lycopersicon esculentum*
DESCRIPTION: phenylalanine ammonia-lyase. PAL5.

45

BAA07860.1 D43802 *Populus kitakamiensis*
DESCRIPTION: phenylalanine ammonia-lyase.

AAA84889.1 U39792 *Pinus taeda*
DESCRIPTION: phenylalanine ammonia-lyase. lpPAL.

CAA73065.1 Y12461 *Helianthus annuus*

DESCRIPTION: phenylalanine ammonia lyase. PAL.

5 BAA95629.1 AB042520 Catharanthus roseus
DESCRIPTION: phenylalanine ammonia lyase.

10 BAA05643.1 D26596 Camellia sinensis
DESCRIPTION: phenylalanine ammonia-lyase.

BAA24929.1 D83076 Lithospermum erythrorhizon
DESCRIPTION: phenylalanine ammonia-lyase.

15 BAA21643.1 D30656 Populus kitakamiensis
DESCRIPTION: phenylalanine ammonia-lyase.

20 CAA37129.1 X52953 Glycine max
DESCRIPTION: phenylalanine ammonia-lyase. PAL1.

25 AAA34122.1 M84466 Nicotiana tabacum
DESCRIPTION: phenylalanine ammonia lyase. tpa1.

30 BAA22948.1 AB008200 Nicotiana tabacum
DESCRIPTION: phenylalanine ammonia-lyase. palB.

AAA99500.1 L36822 Stylosanthes humilis
DESCRIPTION: phenylalanine ammonia lyase. PAL17.1.

35 CAB42793.1 AJ238753 Citrus clementina x Citrus reticulata
DESCRIPTION: phenylalanine-ammonia lyase. pal1.

40 AAG49585.1 AF325496 Ipomoea nil
DESCRIPTION: phenylalanine ammonia-lyase.

45 CAA55075.1 X78269 Nicotiana tabacum
DESCRIPTION: phenylalanine ammonia-lyase.

- BAA22963.1 D17467 *Nicotiana tabacum*
DESCRIPTION: phenylalanine ammonia-lyase. TOBPAL1.
- 5 BAA22947.1 AB008199 *Nicotiana tabacum*
DESCRIPTION: phenylalanine ammonia-lyase. palA.
- 10 AAA34179.2 M83314 *Lycopersicon esculentum*
DESCRIPTION: deamination of phenylalanine to coumarate. phenylalanine ammonia lyase. pal.
- 15 BAA11459.1 D78640 *Ipomoea batatas*
DESCRIPTION: Phenylalanine Ammonia-Lyase.
- 20 AAA33389.1 M29232 *Ipomoea batatas*
DESCRIPTION: phenylalanine ammonia-lyase.
- 25 CAA68036.1 X99705 *Triticum aestivum*
DESCRIPTION: phenylalanine ammonia-lyase. PAL.
- CAA61198.1 X87946 *Oryza sativa*
DESCRIPTION: phenylalanine ammonia-lyase. ZB8.
- 30 BAA06337.1 D30657 *Populus kitakamiensis*
DESCRIPTION: phenylalanine ammonia-lyase.
- 35 AAD45384.1 AF165998 *Vigna unguiculata*
DESCRIPTION: phenylalanine ammonia-lyase.
- 40 CAA53733.1 X76130 *Cucumis melo*
DESCRIPTION: phenylalanine ammonia-lyase. pal.
- 45 AAA51873.1 U16130 *Persea americana*
DESCRIPTION: phenylalanine ammonia lyase. PAL.

BAB19128.1 AB041361 *Dianthus caryophyllus*
DESCRIPTION: phenylalanine ammonia-lyase. Dcpal1.

5 CAA34715.1 X16772 *Petroselinum crispum*
DESCRIPTION: phenylalanine ammonia-lyase (AA 137 - 716) (1 is 3rd base in codon).

10 BAA07861.1 D43803 *Populus kitakamiensis*
DESCRIPTION: phenylalanine ammonia-lyase.

48

15 CAB94692.1 AJ242742 *Ipomoea batatas*
DESCRIPTION: Removal of H₂O₂, oxidation of toxic reductants, defence response toward wounding. peroxidase. pod.

20 AAD37430.1 AF149280 *Phaseolus vulgaris*
DESCRIPTION: peroxidase 5 precursor. FBP5. secretory peroxidase.

CAA66037.1 X97351 *Populus balsamifera* subsp. *trichocarpa*
25 DESCRIPTION: signal for ER. peroxidase.

BAA06335.1 D30653 *Populus kitakamiensis*
DESCRIPTION: peroxidase.

30

AAA34108.1 J02979 *Nicotiana tabacum*
DESCRIPTION: lignin-forming peroxidase precursor (EC 1.11.1.7).

35

BAA01992.1 D11396 *Nicotiana tabacum*
DESCRIPTION: 'peroxidase'.

40 CAA50597.1 X71593 *Lycopersicon esculentum*
DESCRIPTION: peroxidase. CEVI-1.

CAB67121.1 Y19023 *Lycopersicon esculentum*
45 DESCRIPTION: peroxidase. cevi-1.

BAA11853.1 D83225 Populus nigra
DESCRIPTION: peroxidase.

5

CAA66034.1 X97348 Populus balsamifera subsp. trichocarpa
DESCRIPTION: signal for ER. peroxidase.

10 BAA01877.1 D11102 Populus kitakamiensis
DESCRIPTION: peroxidase. prxA1.

15 BAA11852.1 D83224 Populus nigra
DESCRIPTION: peroxidase.

20 CAA66035.1 X97349 Populus balsamifera subsp. trichocarpa
DESCRIPTION: signal for ER. peroxidase.

AAB47602.1 L07554 Linum usitatissimum
DESCRIPTION: peroxidase. FLXPER1.

25

AAD37427.1 AF149277 Phaseolus vulgaris
DESCRIPTION: peroxidase 1 precursor. FBP1. secretory peroxidase.

30 CAA66036.1 X97350 Populus balsamifera subsp. trichocarpa
DESCRIPTION: signal for ER. peroxidase.

35 AAB97734.1 AF014502 Glycine max
DESCRIPTION: seed coat peroxidase precursor. Ep. H2O2 oxidoreductase;
class III plant peroxidase.

40 BAA06334.1 D30652 Populus kitakamiensis
DESCRIPTION: peroxidase.

45 BAA07241.1 D38051 Populus kitakamiensis
DESCRIPTION: peroxidase. prxA4a.

- CAA62226.1 X90693 *Medicago sativa*
DESCRIPTION: peroxidase1B. prx1B.
- 5 CAA62225.1 X90692 *Medicago sativa*
DESCRIPTION: peroxidase1A. prx1A.
- 10 CAA62227.1 X90694 *Medicago sativa*
DESCRIPTION: peroxidase1C. prx1C.
- 15 AAB41811.1 L36157 *Medicago sativa*
DESCRIPTION: peroxidase. pxdC. amino acid feature: conserved domains, aa
123 .. 129, 191 .. 198; amino acid feature: heme-binding domain, aa 68 ..
73.
- 20 AAB41810.1 L36156 *Medicago sativa*
DESCRIPTION: peroxidase. pxdA. amino acid feature: conserved motifs, aa
181 .. 188; amino acid feature: heme-binding domain, aa 60 .. 65.
- 25 AAC98519.1 AF007211 *Glycine max*
DESCRIPTION: peroxidase precursor. GMIPER1. pathogen-induced.
- 30 BAA02840.1 D13683 *Populus kitakamiensis*
DESCRIPTION: peroxidase. HPOX14.
- 35 BAA14144.1 D90116 *Armoracia rusticana*
DESCRIPTION: peroxidase isozyme.
- 40 BAA14143.1 D90115 *Armoracia rusticana*
DESCRIPTION: peroxidase isozyme.
- 45 BAA08499.1 D49551 *Oryza sativa*
DESCRIPTION: peroxidase. poxN.

- BAA03373.1 D14482 *Oryza sativa*
DESCRIPTION: putative peroxidase.
- 5 AAA34101.1 L02124 *Nicotiana tabacum*
DESCRIPTION: peroxidase.
- 10 BAA82306.1 AB027752 *Nicotiana tabacum*
DESCRIPTION: peroxidase.
- 15 CAA40796.1 X57564 *Armoracia rusticana*
DESCRIPTION: peroxidase. peroxidase precursor.
- 20 AAA33121.1 M32742 *Cucumis sativus*
DESCRIPTION: peroxidase (CuPer2).
- CAA76680.1 Y17192 *Cucurbita pepo*
DESCRIPTION: peroxidase. aprx. type III peroxidase.
- 25 BAA92500.1 AP001383 *Oryza sativa*
DESCRIPTION: ESTs D39300(R3292),AU030751(E60187) correspond to a
region
of the predicted gene. Similar to peroxidase ATP6a. (X98774).
- 30 BAA77388.1 AB024438 *Scutellaria baicalensis*
DESCRIPTION: peroxidase 2.
- 35 AAA33127.1 M91373 *Cucumis sativus*
DESCRIPTION: peroxidase. pre-peroxidase. putative.
- 40 AAD43561.1 AF155124 *Gossypium hirsutum*
DESCRIPTION: bacterial-induced peroxidase precursor. Perx_Goshiko.
- 45 AAB06183.1 M37636 *Arachis hypogaea*
DESCRIPTION: cationic peroxidase. PNC1.

- 5 CAB94692.1 AJ242742 *Ipomoea batatas*
DESCRIPTION: Removal of H₂O₂, oxidation of toxic reductants, defence response toward wounding. peroxidase. pod.
- 10 BAA06335.1 D30653 *Populus kitakamiensis*
DESCRIPTION: peroxidase.
- 15 AAD37427.1 AF149277 *Phaseolus vulgaris*
DESCRIPTION: peroxidase 1 precursor. FBP1. secretory peroxidase.
- 20 AAD37430.1 AF149280 *Phaseolus vulgaris*
DESCRIPTION: peroxidase 5 precursor. FBP5. secretory peroxidase.
- 25 BAA11852.1 D83224 *Populus nigra*
DESCRIPTION: peroxidase.
- 30 CAA66035.1 X97349 *Populus balsamifera* subsp. *trichocarpa*
DESCRIPTION: signal for ER. peroxidase.
- CAA66034.1 X97348 *Populus balsamifera* subsp. *trichocarpa*
DESCRIPTION: signal for ER. peroxidase.
- 35 BAA07241.1 D38051 *Populus kitakamiensis*
DESCRIPTION: peroxidase. prxA4a.
- 40 BAA92500.1 AP001383 *Oryza sativa*
DESCRIPTION: ESTs D39300(R3292), AU030751(E60187) correspond to a region of the predicted gene. Similar to peroxidase ATP6a. (X98774).
- 45 CAA50597.1 X71593 *Lycopersicon esculentum*
DESCRIPTION: peroxidase. CEVI-1.

CAB67121.1 Y19023 *Lycopersicon esculentum*
DESCRIPTION: peroxidase. cevi-1.

5

CAA66036.1 X97350 *Populus balsamifera* subsp. *trichocarpa*
DESCRIPTION: signal for ER. peroxidase.

10

AAB47602.1 L07554 *Linum usitatissimum*
DESCRIPTION: peroxidase. FLXPER1.

15

CAA62226.1 X90693 *Medicago sativa*
DESCRIPTION: peroxidase1B. prx1B.

20

AAA34108.1 J02979 *Nicotiana tabacum*
DESCRIPTION: lignin-forming peroxidase precursor (EC 1.11.1.7).

25

CAA62227.1 X90694 *Medicago sativa*
DESCRIPTION: peroxidase1C. prx1C.

30

BAA06334.1 D30652 *Populus kitakamiensis*
DESCRIPTION: peroxidase.

35

BAA01992.1 D11396 *Nicotiana tabacum*
DESCRIPTION: 'peroxidase'.

40

AAD43561.1 AF155124 *Gossypium hirsutum*
DESCRIPTION: bacterial-induced peroxidase precursor. Perx_Goshiko.

45

BAA82306.1 AB027752 *Nicotiana tabacum*
DESCRIPTION: peroxidase.

AAC98519.1 AF007211 *Glycine max*
DESCRIPTION: peroxidase precursor. GMIPER1. pathogen-induced.

- BAA14143.1 D90115 *Armoracia rusticana*
DESCRIPTION: peroxidase isozyme.
- 5 AAB97734.1 AF014502 *Glycine max*
DESCRIPTION: seed coat peroxidase precursor. Ep. H₂O₂ oxidoreductase;
class III plant peroxidase.
- 10 AAF63027.1 AF244924 *Spinacia oleracea*
DESCRIPTION: hydrogen peroxide catabolism. peroxidase prx15 precursor.
type III peroxidase.
- 15 CAA62225.1 X90692 *Medicago sativa*
DESCRIPTION: peroxidase1A. prx1A.
- 20 BAA01877.1 D11102 *Populus kitakamiensis*
DESCRIPTION: peroxidase. prxA1.
- 25 AAF63026.1 AF244923 *Spinacia oleracea*
DESCRIPTION: hydrogen peroxide catabolism. peroxidase prx14 precursor.
type III peroxidase.
- 30 BAA14144.1 D90116 *Armoracia rusticana*
DESCRIPTION: peroxidase isozyme.
- 35 AAB41810.1 L36156 *Medicago sativa*
DESCRIPTION: peroxidase. pxdA. amino acid feature: conserved motifs, aa
181 .. 188; amino acid feature: heme-binding domain, aa 60 .. 65.
- 40 AAA34050.1 M74103 *Nicotiana sylvestris*
DESCRIPTION: anionic peroxidase.
- CAA62597.1 X91172 *Raphanus sativus*
DESCRIPTION: korean-radish isoperoxidase. prxk1.
- 45 AAB02554.1 L37790 *Stylosanthes humilis*
DESCRIPTION: cationic peroxidase.

CAA76680.1 Y17192 Cucurbita pepo
 DESCRIPTION: peroxidase. aprx. type III peroxidase.

CAA71492.1 Y10466 Spinacia oleracea
 DESCRIPTION: peroxidase. prxr5.

BAA94962.1 AB042103 Asparagus officinalis
 DESCRIPTION: peroxidase. AspPOX1.

BAA77389.1 AB024439 Scutellaria baicalensis
 DESCRIPTION: peroxidase 3.

AAD37428.1 AF149278 Phaseolus vulgaris
 DESCRIPTION: peroxidase 3 precursor. FBP3. secretory peroxidase.

AAB41811.1 L36157 Medicago sativa
 DESCRIPTION: peroxidase. pxdC. amino acid feature: conserved domains, aa
 123 .. 129, 191 .. 198; amino acid feature: heme-binding domain, aa 68 ..
 73.

AAB06183.1 M37636 Arachis hypogaea
 DESCRIPTION: cationic peroxidase. PNC1.

BAA02112.1 D12544 Pisum sativum
 DESCRIPTION: GTP-binding protein.

CAA98184.1 Z73956 Lotus japonicus
 DESCRIPTION: GTP-binding protein. RAB11H. rab11H.

AAK15703.1 AF327517 Oryza sativa
 DESCRIPTION: GTP-binding protein.

BAA02904.1 D13758 Oryza sativa

DESCRIPTION: ras-related GTP binding protein. ss230.

5 BAA02111.1 D12543 Pisum sativum
DESCRIPTION: GTP-binding protein.

10 BAA02113.1 D12545 Pisum sativum
DESCRIPTION: GTP-binding protein.

CAA98180.1 Z73952 Lotus japonicus
DESCRIPTION: GTP-binding protein. RAB11D. rab11D.

15 CAB65172.1 AJ245570 Lycopersicon esculentum
DESCRIPTION: putative role in secretion of cell wall modifying enzymes.
Rab11 GTPase. Rab11a.

20 BAA02114.1 D12546 Pisum sativum
DESCRIPTION: GTP-binding protein.

25 CAA98181.1 Z73953 Lotus japonicus
DESCRIPTION: GTP-binding protein. RAB11E. rab11E.

30 CAA95859.1 Z71276 Mangifera indica
DESCRIPTION: small GTPase. rabX. homologous to Rab11.

35 CAA55865.1 X79278 Medicago sativa
DESCRIPTION: GTP binding protein. Rab.

CAA89049.1 Z49190 Beta vulgaris
DESCRIPTION: GTP-binding. small G protein.

40 CAA98179.1 Z73951 Lotus japonicus
DESCRIPTION: GTP-binding protein. RAB11C. rab11C.

45 BAA02437.1 D13152 Oryza sativa
DESCRIPTION: GTP binding protein. rgp2.

- 5 BAA06701.1 D31905 Zea mays
DESCRIPTION: mgp1 GTP-binding protein. mgp1.
- BAA06702.1 D31906 Zea mays
DESCRIPTION: mgp2 GTP-binding protein. mgp2.
- 10 BAA02110.1 D12542 Pisum sativum
DESCRIPTION: GTP-binding protein.
- 15 CAA98177.1 Z73949 Lotus japonicus
DESCRIPTION: GTP-binding protein. RAB11A. rab11A.
- 20 CAA41966.1 X59276 Oryza sativa
DESCRIPTION: GTP-binding protein. rgp1.
- AAB97114.1 U58853 Glycine max
DESCRIPTION: small GTP-binding protein. sra1.
- 25 CAA98185.1 Z73957 Lotus japonicus
DESCRIPTION: GTP-binding protein. RAB11I. rab11I.
- 30 CAA67153.1 X98540 Fagus sylvatica
DESCRIPTION: FSGTP1.
- 35 CAA98183.1 Z73955 Lotus japonicus
DESCRIPTION: GTP-binding protein. RAB11G. rab11G.
- 40 CAA98182.1 Z73954 Lotus japonicus
DESCRIPTION: GTP-binding protein. RAB11F. rab11F.
- 45 CAA54506.1 X77301 Glycine max
DESCRIPTION: GTPase. gmr2.

BAA02108.1 D12540 Pisum sativum
DESCRIPTION: GTP-binding protein.

5 AAA68983.1 L12395 Brassica napus
DESCRIPTION: signal transduction, membrane vehicle traffic. small
GTP-binding protein. bra. putative.

10 AAD48018.1 AF165095 Gossypium hirsutum
DESCRIPTION: Rab GTP-binding protein Rab11a.

15 BAA02109.1 D12541 Pisum sativum
DESCRIPTION: GTP-binding protein.

20 CAA98186.1 Z73958 Lotus japonicus
DESCRIPTION: GTP-binding protein. RAB11J. rab11J.

25 BAA84640.1 AB007911 Pisum sativum
DESCRIPTION: PRA2. pra2. light-repressible GTP binding protein.

30 AAD48019.1 AF165096 Gossypium hirsutum
DESCRIPTION: Rab GTP-binding protein Rab11b.

35 CAA98178.1 Z73950 Lotus japonicus
DESCRIPTION: GTP-binding protein. RAB11B. rab11B.

40 AAA63901.1 U22432 Zea mays
DESCRIPTION: GTP binding protein. rab2.

45 CAA98165.1 Z73937 Lotus japonicus
DESCRIPTION: GTP-binding protein. RAB2A. rab2A.

AAA34253.1 L08130 Volvox carteri
DESCRIPTION: GTP-binding protein. yptV4.

45 AAA90955.1 U32185 Glycine max

DESCRIPTION: vesicular transport. guanine nucleotide regulatory protein.
rab2. GTP-binding protein; soyrab.

5 AAA63902.1 U22433 Zea mays
DESCRIPTION: GTP binding protein. rab2.

53

10 CAA64327.1 X94624 Brassica napus
DESCRIPTION: acyl-CoA synthetase.

15 CAA96523.1 Z72153 Brassica napus
DESCRIPTION: acyl CoA synthetase.

20 CAC19877.1 AJ401089 Brassica napus
DESCRIPTION: activation of free fatty acids. long chain acyl-CoA
synthetase. acs6. activity confirmed by expression in E. coli.

25 CAA06820.1 AJ006025 Cicer arietinum
DESCRIPTION: acyl-coA synthetase.

BAA08365.1 D49366 Lithospermum erythrorhizon
DESCRIPTION: 4-coumarate:CoA ligase.

30 CAA36850.1 X52623 Oryza sativa
DESCRIPTION: 4-coumarate-CoA ligase.

35 AAF37734.1 AF052223 Lolium perenne
DESCRIPTION: 4-coumarate--CoA ligase 4CL3.

40 AAF91309.1 AF239686 Rubus idaeus
DESCRIPTION: 4-coumarate:coA ligase 2. adenylate-forming enzyme; 4CL2.

45 AAC24503.1 AF041049 Populus tremuloides
DESCRIPTION: 4-coumarate:CoA ligase.

BAA08366.2 D49367 *Lithospermum erythrorhizon*
DESCRIPTION: 4-coumarate:CoA ligase.

5 AAF91308.1 AF239685 *Rubus idaeus*
DESCRIPTION: 4-coumarate:coA ligase 3. adenylate-forming enzyme; 4CL3.

10 AAC39366.1 AF008184 *Populus x generosa*
DESCRIPTION: 4-coumarate:CoA ligase 1. 4CL1.

15 CAA31696.1 X13324 *Petroselinum crispum*
DESCRIPTION: 4-coumarate:CoA ligase Pc4Cl-1 (AA 1-544).

20 AAC39365.1 AF008183 *Populus x generosa*
DESCRIPTION: 4-coumarate:CoA ligase 2. 4CL2.

AAA33842.1 M62755 *Solanum tuberosum*
DESCRIPTION: 4-coumarate--CoA ligase. St4C1-1.

25 CAA31697.1 X13325 *Petroselinum crispum*
DESCRIPTION: 4-coumarate:CoA ligase Pc4Cl-2 (AA 1-544).

30 AAB42383.1 U39405 *Pinus taeda*
DESCRIPTION: 4-coumarate:CoA ligase. lp4CL-1.

35 AAB42382.1 U39404 *Pinus taeda*
DESCRIPTION: 4-coumarate:CoA ligase. lp4CL-2.

AAA92669.1 U12013 *Pinus taeda*
DESCRIPTION: 4-coumarate-CoA ligase enzyme.

40 AAF91310.1 AF239687 *Rubus idaeus*
DESCRIPTION: 4-coumarate:coA ligase 1. adenylate-forming enzyme; 4CL1.

45 AAA92668.1 U12012 *Pinus taeda*
DESCRIPTION: 4-coumarate-CoA ligase enzyme.

- 5 AAF37732.1 AF052221 *Lolium perenne*
DESCRIPTION: 4-coumarate--CoA ligase 4CL1.
- 10 CAA49575.1 X69954 *Glycine max*
DESCRIPTION: 4-coumarate--CoA ligase.
- 15 AAC24504.1 AF041050 *Populus tremuloides*
DESCRIPTION: 4-coumarate:CoA ligase.
- 20 CAB97359.1 AJ278455 *Juglans nigra*
DESCRIPTION: 4-coumarate-CoA ligase. 4CL.
- 25 AAA69580.1 L43362 *Oryza sativa*
DESCRIPTION: 4-coumarate:CoA ligase isoform 2. 4cl.2. putative.
- 30 AAG46175.1 AC018727 *Oryza sativa*
DESCRIPTION: putative 4-coumarate CoA ligase. OSJNBa0056G17.30.
- 35 AAF73997.2 AF144504 *Picea smithiana*
DESCRIPTION: 4-coumarate:CoA ligase. 4CL.
- 40 AAF73998.2 AF144505 *Cathaya argyrophylla*
DESCRIPTION: 4-coumarate:CoA ligase. 4CL.
- 45 AAF73994.2 AF144501 *Pinus armandii*
DESCRIPTION: 4-coumarate:CoA ligase. 4CL.

AAF73996.2 AF144503 Pinus armandii
DESCRIPTION: 4-coumarate:CoA ligase. 4CL.

55

5

CAA87068.1 Z46944 Citrus sinensis
DESCRIPTION: non-photosynthetic ferredoxin.

10 AAK15005.1 AF233452 Impatiens balsamina
DESCRIPTION: ferredoxin. plastidal protein.

15 AAA33461.1 M73831 Zea mays
DESCRIPTION: ferredoxin.

CAB65696.1 AJ270962 Lycopersicon esculentum
DESCRIPTION: electron transfer. putative ferredoxin. ferredoxin.
20

BAA90760.1 AB038037 Ipomoea nil
DESCRIPTION: non-photosynthetic ferredoxin.

25

BAA06456.1 D30794 Oryza sativa
DESCRIPTION: ferredoxin.

30 AAB61593.1 AF003125 Mesembryanthemum crystallinum
DESCRIPTION: ferredoxin I precursor.

35 AAA33665.1 M31713 Pisum sativum
DESCRIPTION: ferredoxin I precursor.

AAD02175.1 AF039662 Capsicum annuum
DESCRIPTION: delays the harpin-mediated hypersensitive response.
40 ferredoxin-like protein. ap1.

CAA73265.1 Y12734 Physcomitrella patens
DESCRIPTION: ferredoxin.
45

CAA52980.1 X75089 *Triticum aestivum*
DESCRIPTION: ferredoxin. petF.

5 BAA06436.1 D30763 *Oryza sativa*
DESCRIPTION: ferredoxin.

CAA99756.1 Z75520 *Lycopersicon esculentum*
10 DESCRIPTION: transfer of electrons in a wide variety of metabolic
reactions. ferredoxin-I. precursor.

AAA33462.1 M73828 *Zea mays*
15 DESCRIPTION: ferredoxin.

AAA34028.1 M35660 *Spinacia oleracea*
20 DESCRIPTION: ferredoxin I precursor.

CAA26281.1 X02432 *Silene latifolia* subsp. *alba*
DESCRIPTION: ferredoxin precursor.

25 AAA33459.1 M73829 *Zea mays*
DESCRIPTION: ferredoxin.

30 AAA33460.1 M73830 *Zea mays*
DESCRIPTION: ferredoxin.

BAA32348.1 AB016810 *Zea mays*
35 DESCRIPTION: ferredoxin. pFD2.

BAA19865.1 D83660 *Oryza sativa*
40 DESCRIPTION: root ferredoxin.

AAA33085.1 L10349 *Chlamydomonas reinhardtii*
DESCRIPTION: ferredoxin. precursor.

45 AAC49171.1 U29516 *Chlamydomonas reinhardtii*

DESCRIPTION: ferredoxin precursor. Method: conceptual translation
supplied by author.

5 AAB65699.1 AF010320 *Oryza sativa*
DESCRIPTION: ferredoxin.

10 AAK14422.1 AC087851 *Oryza sativa*
DESCRIPTION: putative ferredoxin. OSJNBb0072E24.16.

57

15 CAB94692.1 AJ242742 *Ipomoea batatas*
DESCRIPTION: Removal of H₂O₂, oxidation of toxic reductants, defence
response toward wounding. peroxidase. pod.

20 AAD37430.1 AF149280 *Phaseolus vulgaris*
DESCRIPTION: peroxidase 5 precursor. FBP5. secretory peroxidase.

25 CAA66037.1 X97351 *Populus balsamifera* subsp. *trichocarpa*
DESCRIPTION: signal for ER. peroxidase.

BAA06335.1 D30653 *Populus kitakamiensis*
DESCRIPTION: peroxidase.

30 AAA34108.1 J02979 *Nicotiana tabacum*
DESCRIPTION: lignin-forming peroxidase precursor (EC 1.11.1.7).

35 BAA01992.1 D11396 *Nicotiana tabacum*
DESCRIPTION: 'peroxidase'.

40 CAA66034.1 X97348 *Populus balsamifera* subsp. *trichocarpa*
DESCRIPTION: signal for ER. peroxidase.

45 AAB47602.1 L07554 *Linum usitatissimum*
DESCRIPTION: peroxidase. FLXPER1.

BAA11853.1 D83225 *Populus nigra*
DESCRIPTION: peroxidase.

5 CAA50597.1 X71593 *Lycopersicon esculentum*
DESCRIPTION: peroxidase. CEVI-1.

10 CAB67121.1 Y19023 *Lycopersicon esculentum*
DESCRIPTION: peroxidase. cevi-1.

15 BAA11852.1 D83224 *Populus nigra*
DESCRIPTION: peroxidase.

20 CAA66035.1 X97349 *Populus balsamifera* subsp. *trichocarpa*
DESCRIPTION: signal for ER. peroxidase.

AAD37427.1 AF149277 *Phaseolus vulgaris*
DESCRIPTION: peroxidase 1 precursor. FBP1. secretory peroxidase.

25 BAA01877.1 D11102 *Populus kitakamiensis*
DESCRIPTION: peroxidase. prxA1.

30 CAA66036.1 X97350 *Populus balsamifera* subsp. *trichocarpa*
DESCRIPTION: signal for ER. peroxidase.

35 CAA62225.1 X90692 *Medicago sativa*
DESCRIPTION: peroxidase1A. prx1A.

40 AAB97734.1 AF014502 *Glycine max*
DESCRIPTION: seed coat peroxidase precursor. Ep. H2O2 oxidoreductase;
class III plant peroxidase.

CAA62226.1 X90693 *Medicago sativa*
DESCRIPTION: peroxidase1B. prx1B.

45 CAA62227.1 X90694 *Medicago sativa*

DESCRIPTION: peroxidase1C. prx1C.

5 BAA06334.1 D30652 Populus kitakamiensis
DESCRIPTION: peroxidase.

10 BAA07241.1 D38051 Populus kitakamiensis
DESCRIPTION: peroxidase. prxA4a.

15 AAB41810.1 L36156 Medicago sativa
DESCRIPTION: peroxidase. pxdA. amino acid feature: conserved motifs, aa
181 .. 188; amino acid feature: heme-binding domain, aa 60 .. 65.

20 AAB41811.1 L36157 Medicago sativa
DESCRIPTION: peroxidase. pxdC. amino acid feature: conserved domains, aa
123 .. 129, 191 .. 198; amino acid feature: heme-binding domain, aa 68 ..
73.

25 BAA14144.1 D90116 Armoracia rusticana
DESCRIPTION: peroxidase isozyme.

30 AAC98519.1 AF007211 Glycine max
DESCRIPTION: peroxidase precursor. GMIPER1. pathogen-induced.

BAA02840.1 D13683 Populus kitakamiensis
DESCRIPTION: peroxidase. HPOX14.

35 BAA14143.1 D90115 Armoracia rusticana
DESCRIPTION: peroxidase isozyme.

40 AAA33129.1 M91372 Cucumis sativus
DESCRIPTION: peroxidase. pre-peroxidase.

45 BAA08499.1 D49551 Oryza sativa
DESCRIPTION: peroxidase. poxN.

- BAA03373.1 D14482 *Oryza sativa*
DESCRIPTION: putative peroxidase.
- 5 AAA34101.1 L02124 *Nicotiana tabacum*
DESCRIPTION: peroxidase.
- 10 CAA76680.1 Y17192 *Cucurbita pepo*
DESCRIPTION: peroxidase. aprx. type III peroxidase.
- 15 CAA40796.1 X57564 *Armoracia rusticana*
DESCRIPTION: peroxidase. peroxidase precursor.
- 20 AAA33121.1 M32742 *Cucumis sativus*
DESCRIPTION: peroxidase (CuPer2).
- BAA82306.1 AB027752 *Nicotiana tabacum*
DESCRIPTION: peroxidase.
- 25 AAD43561.1 AF155124 *Gossypium hirsutum*
DESCRIPTION: bacterial-induced peroxidase precursor. Perx_Goshiko.
- 30 AAB06183.1 M37636 *Arachis hypogaea*
DESCRIPTION: cationic peroxidase. PNC1.
- 35 AAA33127.1 M91373 *Cucumis sativus*
DESCRIPTION: peroxidase. pre-peroxidase. putative.
- CAA71492.1 Y10466 *Spinacia oleracea*
DESCRIPTION: peroxidase. prxr5.
- 40 AAF63027.1 AF244924 *Spinacia oleracea*
DESCRIPTION: hydrogen peroxide catabolism. peroxidase prx15 precursor.
type III peroxidase.
- 45 AAA33128.1 M91374 *Cucumis sativus*

DESCRIPTION: peroxidase. putative.

5 BAA77389.1 AB024439 *Scutellaria baicalensis*
DESCRIPTION: peroxidase 3.

10 BAA77388.1 AB024438 *Scutellaria baicalensis*
DESCRIPTION: peroxidase 2.

AAB02554.1 L37790 *Stylosanthes humilis*
DESCRIPTION: cationic peroxidase.

15 AAF63026.1 AF244923 *Spinacia oleracea*
DESCRIPTION: hydrogen peroxide catabolism. peroxidase prx14 precursor.
type III peroxidase.

20 58

25 AAG49002.1 AY013246 *Hordeum vulgare*
DESCRIPTION: putative ABC transporter. 635P2.4a; GC splice donor
confirmed by cDNA and comparative sequencing.

30 AAG45492.1 AY013245 *Oryza sativa*
DESCRIPTION: 36I5.4. putative ABC transporter; GC splice donor confirmed
by cDNA alignment and comparative sequence.

AAG49003.1 AY013246 *Hordeum vulgare*
DESCRIPTION: putative ABC transporter. 635P2.4b; GC splice donor
confirmed by cDNA alignment and comparative sequence.

35 BAA83352.1 AP000391 *Oryza sativa*
DESCRIPTION: ESTs AU067992(C11433),AU077424(C11433) correspond to
a
40 region of the predicted gene.; Similar to ABC transporter-7 (U43892).

BAB17113.1 AP002866 *Oryza sativa*
DESCRIPTION: putative white protein; ATP-binding cassette transporter.
45 P0410E01.34.

- 5 BAA90508.1 AP001111 *Oryza sativa*
DESCRIPTION: similar to ABC transporter of *Arabidopsis thaliana* (AC004697).
- 10 BAA90507.1 AP001111 *Oryza sativa*
DESCRIPTION: similar to ABC transporter of *Arabidopsis thaliana* (AC004697).
- 15 BAB40032.1 AP003046 *Oryza sativa*
DESCRIPTION: putative ABC transporter. P0445D12.3.
- 20 BAB16495.1 AP002861 *Oryza sativa*
DESCRIPTION: putative ABC transporter ATP-binding protein. P0665D10.21.
- 25 BAA94511.1 AB041505 *Populus nigra*
DESCRIPTION: ABC transporter homolog. PnATH.
- 30 BAB21275.1 AP002844 *Oryza sativa*
DESCRIPTION: putative ABC transporter protein. P0410E03.6.
- 35 BAB21276.1 AP002844 *Oryza sativa*
DESCRIPTION: putative ABC transporter protein. P0410E03.7. contains EST D22472(C1173).
- 40 BAB21279.1 AP002844 *Oryza sativa*
DESCRIPTION: putative ABC transporter protein. P0410E03.10. contains ESTs AU065360(R3463),AU101680(R3463).
- 45 CAA94437.1 Z70524 *Spirodela polyrrhiza*
DESCRIPTION: multidrug resistance protein. PDR5-like ABC transporter.
- 59 BAB21273.1 AP002844 *Oryza sativa*
DESCRIPTION: putative ABC transporter protein. P0410E03.4.

CAA71369.1 Y10338 Solanum tuberosum
DESCRIPTION: chloride channel Stclcl. putative.

5 AAD29679.1 AF133209 Nicotiana tabacum
DESCRIPTION: CLC-Nt2 protein. putative chloride channel.

60

10 BAB40094.1 AP003210 Oryza sativa
DESCRIPTION: putative receptor protein kinase. OSJNBa0010K01.7.

15 AAG52992.1 U77888 Ipomoea nil
DESCRIPTION: receptor-like protein kinase INRPK1a. inrpkl.

20 AAF59906.1 AF197947 Glycine max
DESCRIPTION: receptor protein kinase-like protein. CLV1B.

25 AAC36318.1 AF053127 Malus x domestica
DESCRIPTION: leucine-rich receptor-like protein kinase. LRPKml.

AAF91323.1 AF244889 Glycine max
DESCRIPTION: receptor-like protein kinase 2. RLK2. GmRLK2.

30 AAF91324.1 AF244890 Glycine max
DESCRIPTION: receptor-like protein kinase 3. RLK3. GmRLK3.

35 AAB36558.1 U77888 Ipomoea nil
DESCRIPTION: receptor-like protein kinase INRPK1. inrpkl. leucine-rich repeat.

40 BAA83373.1 AP000391 Oryza sativa
DESCRIPTION: ESTs C22657(S0014),C22656(S0014) correspond to a region of the predicted gene.; Similar to receptor protein kinase, ERECTA (AC004484).

45 BAA84787.1 AP000559 Oryza sativa

DESCRIPTION: ESTs C22557(S0014),C22656(S0014) correspond to a region of the predicted gene.; Similar to receptor protein kinase, ERECTA (AC004484).

5

AAF91322.1 AF244888 Glycine max
DESCRIPTION: receptor-like protein kinase 1. RLK1. GmRLK1.

10

AAF59905.1 AF197946 Glycine max
DESCRIPTION: receptor protein kinase-like protein. CLV1A.

15

AAB61708.1 U93048 Daucus carota
DESCRIPTION: somatic embryogenesis receptor-like kinase. SERK.

20

CAB51480.1 Y14600 Sorghum bicolor
DESCRIPTION: putative protein serine /threonine kinase. RLK1. accumulates in mesophyll cells.

25

CAC20842.1 AJ250467 Pinus sylvestris
DESCRIPTION: receptor protein kinase. upk.

30

CAA61510.1 X89226 Oryza sativa
DESCRIPTION: leucine-rich repeat/receptor protein kinase. lrk2.

35

BAB19337.1 AP003044 Oryza sativa
DESCRIPTION: putative protein kinase. P0038C05.10. contains ESTs AU056335(S20481),AU056336(S20481).

40

AAG52994.1 U77888 Ipomoea nil
DESCRIPTION: receptor-like protein kinase INRPK1c. inrpkl.
BAB40081.1 AP003074 Oryza sativa
DESCRIPTION: putative receptor protein kinase. OSJNBa0004G10.30.

45

BAB18321.1 AP002865 Oryza sativa
DESCRIPTION: putative receptor protein kinase. P0034C11.11.

AAK00425.1 AC069324 *Oryza sativa*
DESCRIPTION: Putative protein kinase. OSJNBa0071K19.11.

5 AAK27817.1 AC022457 *Oryza sativa*
DESCRIPTION: putative protein kinase. OSJNBa0006L06.16.

10 BAA87853.1 AP000816 *Oryza sativa*
DESCRIPTION: EST AU030604(E51294) corresponds to a region of the
predicted gene. Similar to putative NAK-like Ser/Thr protein kinase.
(AF001308).

15 BAB03621.1 AP002522 *Oryza sativa*
DESCRIPTION: putative protein kinase Xa21. P0009G03.21.

20 AAG59657.1 AC084319 *Oryza sativa*
DESCRIPTION: putative protein kinase. OSJNBa0004B24.20.

25 BAB39873.1 AP002882 *Oryza sativa*
DESCRIPTION: putative protein kinase. P0439B06.8. contains ESTs
AU056701(S20808),AU056702(S20808).

30 BAB03429.1 AP002817 *Oryza sativa*
DESCRIPTION: EST C22619(S11214) corresponds to a region of the predicted
gene. Similar to Arabidopsis thaliana chromosome 2, BAC clone T17D12;
putative protein kinase (AC006587).

35 BAB07999.1 AP002525 *Oryza sativa*
DESCRIPTION: putative protein kinase. P0462H08.22. contains EST
C22619(S11214).

40 AAK21965.1 AY028699 *Brassica napus*
DESCRIPTION: receptor protein kinase PERK1.

45 AAG16628.1 AY007545 *Brassica napus*
DESCRIPTION: protein serine/threonine kinase BNK1.

BAA78575.1 AB028132 Oryza sativa
DESCRIPTION: Dof zinc finger protein.

5

AAB70119.1 U82230 Zea mays
DESCRIPTION: transcription factor. prolamin box binding factor. PBF.
endosperm-specific DOF protein; DNA binding.

10

CAA08755.1 AJ009594 Nicotiana tabacum
DESCRIPTION: Dof zinc finger protein. BBF1.

15

CAA66601.1 X97942 Nicotiana tabacum
DESCRIPTION: Zn finger protein. NtBBF1.1.

20

CAA66606.1 X97947 Nicotiana tabacum
DESCRIPTION: Zn finger protein. NtBBF3.

25

BAA78573.1 AB028130 Oryza sativa
DESCRIPTION: Dof zinc finger protein.

30

BAA78572.1 AB028129 Oryza sativa
DESCRIPTION: Dof zinc finger protein.

35

CAA56287.1 X79934 Zea mays
DESCRIPTION: Dof2. No start codon.

CAA66604.1 X97945 Nicotiana tabacum
DESCRIPTION: Zn finger protein. NtBBF2a.

40

CAA66605.1 X97946 Nicotiana tabacum
DESCRIPTION: Zn finger protein. NtBBF2b.

45

BAA78574.1 AB028131 Oryza sativa
DESCRIPTION: Dof zinc finger protein. Rice cDNA for protein that binds to
AT-rich sequence of rice carboxypeptidase-3 promoter.

BAA78576.1 AB028133 *Oryza sativa*
DESCRIPTION: Dof zinc finger protein.

5 68

CAA83453.1 Z31581 *Pisum sativum*
DESCRIPTION: chloroplast outer envelope protein 86.

10

AAA53276.1 L36857 *Pisum sativum*
DESCRIPTION: component of chloroplast outer membrane protein import
apparatus. GTP-binding protein. IAP86.

15

AAF75761.1 AF262939 *Pisum sativum*
DESCRIPTION: chloroplast protein import component Toc159. major receptor
of the chloroplast outer envelope membrane protein import apparatus.

20

AAG48839.1 AC084218 *Oryza sativa*
DESCRIPTION: similar to *Arabidopsis thaliana* putative chloroplast outer
envelope 86-like protein (AC002330).

25

AAC25785.1 L36856 *Pisum sativum*
DESCRIPTION: component of chloroplast outer membrane protein import
apparatus. GTP-binding protein. IAP34.

30

CAB77551.1 AJ271049 *Zea mays*
DESCRIPTION: a component of the protein translocon at the outer envelope
of chloroplast. Toc34-2 protein. toc34B.

35

CAB65537.1 AJ245968 *Zea mays*
DESCRIPTION: a component of the protein translocon at the outer envelope
of chloroplast. Toc34-1 protein. toc34A.

40 70

AAB71887.1 AF020791 *Hordeum vulgare*
DESCRIPTION: inserts Fe²⁺ into protoporphyrin IX. ferrochelatase. hemH.
protoheme IX ferro-lyase.

45

- BAA05101.1 D26105 *Hordeum vulgare*
DESCRIPTION: ferrochelatase. hemH.
- 5 BAA05102.1 D26106 *Cucumis sativus*
DESCRIPTION: ferrochelatase. hemH.
- 10 BAB20760.1 AB037113 *Cucumis sativus*
DESCRIPTION: ferrochelatase. hemH.
- 15 BAA22284.1 AB007120 *Oryza sativa*
DESCRIPTION: ferrochelatase. hemH.
- 20 CAA06705.1 AJ005802 *Solanum tuberosum*
DESCRIPTION: tetrapyrrole biosynthesis. ferrochelatase.
- 25 AAK16728.1 AF332962 *Chlamydomonas reinhardtii*
DESCRIPTION: ferrochelatase.
- 30 AAK16729.1 AF332963 *Polytomella* sp. 'Pringsheim 198.80'
DESCRIPTION: ferrochelatase.
- 71
-
- 35 CAA64442.1 X94986 *Manihot esculenta*
DESCRIPTION: beta glucosidase. bglA.
- 40 AAB22162.1 S35175 *Manihot esculenta*
DESCRIPTION: linamarase. linamarase. beta-glucosidase; Method: conceptual translation with partial peptide sequencing; This sequence comes from Fig. 4.
- 45 AAA93032.1 U50201 *Prunus serotina*
DESCRIPTION: hydrolysis of the cyanogenic glucoside (R)-prunasin. prunasin hydrolase precursor. located in protein bodies of *Prunus* seeds;

encodes 8 putative N-glycosylation sites (N-X-S/T); encodes NEP and ITENG motifs characteristic of the BGA family of beta-glucosidases.

- 5 AAA91166.1 U39228 *Prunus avium*
DESCRIPTION: beta-glucosidase.
- 10 AAF34650.1 AF221526 *Prunus serotina*
DESCRIPTION: hydrolysis of the cyanogenic glucoside (R)-prunasin. prunasin hydrolase isoform PHA precursor. beta-glucosidase; contains 6 potential N-glycosylation sites (N-X-S/T); glycosyl hydrolase family 1 member.
- 15 AAF03675.1 AF149311 *Rauvolfia serpentina*
DESCRIPTION: hydrolyses the glucoalkaloid raucaffricine. raucaffricine-O-beta-D-glucosidase. beta glucosidase; RG; part of the Ajmaline biosynthesis pathway; belongs to family 1 of the glucosyl hydrolases.
- 20 CAA57913.1 X82577 *Brassica napus*
DESCRIPTION: beta-glucosidase. bgl.
- 25 BAA78708.1 AB003089 *Polygonum tinctorium*
DESCRIPTION: beta-glucosidase.
- 30 BAA11831.1 D83177 *Costus speciosus*
DESCRIPTION: saponin metabolite. furostanol glycoside 26-O-beta-glucosidase (F26G). functional expression in *E. coli*; one of the F26G isozymes.
- 35 AAG25897.1 AF170087 *Cucurbita pepo*
DESCRIPTION: silverleaf whitefly-induced protein 3. SLW3. similar to beta-glucosidase.
- 40 AAF04007.1 AF163097 *Dalbergia cochinchinensis*
DESCRIPTION: beta-fucosidase beta-glucosidase. dalcochinin 8'-O-beta-glucoside beta-glucosidase precursor. BGLU1. rotenoid beta-glucosidase.
- 45

- AAC69619.1 AF072736 *Pinus contorta*
DESCRIPTION: beta-glucosidase.
- 5 AAB38784.1 U72154 *Brassica nigra*
DESCRIPTION: beta-glucosidase. psr3.1. PSR3.1; phosphate-starvation responsive enzyme.
- 10 AAD02839.1 AF082991 *Avena sativa*
DESCRIPTION: beta-D-glucosidase beta subunit precursor. P60b. avenacosidase.
- 15 AAA87339.1 L41869 *Hordeum vulgare*
DESCRIPTION: beta-glucosidase. BGQ60. expression specific to starchy endosperm of seed.
- 20 AAB71381.1 U95298 *Manihot esculenta*
DESCRIPTION: linamarase. pLIN-GEN. beta-glucosidase.
- 25 CAA55196.1 X78433 *Avena sativa*
DESCRIPTION: beta-D-glucosidase.
- 30 AAC49177.1 U33817 *Sorghum bicolor*
DESCRIPTION: beta-glucosidase, catalyzes the hydrolysis of the cyanogenic beta-glucoside dhurrin. dhurrinase.
- 35 AAD09850.1 U44087 *Zea mays*
DESCRIPTION: beta-D-glucosidase precursor. glu2. product subunit structure: autodimer of 58.4 kDa monomers Allele: glu2-B73.
- 40 AAG00614.1 AF293849 *Secale cereale*
DESCRIPTION: beta-glucosidase.
- 45 AAF28800.1 AF112888 *Catharanthus roseus*
DESCRIPTION: plays a role in secondary metabolism by hydrolyzing strictosidine to cathenamine during indole alkaloid biosynthesis. strictosidine beta-glucosidase. localized in the endoplasmic reticulum.

- CAA40058.1 X56734 *Trifolium repens*
DESCRIPTION: beta-glucosidase. non-cyanogenic.
- CAA40057.1 X56733 *Trifolium repens*
DESCRIPTION: beta-glucosidase. Li.
- AAD10503.1 U33816 *Zea mays*
DESCRIPTION: functions in defense of young plant parts against pests via the production of hydroxamic acids from hydroxamic acid glucosides. beta-D-glucosidase.
- AAA65946.1 U25157 *Zea mays*
DESCRIPTION: functions in defense of young plant parts against pests via the production of hydroxamic acids from hydroxamic acid glucosides. beta-D-glucosidase.
- CAA52293.1 X74217 *Zea mays*
DESCRIPTION: beta-glucosidase. p60.1.
- AAB03266.1 U44773 *Zea mays*
DESCRIPTION: beta-D-glucosidase. glu1. autodimer of 58.4 kD monomers.
- AAK07429.1 AF321287 *Musa acuminata*
DESCRIPTION: beta-glucosidase.
- CAA79989.2 Z21977 *Brassica napus*
DESCRIPTION: beta thioglucosidase. myrosinase, thioglucoside glucosylhydrolase. Myr1.Bn1.
- AAF34651.1 AF221527 *Prunus serotina*
DESCRIPTION: putative prunasin hydrolase precursor. beta-glucosidase; glycosyl hydrolase family 1 member.
- AAA84906.1 U28047 *Oryza sativa*
DESCRIPTION: catalyzes the release of either giberellin or cyanogenic

substances from their glucoconjugates. beta glucosidase. beta-D-glucoside glucohydrolase; dimer of 60 kDa monomers; localized in the plastid.

5 CAC08209.1 AJ005950 Cicer arietinum
DESCRIPTION: beta-glucosidase.

72

10 CAA56570.1 X80301 Nicotiana tabacum
DESCRIPTION: axi 1.

15 AAB72114.1 U81288 Pisum sativum
DESCRIPTION: PsRT17-1. similar to the Nicotiana tabacum axi 1 gene product encoded by the sequence presented in GenBank Accession Number X80301.

74

20 AAG23130.1 AF198260 Lycopersicon esculentum
DESCRIPTION: diacylglycerol kinase variant A. Dgk1. DGK-1; alternatively spliced.

25 AAG23129.1 AF198259 Lycopersicon esculentum
DESCRIPTION: phosphorylates diacylglycerol to yield phosphatidic acid. diacylglycerol kinase. DGK1. LeDGK1; lipid kinase; non-calmodulin-binding isoform; alternatively spliced product.

30

AAG23131.1 AF198260 Lycopersicon esculentum
DESCRIPTION: diacylglycerol kinase variant B. Dgk1. CBDGK; calmodulin-binding; alternatively spliced.

35

AAG23128.1 AF198258 Lycopersicon esculentum
DESCRIPTION: phosphorylates diacylglycerol to yield phosphatidic acid. calmodulin-binding diacylglycerol kinase. DGK1. LeCBDGK; lipid kinase; alternatively spliced product.

40

75

45 CAC09580.1 AJ298992 Fagus sylvatica
DESCRIPTION: Absciscic acid (ABA) and calcium induced protein kinase. protein kinase (PK). pk1.

5 AAA34002.1 M67449 Glycine max
 DESCRIPTION: protein kinase. PK6.

10 AAG31141.1 AF305911 Oryza sativa
 DESCRIPTION: EDR1. EDR1. MAP kinase kinase kinase; similar to
 Arabidopsis
 thaliana EDR1.

15 AAG31142.1 AF305912 Hordeum vulgare
 DESCRIPTION: EDR1. EDR1. MAP kinase kinase kinase; similar to
 Arabidopsis
 thaliana EDR1.

20 CAA73722.1 Y13273 Lycopersicon esculentum
 DESCRIPTION: putative protein kinase.

25 AAD46406.1 AF096250 Lycopersicon esculentum
 DESCRIPTION: ethylene-responsive protein kinase TCTR1. ER50.
 serine/threonine kinase; similar to Arabidopsis thaliana negative
 regulator of the ethylene response pathway encoded by GenBank Accession
 Number L08789.

30 AAD10056.1 AF110518 Lycopersicon esculentum
 DESCRIPTION: ethylene-inducible CTR1-like protein kinase. protein kinase
 homolog; ethylene and fruit ripening inducible CTR1-like protein kinase;
 TCTR1.

35 AAD10057.1 AF110519 Lycopersicon esculentum
 DESCRIPTION: ethylene-inducible CTR1-like protein kinase. protein kinase
 homolog; ethylene and fruit ripening inducible CTR1-like protein kinase;
 TCTR1v.

40 CAA06334.1 AJ005077 Lycopersicon esculentum
 DESCRIPTION: protein kinase. TCTR2 protein. TCTR2.

45 AAK30005.1 AY029067 Rosa hybrid cultivar

DESCRIPTION: CTR2 protein kinase.

- 5 AAK11734.1 AY027437 *Arachis hypogaea*
DESCRIPTION: serine/threonine/tyrosine kinase.
- 10 CAA73067.1 Y12464 *Sorghum bicolor*
DESCRIPTION: serine/threonine kinase. SNFL1.
- 15 CAA73068.1 Y12465 *Sorghum bicolor*
DESCRIPTION: serine/threonine kinase. SNFL2.
- 20 AAK31267.1 AC079890 *Oryza sativa*
DESCRIPTION: putative protein kinase. OSJNBb0089A17.2.
- 25 AAF66615.1 AF142596 *Nicotiana tabacum*
DESCRIPTION: LRR receptor-like protein kinase.
- 30 BAB39451.1 AP003338 *Oryza sativa*
DESCRIPTION: putative receptor kinase. OJ1212_B09.24.
- 35 BAB17126.1 AP002867 *Oryza sativa*
DESCRIPTION: putative receptor kinase. P0463F06.16.
- 40 BAB17321.1 AP002747 *Oryza sativa*
DESCRIPTION: putative receptor kinase. P0698G03.1.
- 45 AAF68398.1 AF237568 *Oryza sativa*
DESCRIPTION: receptor-like protein kinase. RLG2.
- BAB17129.1 AP002867 *Oryza sativa*
DESCRIPTION: putative receptor kinase. P0463F06.20.
- BAB17348.1 AP002747 *Oryza sativa*
DESCRIPTION: putative receptor kinase. P0698G03.32.

DESCRIPTION: receptor protein kinase-like protein. CLV1A.

5 AAF91323.1 AF244889 Glycine max
DESCRIPTION: receptor-like protein kinase 2. RLK2. GmRLK2.

10 AAD46917.1 AF164021 Oryza sativa
DESCRIPTION: receptor kinase.

15 AAF59906.1 AF197947 Glycine max
DESCRIPTION: receptor protein kinase-like protein. CLV1B.

AAF78018.1 AF238474 Oryza sativa
DESCRIPTION: receptor-like kinase. RLG16. protein kinase.

20 BAB39438.1 AP003338 Oryza sativa
DESCRIPTION: putative receptor kinase. OJ1212_B09.7.

25 BAA05649.1 D26602 Nicotiana tabacum
DESCRIPTION: protein kinase.

30 AAC01746.1 AF044489 Oryza sativa
DESCRIPTION: receptor-like protein kinase. drpk1.

CAA71142.1 Y10036 Cucumis sativus
DESCRIPTION: SNF1-related protein kinase.

35 AAA62232.1 U00443 Brassica napus
DESCRIPTION: S-receptor kinase. protein contains an immunoglobulin-like domain.

40 CAA61510.1 X89226 Oryza sativa
DESCRIPTION: leucine-rich repeat/receptor protein kinase. lrk2.

77
45 -----
AAD03693.1 AF084554 Brassica napus

DESCRIPTION: fibrillin.

CAA10372.1 AJ131455 Plastid Solanum demissum
5 DESCRIPTION: carotenoid-associated. fibrillin. c40.4.

CAA50750.1 X71952 Capsicum annuum
10 DESCRIPTION: fibrillin.
79

AAB53155.1 U43629 Beta vulgaris
15 DESCRIPTION: putative sugar transporter. integral membrane protein.
member of major facilitator superfamily.

AAF74566.1 AF215852 Nicotiana tabacum
20 DESCRIPTION: transport of hexoses across the plastid inner envelope
membrane. hexose transporter. pGlcT.

AAG00995.1 AF286906 Mesembryanthemum crystallinum
25 DESCRIPTION: putative glucose translocator. metabolite transporter;
targeted to plastid inner envelope membrane.

AAF74565.1 AF215851 Spinacia oleracea
30 DESCRIPTION: transport of hexoses across the plastid inner envelope
membrane. hexose transporter. pGlcT.

AAF74567.1 AF215853 Solanum tuberosum
35 DESCRIPTION: transport of hexoses across the plastid inner envelope
membrane. hexose transporter. pGlcT.

AAF74568.1 AF215854 Zea mays
40 DESCRIPTION: transport of hexoses across the plastid inner envelope
membrane. hexose transporter. pGlcT.

AAG46179.1 AC018727 Oryza sativa
45 DESCRIPTION: putative sugar transporter protein. OSJNBa0056G17.3.

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- AAB88879.1 AF00952 *Prunus armeniaca*
DESCRIPTION: putative sugar transporter.
- 5 AAG43998.1 AF215837 *Apium graveolens* var. dulce
DESCRIPTION: mannitol transporter. Mat1.
- 10 CAA68813.1 Y07520 *Chlorella kessleri*
DESCRIPTION: H(+)/hexose cotransporter (AA 1-533).
- 15 CAA53192.1 X75440 *Chlorella kessleri*
DESCRIPTION: hexose transporter like protein. HUP3.
- 20 CAB52689.1 AJ132224 *Lycopersicon esculentum*
DESCRIPTION: hexose transporter. ht2.
- CAA39036.1 X55349 *Chlorella kessleri*
DESCRIPTION: H(+)/hexose-cotransporter. HUP1.
- 25 CAA47324.1 X66856 *Nicotiana tabacum*
DESCRIPTION: monosaccharid transporter. MST1.
- 30 AAB68028.1 U64902 *Beta vulgaris*
DESCRIPTION: BvcDNA-205. putative sugar transporter; member of major facilitative superfamily; integral membrane protein.
- 35 AAB68029.1 U64903 *Beta vulgaris*
DESCRIPTION: BvcDNA-397. putative sugar transporter; member of major facilitative superfamily; integral membrane protein.
- 40 CAA09419.1 AJ010942 *Lycopersicon esculentum*
DESCRIPTION: hexose transporter protein.
- 45 CAB07812.1 Z93775 *Vicia faba*
DESCRIPTION: sugar transport. monosaccharid transport protein. hext.

- BAB19864.1 AB052885 *Oryza sativa*
DESCRIPTION: monosaccharide transporter 3. OsmST3.
- 5 AAA79761.1 L08196 *Ricinus communis*
DESCRIPTION: hexose transport. sugar carrier protein. RCSTC.
- 10 AAK13147.1 AC083945 *Oryza sativa*
DESCRIPTION: Putative sugar transporter. OSJNBa0058E19.22.
- 15 AAB06594.1 U38651 *Medicago truncatula*
DESCRIPTION: sugar transporter.
- 20 CAA04511.1 AJ001061 *Vitis vinifera*
DESCRIPTION: hexose uptake. hexose transporter.
- AAC61852.1 AF061106 *Petunia x hybrida*
DESCRIPTION: putative monosaccharide transporter 1. pmt1. similar to hexose transporter protein; PMT1.
- 25 CAA70777.1 Y09590 *Vitis vinifera*
DESCRIPTION: hexose transporter.
- 30 AAA79769.1 L08197 *Ricinus communis*
DESCRIPTION: sugar transport. sugar carrier protein. RCSTA. putative.
- 35 CAB06079.1 Z83829 *Picea abies*
DESCRIPTION: monosaccharide transporter. PaMst-1. PaMst-1.
- 40 AAA18534.1 L21753 *Saccharum hybrid cultivar H65-7052*
DESCRIPTION: glucose transporter. putative.
- CAC00697.1 AJ278765 *Lycopersicon esculentum*
DESCRIPTION: putative sugar transporter. st3.
- 45 AAA79857.1 L08188 *Ricinus communis*

DESCRIPTION: hexose transport. hexose carrier protein. HEX6.

BAB19863.1 AB052884 Oryza sativa

5 DESCRIPTION: monosaccharide transporter 2. OsMST2.

BAB19862.1 AB052883 Oryza sativa

10 DESCRIPTION: monosaccharide transporter 1. OsMST1.

AAF91432.1 AF280432 Mesembryanthemum crystallinum

15 DESCRIPTION: putative Na⁺/myo-inositol symporter. Itr2. membrane transport protein.

CAB52688.1 AJ132223 Lycopersicon esculentum

20 DESCRIPTION: hexose transporter. ht1.

BAA85398.1 AP000615 Oryza sativa

DESCRIPTION: similar to sugar transporter protein. (AL022604).

25 AAG46115.1 AC073166 Oryza sativa

DESCRIPTION: putative sugar transporter. OSJNBb0064P21.3.

CAB52690.1 AJ132225 Lycopersicon esculentum

30 DESCRIPTION: hexose transporter. ht3.

AAA18533.1 L21752 Saccharum hybrid cultivar H65-7052

35 DESCRIPTION: glucose transporter. putative.

AAD55054.1 AF173655 Beta vulgaris

DESCRIPTION: glucose transporter. Gt.

40

BAB39246.1 AP002869 Oryza sativa

DESCRIPTION: putative transport protein homolog. P0554D10.30.

45 AAA79764.1 L08191 Ricinus communis

DESCRIPTION: sugar transport. sugar carrier protein. RCSTC. Nucleotides 1

to 23 and 226 to 246 are originated from degenerated primers; putative.

5 AAA79762.1 L08189 Ricinus communis
DESCRIPTION: sugar transport. sugar carrier protein. RCSTA. Nucleotides 1 to 23 and 226 to 246 are originated from degenerated primers; putative.

10 AAA79767.1 L08194 Ricinus communis
DESCRIPTION: sugar transport. sugar carrier protein. RCSTG. Nucleotides 1 to 23 and 226 to 246 are originated from degenerated primers; putative.

15 AAA79766.1 L08193 Ricinus communis
DESCRIPTION: sugar transport. sugar carrier protein. RCSTF. Nucleotides 1 to 23 and 226 to 246 are originated from degenerated primers; putative.

82

20 CAA78386.1 Z13996 Petunia x hybrida
DESCRIPTION: DNA binding protein; transcriptional activator. protein 1. myb.Ph3. Product related to animal myb proto-oncoproteins. Sequence from nucleotide 992 is not included in clone cPF1 and has been obtained by PCR amplification of cDNA.

25 CAB43399.1 AJ006292 Antirrhinum majus
DESCRIPTION: Myb-related transcription factor mixta-like 1. mybm11.

30 CAA67600.1 X99210 Lycopersicon esculentum
DESCRIPTION: myb-related transcription factor. THM16.

35 BAA93038.1 AP001552 Oryza sativa
DESCRIPTION: EST AU082058(C12976) corresponds to a region of the predicted gene. Similar to Arabidopsis thaliana putative transcription factor (AF062916).

40 BAA23337.1 D88617 Oryza sativa
DESCRIPTION: transfactor. OSMYB1. Osmyb1.

45 CAA64614.1 X95296 Lycopersicon esculentum
DESCRIPTION: transcription factor. THM27. myb-related.

- CAA72186.1 Y11351 *Oryza sativa*
 DESCRIPTION: myb factor. myb.
 5
- AAF22256.1 AF161711 *Pimpinella brachycarpa*
 DESCRIPTION: myb-related transcription factor.
 10
- AAC04720.1 AF034134 *Gossypium hirsutum*
 DESCRIPTION: putative MYB-like transcription factor. MYB-like DNA-binding
 domain protein. CmY-O. similar to MYB A encoded by GenBank Accession
 Number L04497.
 15
- AAA82943.1 U39448 *Picea mariana*
 DESCRIPTION: MYB-like transcriptional factor MBF1. putative DNA binding
 region highly similar to the maize C1.
 20
- BAB39987.1 AP003020 *Oryza sativa*
 DESCRIPTION: putative transcription factor (myb). P0498A12.16. contains
 ESTs AU097474(S5087),D40175(S1959).
 25
- BAB39972.1 AP003018 *Oryza sativa*
 DESCRIPTION: putative transcription factor (myb). OSJNBa0004B13.27.
 contains ESTs AU097474(S5087),D40175(S1959).
 30
- BAA23338.1 D88618 *Oryza sativa*
 DESCRIPTION: transfactor. OSMYB2. OsmYb2.
 35
- CAA67575.1 X99134 *Lycopersicon esculentum*
 DESCRIPTION: transcription factor. THM6. myb-related.
 40
- CAA78387.1 Z13997 *Petunia x hybrida*
 DESCRIPTION: DNA-binding protein, transcriptional activator. protein 2.
 myb.Ph2. related to animal myb proto-oncoproteins.
 45
- AAA19821.1 L19495 *Zea mays*

DESCRIPTION: transcriptional activator for anthocyanin synthesis.
transcriptional activator.

- 5 AAC49394.1 U57002 Zea mays
DESCRIPTION: P protein. P. allele P-wr; Myb-like transcriptional
regulator with a putative zinc-finger at the C-terminal.
- 10 AAA33500.1 M73028 Zea mays
DESCRIPTION: myb-like transcription factor. P.
- 15 AAG36774.1 AF210616 Zea mays
DESCRIPTION: P2 protein. P2. myb-like transcriptional factor; similar to
Zea mays P gene.
- 20 BAA88222.1 AB028650 Nicotiana tabacum
DESCRIPTION: myb-related transcription factor LBM2. lbm2.
- 25 CAA72185.1 Y11350 Oryza sativa
DESCRIPTION: myb factor. myb.
- 30 AAG13574.1 AC037425 Oryza sativa
DESCRIPTION: myb factor. OSJNBa0055P24.4.
- 35 AAB41101.1 U72762 Nicotiana tabacum
DESCRIPTION: transcription factor Myb1. myb1. TMV-inducible Myb
homolog;
contains helix-turn-helix motif; contains redox-sensitive cysteine.
- 40 BAA88223.1 AB028651 Nicotiana tabacum
DESCRIPTION: myb-related transcription factor LBM3. lbm3.
- 45 AAA19819.1 L19496 Zea mays
DESCRIPTION: transcriptional activator for anthocyanin synthesis.
transcriptional activator.
- BAA88224.1 AB028652 Nicotiana tabacum

DESCRIPTION: myb-related transcription factor LBM4. lbm4.

5 AAB67720.1 AF015268 Zea mays
DESCRIPTION: activator of anthocyanin structural genes. PL transcription factor. Pl.

10 AAA33492.1 L13454 Zea mays
DESCRIPTION: transcriptional activator for anthocyanin biosynthesis. Pl-Bh (Blotched1).

83

15 CAA78387.1 Z13997 Petunia x hybrida
DESCRIPTION: DNA-binding protein, transcriptional activator. protein 2. myb.Ph2. related to animal myb proto-oncoproteins.

20 BAA81736.1 AB029165 Glycine max
DESCRIPTION: GmMYB29B2.

25 BAA81732.1 AB029161 Glycine max
DESCRIPTION: GmMYB29A2.

30 BAA81731.1 AB029160 Glycine max
DESCRIPTION: GmMYB29A1.

BAA81730.1 AB029159 Glycine max
DESCRIPTION: GmMYB29A1.

35 BAA88221.1 AB028649 Nicotiana tabacum
DESCRIPTION: myb-related transcription factor LBM1. lbm1.

40 BAA88224.1 AB028652 Nicotiana tabacum
DESCRIPTION: myb-related transcription factor LBM4. lbm4.

45 CAA66952.1 X98308 Lycopersicon esculentum
DESCRIPTION: THM18. myb-related transcription factor.

BAA81733.2 AB029162 Glycine max
DESCRIPTION: GmMYB29A2.

5

CAA72217.1 Y11414 Oryza sativa
DESCRIPTION: myb.

10 BAA88222.1 AB028650 Nicotiana tabacum
DESCRIPTION: myb-related transcription factor LBM2. lbm2.

15 AAB41101.1 U72762 Nicotiana tabacum
DESCRIPTION: transcription factor Myb1. myb1. TMV-inducible Myb
homolog;
contains helix-turn-helix motif; contains redox-sensitive cysteine.

20 BAA88223.1 AB028651 Nicotiana tabacum
DESCRIPTION: myb-related transcription factor LBM3. lbm3.

25 CAA72185.1 Y11350 Oryza sativa
DESCRIPTION: myb factor. myb.

30 AAG13574.1 AC037425 Oryza sativa
DESCRIPTION: myb factor. OSJNBa0055P24.4.

35 AAK19616.1 AF336283 Gossypium hirsutum
DESCRIPTION: GHMYB25. ghmyb25. similar to myb; contains an unspliced
intron.

40 CAA78386.1 Z13996 Petunia x hybrida
DESCRIPTION: DNA binding protein; transcriptional activator. protein 1.
myb.Ph3. Product related to animal myb proto-oncoproteins. Sequence from
nucleotide 992 is not included in clone cPF1 and has been obtained by PCR
amplification of cDNA.

45 CAA72218.1 Y11415 Oryza sativa
DESCRIPTION: myb.

- AAK19615.1 AF336282 *Gossypium hirsutum*
DESCRIPTION: GHMYB10. ghmyb10. similar to myb.
- 5 AAK19618.1 AF336285 *Gossypium hirsutum*
DESCRIPTION: GHMYB38. ghmyb38. similar to myb.
- 10 CAA72186.1 Y11351 *Oryza sativa*
DESCRIPTION: myb factor. myb.
- 15 CAA64614.1 X95296 *Lycopersicon esculentum*
DESCRIPTION: transcription factor. THM27. myb-related.
- 20 CAA50221.1 X70876 *Hordeum vulgare*
DESCRIPTION: MybHv5. myb2.
- 25 BAA23338.1 D88618 *Oryza sativa*
DESCRIPTION: transfactor. OSMYB2. Osmyb2.
- 30 AAK19619.1 AF336286 *Gossypium hirsutum*
DESCRIPTION: GHMYB9. ghmyb9. similar to myb.
- 35 AAA82943.1 U39448 *Picea mariana*
DESCRIPTION: MYB-like transcriptional factor MBF1. putative DNA binding region highly similar to the maize C1.
- 40 AAC04720.1 AF034134 *Gossypium hirsutum*
DESCRIPTION: putative MYB-like transcription factor. MYB-like DNA-binding domain protein. Cmy-O. similar to MYB A encoded by GenBank Accession Number L04497.
- 45 AAK19611.1 AF336278 *Gossypium hirsutum*
DESCRIPTION: BNLGHi233. bnlghi6233. similar to myb.
- 45 BAA23337.1 D88617 *Oryza sativa*
DESCRIPTION: transfactor. OSMYB1. Osmyb1.

5 BAB39987.1 AP003020 Oryza sativa
DESCRIPTION: putative transcription factor (myb). P0498A12.16. contains
ESTs AU097474(S5087),D40175(S1959).

10 BAB39972.1 AP003018 Oryza sativa
DESCRIPTION: putative transcription factor (myb). OSJNBa0004B13.27.
contains ESTs AU097474(S5087),D40175(S1959).

15 CAA65525.1 X96749 Oryza sativa
DESCRIPTION: myb7.

20 AAK19617.1 AF336284 Gossypium hirsutum
DESCRIPTION: GHMYB36. ghmyb36. similar to myb.

CAA67575.1 X99134 Lycopersicon esculentum
DESCRIPTION: transcription factor. THM6. myb-related.

25 CAA50224.1 X70879 Hordeum vulgare
DESCRIPTION: MybHv1. myb1.

84

30 -----
BAA88222.1 AB028650 Nicotiana tabacum
DESCRIPTION: myb-related transcription factor LBM2. lbm2.

35 BAA88221.1 AB028649 Nicotiana tabacum
DESCRIPTION: myb-related transcription factor LBM1. lbm1.

40 BAA88224.1 AB028652 Nicotiana tabacum
DESCRIPTION: myb-related transcription factor LBM4. lbm4.

45 CAA78387.1 Z13997 Petunia x hybrida
DESCRIPTION: DNA-binding protein, transcriptional activator. protein 2.
myb.Ph2. related to animal myb proto-oncoproteins.

CAA66952.1 X98308 *Lycopersicon esculentum*
DESCRIPTION: THM18. myb-related transcription factor.

5 AAB41101.1 U72762 *Nicotiana tabacum*
DESCRIPTION: transcription factor Myb1. myb1. TMV-inducible Myb
homolog;
contains helix-turn-helix motif; contains redox-sensitive cysteine.

10 BAA88223.1 AB028651 *Nicotiana tabacum*
DESCRIPTION: myb-related transcription factor LBM3. lbm3.

15 BAA81733.2 AB029162 *Glycine max*
DESCRIPTION: GmMYB29A2.

20 BAA81731.1 AB029160 *Glycine max*
DESCRIPTION: GmMYB29A1.

25 BAA81730.1 AB029159 *Glycine max*
DESCRIPTION: GmMYB29A1.

BAA81736.1 AB029165 *Glycine max*
DESCRIPTION: GmMYB29B2.

30 CAA72217.1 Y11414 *Oryza sativa*
DESCRIPTION: myb.

35 BAA81732.1 AB029161 *Glycine max*
DESCRIPTION: GmMYB29A2.

40 CAA72185.1 Y11350 *Oryza sativa*
DESCRIPTION: myb factor. myb.

45 AAG13574.1 AC037425 *Oryza sativa*
DESCRIPTION: myb factor. OSJNBa0055P24.4.

CAA72218.1 Y11415 Oryza sativa
DESCRIPTION: myb.

5 CAA78386.1 Z13996 Petunia x hybrida
DESCRIPTION: DNA binding protein; transcriptional activator. protein 1.
myb.Ph3. Product related to animal myb proto-oncoproteins. Sequence from
nucleotide 992 is not included in clone cPF1 and has been obtained by PCR
amplification of cDNA.

10

AAC49394.1 U57002 Zea mays
DESCRIPTION: P protein. P. allele P-wr; Myb-like transcriptional
regulator with a putative zinc-finger at the C-terminal.

15

CAB43399.1 AJ006292 Antirrhinum majus
DESCRIPTION: Myb-related transcription factor mixta-like 1. mybml1.

20

AAK19616.1 AF336283 Gossypium hirsutum
DESCRIPTION: GHMYB25. ghmyb25. similar to myb; contains an unspliced
intron.

25

AAG36774.1 AF210616 Zea mays
DESCRIPTION: P2 protein. P2. myb-like transcriptional factor; similar to
Zea mays P gene.

30

AAA33500.1 M73028 Zea mays
DESCRIPTION: myb-like transcription factor. P.

35 CAA68235.1 X99973 Hordeum vulgare
DESCRIPTION: myb4 transcription factor. myb4.

40 CAA72187.1 Y11352 Oryza sativa
DESCRIPTION: myb factor. myb.

AAA33067.1 L04497 Gossypium hirsutum
DESCRIPTION: MYB A; putative.

45

- CAA72186.1 Y11351 *Oryza sativa*
DESCRIPTION: myb factor. myb.
- 5 CAA67600.1 X99210 *Lycopersicon esculentum*
DESCRIPTION: myb-related transcription factor. THM16.
- 10 AAK19618.1 AF336285 *Gossypium hirsutum*
DESCRIPTION: GHMYB38. ghmyb38. similar to myb.
- 15 AAK19611.1 AF336278 *Gossypium hirsutum*
DESCRIPTION: BNLGHi233. bnlghi6233. similar to myb.
- 20 AAC04718.1 AF034132 *Gossypium hirsutum*
DESCRIPTION: putative MYB-like transcription factor. MYB-like DNA-binding
domain protein. CmY-J. similar to MYB A encoded by GenBank Accession
Number L04497.
- 25 AAK19619.1 AF336286 *Gossypium hirsutum*
DESCRIPTION: GHMYB9. ghmyb9. similar to myb.
- 30 AAK19615.1 AF336282 *Gossypium hirsutum*
DESCRIPTION: GHMYB10. ghmyb10. similar to myb.
- 35 CAA64614.1 X95296 *Lycopersicon esculentum*
DESCRIPTION: transcription factor. THM27. myb-related.
- 40 BAA23338.1 D88618 *Oryza sativa*
DESCRIPTION: transfactor. OSMYB2. Osmyb2.
- 45 BAA23337.1 D88617 *Oryza sativa*
DESCRIPTION: transfactor. OSMYB1. Osmyb1.
- CAA67575.1 X99134 *Lycopersicon esculentum*
DESCRIPTION: transcription factor. THM6. myb-related.

- CAA65525.1 X96749 *Oryza sativa*
DESCRIPTION: myb7.
- 5 BAB39987.1 AP003020 *Oryza sativa*
DESCRIPTION: putative transcription factor (myb). P0498A12.16. contains
ESTs AU097474(S5087),D40175(S1959).
- 10 BAB39972.1 AP003018 *Oryza sativa*
DESCRIPTION: putative transcription factor (myb). OSJNBa0004B13.27.
contains ESTs AU097474(S5087),D40175(S1959).
- 15 CAA50221.1 X70876 *Hordeum vulgare*
DESCRIPTION: MybHv5. myb2.
- 20 AAA82943.1 U39448 *Picea mariana*
DESCRIPTION: MYB-like transcriptional factor MBF1. putative DNA binding
region highly similar to the maize C1.
- 25 AAF22256.1 AF161711 *Pimpinella brachycarpa*
DESCRIPTION: myb-related transcription factor.
- 30 AAK19617.1 AF336284 *Gossypium hirsutum*
DESCRIPTION: GHMYB36. ghmyb36. similar to myb.
- CAA50222.1 X70877 *Hordeum vulgare*
DESCRIPTION: MybHv1. myb1.
- 35 CAA50224.1 X70879 *Hordeum vulgare*
DESCRIPTION: MybHv1. myb1.
- 40 85

AAD11575.1 AF064029 *Helianthus tuberosus*
DESCRIPTION: lectin 1. LECHeltubal; agglutinin.
- 45 AAD11578.1 AF064030 *Helianthus tuberosus*

DESCRIPTION: lectin 2. LECHeltuba2; agglutinin.

5 AAD11577.1 AF064032 Helianthus tuberosus
DESCRIPTION: lectin HE17.

10 AAG10403.1 AF233284 Convolvulus arvensis
DESCRIPTION: mannose-binding lectin. cr8. Conarva.

AAD11576.1 AF064031 Helianthus tuberosus
DESCRIPTION: lectin 3.

15 AAB82776.2 AF001527 Musa acuminata
DESCRIPTION: ripening-associated protein. similar to lectin.

20 AAC49564.1 U56820 Calystegia sepium
DESCRIPTION: lectin.

25 CAB40792.1 AJ237754 Hordeum vulgare
DESCRIPTION: putative lectin. hl#2.

88

30 AAB65163.1 AF002692 Solanum commersonii
DESCRIPTION: glutathione S-transferase, class-phi. GST1. low temperature
induced.

35 CAA55039.1 X78203 Hyoscyamus muticus
DESCRIPTION: glutathione transferase.

40 AAA33930.1 M84968 Silene vulgaris
DESCRIPTION: glutathione-S-transferase.

AAA33931.1 M84969 Silene vulgaris
DESCRIPTION: glutathione-S-transferase.

45 AAF65767.1 AF242309 Euphorbia esula

DESCRIPTION: glutathione S-transferase. putative auxin-binding GST.

5 BAA01394.1 D10524 *Nicotiana tabacum*
DESCRIPTION: glutathione S-transferase. parB.

10 CAA96431.1 Z71749 *Nicotiana plumbaginifolia*
DESCRIPTION: glutathione S-transferase.

AAF61392.1 AF133894 *Persea americana*
DESCRIPTION: glutathione S-transferase. GTH.

15 CAB38119.1 AJ010296 *Zea mays*
DESCRIPTION: Glutathione transferase III(b). gst3b.

20 CAB38118.1 AJ010295 *Zea mays*
DESCRIPTION: Glutathione transferase III(a). gst3a.

25 BAB39935.1 AP002914 *Oryza sativa*
DESCRIPTION: putative glutathione S-transferase. P0493G01.17.

30 CAA09190.1 AJ010451 *Alopecurus myosuroides*
DESCRIPTION: glutathione transferase. GST2a.

CAA09192.1 AJ010453 *Alopecurus myosuroides*
DESCRIPTION: glutathione transferase. GST2c.

35 CAA09193.1 AJ010454 *Alopecurus myosuroides*
DESCRIPTION: glutathione transferase. GST2d.

40 CAA09191.1 AJ010452 *Alopecurus myosuroides*
DESCRIPTION: glutathione transferase. GST2b.

45 BAB39941.1 AP002914 *Oryza sativa*
DESCRIPTION: putative glutathione S-transferase. P0493G01.23.

CAA39480.1 X56004 *Triticum aestivum*
DESCRIPTION: glutathione transferase, gstA2.

5 AAA33469.1 M16902 *Zea mays*
DESCRIPTION: glutathione S-transferase I.

10 AAG32475.1 AF309382 *Oryza sativa* subsp. *japonica*
DESCRIPTION: putative glutathione S-transferase OsGSTF5.

15 AAA33470.1 M16901 *Zea mays*
DESCRIPTION: glutathione S-transferase I.

AAG32477.1 AF309384 *Oryza sativa* subsp. *japonica*
DESCRIPTION: putative glutathione S-transferase OsGSTF3.

20 CAA68993.1 Y07721 *Petunia x hybrida*
DESCRIPTION: conjugates glutathione to anthocyanin to facilitate
transport to the vacuole. glutathione S-transferase. an9 locus.

25 BAB39940.1 AP002914 *Oryza sativa*
DESCRIPTION: putative glutathione S-transferase. P0493G01.22.

30 AAC64007.1 AF062403 *Oryza sativa*
DESCRIPTION: glutathione S-transferase II.

35 AAG34823.1 AF244680 *Zea mays*
DESCRIPTION: glutathione S-transferase GST 15.

40 AAG34817.1 AF244674 *Zea mays*
DESCRIPTION: glutathione S-transferase GST 9.

CAB66333.1 AJ279691 *Betula pendula*
DESCRIPTION: glutathione-S-transferase. gst.

45 AAG34820.1 AF244677 *Zea mays*

DESCRIPTION: glutathione S-transferase GST 11.

5 AAG34821.1 AF244678 Zea mays
DESCRIPTION: glutathione S-transferase GST 13.

10 CAA05354.1 AJ002380 Oryza sativa
DESCRIPTION: glutathione S-transferase. Rgst I.

15 AAG34816.1 AF244673 Zea mays
DESCRIPTION: glutathione S-transferase GST 8.

AAG34818.1 AF244675 Zea mays
DESCRIPTION: glutathione S-transferase GST 10.

20 CAA05355.1 AJ002381 Oryza sativa
DESCRIPTION: glutathione S-transferase. Rgst II.

25 AAG34824.1 AF244681 Zea mays
DESCRIPTION: glutathione S-transferase GST 16.

91

30 AAG34695.1 AF313492 Matthiola incana
DESCRIPTION: putative cytochrome P450.

35 CAA71516.1 Y10492 Glycine max
DESCRIPTION: putative cytochrome P450.

BAA12159.1 D83968 Glycine max
DESCRIPTION: Cytochrome P-450 (CYP93A1).

40 AAC32274.1 AF081575 Petunia x hybrida
DESCRIPTION: flavonoid 3',5'-hydroxylase. Hfl. P450 enzyme.

45 AAA32913.1 M32885 Persea americana
DESCRIPTION: cytochrome P-450LXXIA1 (cyp71A1).

- 5 BAA13076.1 D86351 Glycine max
DESCRIPTION: cytochrome P-450 (CYP93A2).
- CAA64635.1 X95342 Nicotiana tabacum
DESCRIPTION: cytochrome P450. hsr515. hypersensitivity-related gene.
- 10 CAA65580.1 X96784 Nicotiana tabacum
DESCRIPTION: cytochrome P450. hsr515.
- 15 AAD56282.1 AF155332 Petunia x hybrida
DESCRIPTION: flavonoid 3'-hydroxylase. Ht1. cytochrome P450; CYP75B2.
- 20 BAB12433.1 AB025030 Coptis japonica
DESCRIPTION: p450.
- AAG44132.1 AF218296 Pisum sativum
DESCRIPTION: cytochrome P450. P450 isolog.
- 25 CAA50155.1 X70824 Solanum melongena
DESCRIPTION: flavonoid hydroxylase (P450). CYP75.
- 30 AAB17562.1 U72654 Eustoma grandiflorum
DESCRIPTION: flavonoid 3'5'-hydroxylase. F3'5'H. cytochrome P450; CYP75.
- 35 AAF05621.1 AF191772 Papaver somniferum
DESCRIPTION: hydroxylase involved in benzylisoquinoline alkaloid
biosynthesis. (S)-N-methylcoclaurine 3'-hydroxylase. CYP80B1. cytochrome
P450-dependent monooxygenase.
- 40 CAB56503.1 AJ238612 Catharanthus roseus
DESCRIPTION: cytochrome P450.
- 45 CAA70575.1 Y09423 Nepeta racemosa
DESCRIPTION: cytochrome P450. CYP71A5.

- 5 BAA74466.1 AB022733 *Glycyrrhiza echinata*
DESCRIPTION: cytochrome P450. CYP Ge-51.
- CAA50648.1 X71657 *Solanum melongena*
DESCRIPTION: P450 hydroxylase.
- 10 BAA22423.1 AB001380 *Glycyrrhiza echinata*
DESCRIPTION: cytochrome P450. CYP93B1.
- 15 BAB40324.1 AB037245 *Asparagus officinalis*
DESCRIPTION: cytochrome P450. ASPI-2.
- 20 AAB94588.1 AF022459 *Glycine max*
DESCRIPTION: CYP71D10p. CYP71D10. cytochrome P450 monooxygenase.
- 25 AAG14961.1 AF214007 *Brassica napus*
DESCRIPTION: cytochrome p450-dependent monooxygenase. BNF5H1.
- BAB40323.1 AB037244 *Asparagus officinalis*
DESCRIPTION: cytochrome P450. ASPI-1.
- 30 AAB61965.1 U48435 *Solanum chacoense*
DESCRIPTION: putative cytochrome P450.
- 35 AAC39452.1 AF014800 *Eschscholzia californica*
DESCRIPTION: hydroxylase involved in the biosynthesis of
tetrahydrobenzylisoquinoline alkaloids in plants. (S)-N-methylcoclaurine
3'-hydroxylase. CYP80B1. cytochrome P-450-dependent monooxygenase;
CYP80B1v1.
- 40 AAG14962.1 AF214008 *Brassica napus*
DESCRIPTION: cytochrome p450-dependent monooxygenase. BNF5H2.
- 45 BAA84072.1 AB028152 *Torenia hybrida*

DESCRIPTION: flavone synthase II. cytochrome P450. TFNS5.

AAC39453.1 AF014801 *Eschscholzia californica*

5 DESCRIPTION: hydroxylase involved in the biosynthesis of tetrahydrobenzylisoquinoline alkaloids in plants. (S)-N-methylcoclaurine 3'-hydroxylase. CYP80B1. cytochrome P-450-dependent monooxygenase; CYP80B1v2.

10

AAD47832.1 AF166332 *Nicotiana tabacum*

DESCRIPTION: cytochrome P450.

92

15

AAG42490.1 AF321001 *Suaeda maritima* subsp. *salsa*

DESCRIPTION: S-adenosylmethionine synthetase 2.

20

AAG17666.1 AF271220 *Brassica juncea*

DESCRIPTION: S-adenosylmethionine synthetase. MSAMS2.

25

BAA96637.1 AP002482 *Oryza sativa*

DESCRIPTION: Similar to *Oryza sativa* S-adenosylmethionine synthetase 1 (P46611).

30

AAG17036.1 AF187821 *Pinus contorta*

DESCRIPTION: catalyzes the reaction between methionine and ATP to S-adenosylmethionine. S-adenosylmethionine synthetase. sams2.

35

BAA94605.1 AB041534 *Camellia sinensis*

DESCRIPTION: s-adenosylmethionine synthetase. SAM.

40

AAA81377.1 U17239 *Actinidia chinensis*

DESCRIPTION: S-adenosylmethionine synthetase.

45

AAB38500.1 U79767 *Mesembryanthemum crystallinum*

DESCRIPTION: S-adenosylmethionine synthetase. methionine adenosyltransferase.

- AAA81378.1 U17240 *Actinidia chinensis*
DESCRIPTION: S-adenosylmethionine synthetase.
- 5 BAA09895.1 D63835 *Hordeum vulgare*
DESCRIPTION: S-adenosylmethionine synthetase.
- 10 AAA33274.1 M61882 *Dianthus caryophyllus*
DESCRIPTION: S-adenosylmethionine synthetase. CARSAM2.
- 15 AAA58773.1 L36681 *Pisum sativum*
DESCRIPTION: S-adenosylmethionine synthase. precursor for ethylene and polyamine biosynthesis.
- 20 AAA58772.1 L36680 *Pisum sativum*
DESCRIPTION: precursor for ethylene and polyamine biosynthesis. S-adenosylmethionine synthase.
- 25 AAA81379.1 U17241 *Actinidia chinensis*
DESCRIPTION: S-adenosylmethionine synthetase.
- 30 AAA33857.1 M62758 *Petroselinum crispum*
DESCRIPTION: S-adenosylmethionine synthetase. SMS-1.
- AAG17035.1 AF187820 *Pinus contorta*
DESCRIPTION: catalyzes the reaction between methionine and ATP to S-adenosylmethionine. S-adenosylmethionine synthetase. sams1.
- 35 AAB71833.1 AF008568 *Chlamydomonas reinhardtii*
DESCRIPTION: S-adenosylmethionine synthetase. CHRSAMS.
- 40 AAA33858.1 M62757 *Petroselinum crispum*
DESCRIPTION: S-adenosylmethionine synthetase. SMS-2.
- 45 BAA21726.1 AB006187 *Nicotiana tabacum*
DESCRIPTION: S-adenosylmethionine synthase. BYJ90.

AAF78525.1 AF195233 *Pyrus pyrifolia*
DESCRIPTION: S-adenosylmethionine synthase. SAMS.

5 94

AAB36543.1 U77935 *Phaseolus vulgaris*
DESCRIPTION: DnaJ-like protein. synthesis and expression are regulated by
heavy metal stress, virus infection and wounding treatment, suggesting
that DnaJ-like protein plays a role in plant defense.

10

95

AAB36546.1 U77940 *Phaseolus vulgaris*
DESCRIPTION: polyubiquitin. expression is regulated by heavy metal
stress, UV, virus infection, heat shock and wounding treatment, this
suggests that ubiquitin plays a role in plant defense.

15

98

AAF22109.1 AF119411 *Lupinus albus*
DESCRIPTION: ethylene biosynthesis enzyme.
1-aminocyclopropane-1-carboxylate synthase 1. ACS1. ACC synthase;
S-adenosyl-L-methionine methylthioadenosine-lyase.

20

25

AAC83146.1 AF057562 *Nicotiana glutinosa*
DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase. ACS1. ACC
synthase.

30

AAB06724.1 U64804 *Petunia x hybrida*
DESCRIPTION: ethylene biosynthesis enzyme.
1-aminocyclopropane-1-carboxylate synthase. PH-ACS1.

35

CAA79478.1 Z18953 *Petunia x hybrida*
DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase.

40

AAB17279.1 U72390 *Lycopersicon esculentum*
DESCRIPTION: converts S-adenosylmethionine to
1-aminocyclopropane-1-carboxylate hormone biosynthesis.
1-aminocyclopropane-1-carboxylate synthase. LE-ACS1B.

45

BAA94600.1 AB033503 *Populus euramericana*
DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase. peacs-2.

5 BAA96743.1 AB044662 *Prunus persica*
DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase. PP-ACS1.

10 CAB60831.1 AJ012696 *Citrus sinensis*
DESCRIPTION: ACC synthase. acs2.

15 CAA09477.1 AJ011095 *Citrus sinensis*
DESCRIPTION: ACC synthase. acs-1.

CAA41855.1 X59139 *Lycopersicon esculentum*
DESCRIPTION: 1-aminocyclopropane 1-carboxylate synthase. LE-Acc2.

20 BAA90549.1 AB031026 *Prunus mume*
DESCRIPTION: ACC synthase. PM-ACS1. 1-aminocyclopropane-1-carboxylic
acid
synthase.
25

AAA81580.1 M34289 *Lycopersicon esculentum*
DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase.

30 CAA44397.1 X62536 *Lycopersicon esculentum*
DESCRIPTION: 1-aminocyclopropane 1-carboxylate synthase.

35 CAA46797.1 X65982 *Nicotiana tabacum*
DESCRIPTION: 1-aminocyclopropane 1-carboxylate synthase.

40 BAA78333.1 AB015625 *Pyrus pyrifolia*
DESCRIPTION: 1-aminocyclopropane-1-carboxylic acid synthase. pPPACS3.

45 CAA41856.1 X59145 *Lycopersicon esculentum*
DESCRIPTION: 1-aminocyclopropane 1-carboxylate synthase. LE-ACC2.

- 5 AAB17278.1 U72389 *Lycopersicon esculentum*
DESCRIPTION: converts S-adenosylmethionine to
1-aminocyclopropane-1-carboxylate hormone biosynthesis.
1-aminocyclopropane-1-carboxylate synthase. LE-ACS1A.
- 10 AAF97614.1 U18056 *Lycopersicon esculentum*
DESCRIPTION: converts SAM to ACC; plant hormone biosynthesis.
1-amino-cyclopropane-1-carboxylate synthase. LE-ACS1A. ACC synthase;
direct precursor of ethylene; one member of a multigene family.
- 15 BAB16433.1 AB041521 *Solanum tuberosum*
DESCRIPTION: ACC synthase. ppACS1.
- 20 BAA34923.1 AB013100 *Lycopersicon esculentum*
DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase. LE-ACS6. ACC
synthase.
- 25 BAA25916.1 AB013346 *Lycopersicon esculentum*
DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase.
- 30 AAF97615.1 U18057 *Lycopersicon esculentum*
DESCRIPTION: converts SAM to ACC; plant hormone biosynthesis.
1-amino-cyclopropane-1-carboxylate synthase. LE-ACS1B. ACC synthase; · ·
direct precursor of ethylene; one member of a multigene family.
- 35 BAA92350.1 AB034992 *Malus x domestica*
DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase. MdACS-5A.
- BAA92351.1 AB034993 *Malus x domestica*
DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase. MdACS-5B.
- 40 BAA93712.1 AB032935 *Cucumis melo*
DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase. CMe-ACS1.
- 45 BAA94599.1 AB033502 *Populus euphratica*
DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase. peacs-1.

- BAA33374.1 AB006803 *Cucumis sativus*
DESCRIPTION: ACC synthase. CS-ACS1.
- 5 BAA93714.1 AB032937 *Cucumis sativus*
DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase. CS-ACS1.
- 10 AAC49153.1 U17229 *Pelargonium x hortorum*
DESCRIPTION: 1-aminocyclopropane 1-carboxylate synthase. ACC synthase.
- 15 CAA06288.1 AJ005002 *Nicotiana tabacum*
DESCRIPTION: 1-cyclopropane-1-carboxylate synthase. acs2.
- 20 CAB65314.1 AJ131836 *Nicotiana tabacum*
DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase. acs2.
- AAC15777.1 AF061605 *Nicotiana glutinosa*
DESCRIPTION: ACC synthase. ACS3.
- 25 AAC83147.1 AF057563 *Nicotiana glutinosa*
DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase. ACS2. ACC
synthase.
- 30 BAA06464.1 D30805 *Cucumis melo*
DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase.
- 35 BAA83618.1 AB025906 *Cucumis melo*
DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase. CMe-ACS1
(ME-ACS1).
- 40 AAB70885.1 U88971 *Pelargonium x hortorum*
DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase. GACS2. similar
to *Pelargonium hortorum* clone pGAC-2, Genbank Accession Number U17231.
- 45 AAA33113.1 M58323 *Cucurbita pepo*
DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase.

- 5 AAA33111.1 M61195 Cucurbita pepo
DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase. CP-ACC1A.
- 10 CAA57724.1 X82273 Brassica oleracea
DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase.
- 15 CAA47474.1 X67100 Glycine max
DESCRIPTION: 1-aminocyclopropane 1-carboxylate synthase.
- 20 AAC98809.1 U68216 Carica papaya
DESCRIPTION: ACC synthase. fruit specific; ripening related.
- 25 CAA51227.1 X72676 Brassica juncea
DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase. MACC.
- 30 BAA00838.1 D01032 Cucurbita maxima
DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase. accW.
- 35 AAA34131.1 M63490 Lycopersicon esculentum
DESCRIPTION: enzyme. 1-aminocyclopropane-1-carboxylate synthase.
- 40 CAA41857.1 X59146 Lycopersicon esculentum
DESCRIPTION: 1-aminocyclopropane 1-carboxylate synthase. LE-ACC4.
- 45 CAA77688.1 Z11613 Vigna radiata
DESCRIPTION: 1-aminocyclopropane 1-carboxylate synthase.

CAA67118.1 X98492 *Nicotiana tabacum*
DESCRIPTION: ACC synthase. ACCS2.

99

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BAA22976.1 D63457 *Arabis gemmifera*
DESCRIPTION: alcohol dehydrogenase. Adh. ADH.

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BAA22973.1 D63454 *Arabis gemmifera*
DESCRIPTION: alcohol dehydrogenase. Adh. ADH.

15

AAF23537.1 AF110439 *Arabis glabra*
DESCRIPTION: alcohol dehydrogenase.

20

BAA22978.1 D63459 *Arabis gemmifera*
DESCRIPTION: alcohol dehydrogenase. Adh. ADH.

25

BAA22974.1 D63455 *Arabis gemmifera*
DESCRIPTION: alcohol dehydrogenase. Adh. ADH.

30

AAF23540.1 AF110442 *Arabidopsis halleri*
DESCRIPTION: alcohol dehydrogenase.

35

AAF23551.1 AF110453 *Arabidopsis lyrata* subsp. *petraea*
DESCRIPTION: alcohol dehydrogenase.

40

AAF23539.1 AF110441 *Halimolobos perplexa* var. *lemhiensis*
DESCRIPTION: alcohol dehydrogenase.

BAA22975.1 D63456 *Arabis gemmifera*
DESCRIPTION: alcohol dehydrogenase. Adh. ADH.

AAF23546.1 AF110448 *Arabis lyallii*
DESCRIPTION: alcohol dehydrogenase.

45

AAF23548.1 AF110450 *Arabis parishii*

DESCRIPTION: alcohol dehydrogenase.

5 AAF23550.1 AF110452 Arabidopsis lyrata subsp. petraea
DESCRIPTION: alcohol dehydrogenase.

10 BAA22972.1 D63453 Arabis gemmifera
DESCRIPTION: alcohol dehydrogenase. Adh. ADH.

BAA22971.1 D63452 Arabis gemmifera
DESCRIPTION: alcohol dehydrogenase. Adh. ADH.

15 BAA22977.1 D63458 Arabis gemmifera
DESCRIPTION: alcohol dehydrogenase. Adh. ADH.

20 AAF23549.1 AF110451 Arabis pauciflora
DESCRIPTION: alcohol dehydrogenase.

25 AAF23545.1 AF110447 Arabis lignifera
DESCRIPTION: alcohol dehydrogenase.

30 AAF23536.1 AF110438 Arabis fendleri
DESCRIPTION: alcohol dehydrogenase.

AAF23541.1 AF110443 Arabis hirsuta
DESCRIPTION: alcohol dehydrogenase.

35 AAF23531.1 AF110433 Arabis blepharophylla
DESCRIPTION: alcohol dehydrogenase.

40 AAF23530.1 AF110432 Arabis blepharophylla
DESCRIPTION: alcohol dehydrogenase.

45 AAF23523.1 AF110425 Aubrieta deltoidea
DESCRIPTION: alcohol dehydrogenase.

- AAAF23529.1 AF110431 *Arabis blepharophylla*
DESCRIPTION: alcohol dehydrogenase.
- 5
AAAF23547.1 AF110449 *Arabidopsis lyrata* subsp. *lyrata*
DESCRIPTION: alcohol dehydrogenase.
- 10
AAAF23533.1 AF110435 *Capsella rubella*
DESCRIPTION: alcohol dehydrogenase.
- 15
AAAF23534.1 AF110436 *Arabis drummondii*
DESCRIPTION: alcohol dehydrogenase.
- 20
AAAF23532.1 AF110434 *Brassica oleracea*
DESCRIPTION: alcohol dehydrogenase.
- 25
AAAF23556.1 AF110458 *Barbarea vulgaris*
DESCRIPTION: alcohol dehydrogenase.
- 30
AAAF23555.1 AF110457 *Arabis turrita*
DESCRIPTION: alcohol dehydrogenase.
- 35
AAAF23538.1 AF110440 *Arabidopsis griffithiana*
DESCRIPTION: alcohol dehydrogenase.
- 40
AAAF23524.1 AF110426 *Arabis alpina*
DESCRIPTION: alcohol dehydrogenase.
- 45
AAAF23525.1 AF110427 *Arabis alpina*
DESCRIPTION: alcohol dehydrogenase.
- AAAF23527.1 AF110429 *Arabis alpina*

DESCRIPTION: alcohol dehydrogenase.

5 AAF23535.1 AF110437 *Arabis drummondii*
DESCRIPTION: alcohol dehydrogenase.

10 AAF23553.1 AF110455 *Arabis procurrens*
DESCRIPTION: alcohol dehydrogenase.

AAF23544.1 AF110446 *Arabis jacquinii*
DESCRIPTION: alcohol dehydrogenase.

15 AAF23526.1 AF110428 *Arabis alpina*
DESCRIPTION: alcohol dehydrogenase.

20 AAF23528.1 AF110430 *Cardamine amara*
DESCRIPTION: alcohol dehydrogenase.

25 AAF23552.1 AF110454 *Arabis procurrens*
DESCRIPTION: alcohol dehydrogenase.

30 AAF23542.1 AF110444 *Arabis hirsuta*
DESCRIPTION: alcohol dehydrogenase.

AAC79418.1 AF037560 *Leavenworthia stylosa*
DESCRIPTION: alcohol dehydrogenase 3. Adh3.

35 BAA34682.1 AB015504 *Arabidopsis griffithiana*
DESCRIPTION: alcohol dehydrogenase. Adh.

40 BAA34685.1 AB015507 *Arabidopsis suecica*
DESCRIPTION: alcohol dehydrogenase. Adh.

45 BAA34683.1 AB015505 *Arabidopsis korshinskyi*
DESCRIPTION: alcohol dehydrogenase. Adh.

AAC19393.1 AF069315 *Mesembryanthemum crystallinum*
DESCRIPTION: thylakoid-bound L-ascorbate peroxidase precursor.

5

BAA78553.1 AB022274 *Chloroplast Nicotiana tabacum*
DESCRIPTION: stromal ascorbate peroxidase.

10 BAA78552.1 AB022273 *Chloroplast Nicotiana tabacum*
DESCRIPTION: thylakoid-bound ascorbate peroxidase.

15 BAA22196.1 D88420 *Cucurbita* sp.
DESCRIPTION: a hydrogen peroxide-scavenging enzyme. stromal ascorbate peroxidase.

20 BAA12029.1 D83656 *Cucurbita* sp.
DESCRIPTION: $2AsA + H_2O_2 \rightarrow 2MDA + 2H_2O$. thylakoid-bound ascorbate peroxidase.

25 CAA11265.1 AJ223325 *Chlamydomonas reinhardtii*
DESCRIPTION: ascorbate peroxidase. apx1.

30 BAA83595.1 AB009084 *Chlamydomonas* sp. W80
DESCRIPTION: chloroplast ascorbate peroxidase.

35 AAD30294.1 AF139190 *Mesembryanthemum crystallinum*
DESCRIPTION: cytosolic ascorbate peroxidase. similar to L0-328, R6-3, L72-2.

AAB52954.1 U37060 *Gossypium hirsutum*
DESCRIPTION: ascorbate peroxidase. glyoxysomal membrane-bound protein.

40

AAD43334.1 AF159254 *Zantedeschia aethiopica*
DESCRIPTION: ascorbate peroxidase. apx2. putative glyoxysomal membrane-bound protein.

45

AAC08576.1 AF053474 *Zantedeschia aethiopica*

DESCRIPTION: cytosolic ascorbate peroxidase. apx.

5 AAD43338.1 AF158654 Fragaria x ananassa
DESCRIPTION: cytosolic ascorbate peroxidase APX26.

10 AAD43336.1 AF158652 Fragaria x ananassa
DESCRIPTION: cytosolic ascorbate peroxidase. ApxSC. corresponds to mRNA
sequence deposited in GenBank Accession Number AF039953.

15 AAB95222.1 AF039953 Fragaria x ananassa
DESCRIPTION: cytosolic ascorbate peroxidase. ApxSC.

20 AAD41408.1 AF159633 Fragaria x ananassa
DESCRIPTION: cytosolic ascorbate peroxidase. APX.

AAD41407.1 AF159632 Fragaria x ananassa
DESCRIPTION: cytosolic ascorbate peroxidase. APX.

25 AAD41403.1 AF159628 Fragaria x ananassa
DESCRIPTION: cytosolic ascorbate peroxidase. APX.

30 AAD41402.1 AF159627 Fragaria x ananassa
DESCRIPTION: cytosolic ascorbate peroxidase. APX.

35 AAD43337.1 AF158653 Fragaria x ananassa
DESCRIPTION: cytosolic ascorbate peroxidase APX19.

AAD41406.1 AF159631 Fragaria x ananassa
DESCRIPTION: cytosolic ascorbate peroxidase. APX.

40 AAD41404.1 AF159629 Fragaria x ananassa
DESCRIPTION: cytosolic ascorbate peroxidase. APX.

45 AAB94574.1 AF022213 Fragaria x ananassa
DESCRIPTION: cytosolic ascorbate peroxidase. APX-c.

- 5 AAD41405.1 AF159630 *Fragaria x ananassa*
DESCRIPTION: cytosolic ascorbate peroxidase. APX.
- 10 BAA08264.1 D45423 *Oryza sativa*
DESCRIPTION: ascorbate peroxidase.
- 15 BAA13671.1 D88649 *Cucumis sativus*
DESCRIPTION: cytosolic ascorbate peroxidase.
- 20 CAA55209.1 X78452 *Raphanus sativus*
DESCRIPTION: L-ascorbate peroxidase. APX.
- 25 BAA12890.1 D85864 *Spinacia oleracea*
DESCRIPTION: cytosolic ascorbate peroxidase.
- 30 AAA99518.1 L20864 *Spinacia oleracea*
DESCRIPTION: ascorbate peroxidase.
- 35 BAA12918.1 D85912 *Nicotiana tabacum*
DESCRIPTION: cytosolic ascorbate peroxidase.
- 40 AAB03844.1 U61379 *Vigna unguiculata*
DESCRIPTION: ascorbate peroxidase.
- 45 CAB58361.1 Y16773 *Lycopersicon esculentum*
DESCRIPTION: ascorbate peroxidase. Apx. H₂O₂ scavenger, cytosolic protein.
- CAA57140.1 X81376 *Capsicum annuum*
DESCRIPTION: L-ascorbate peroxidase.
- CAA06996.1 AJ006358 *Hordeum vulgare*
DESCRIPTION: ascorbate peroxidase. apx.

AAF22246.1 AF159380 Pimpinella brachycarpa
DESCRIPTION: ascorbate peroxidase. APX.

5

AAA86689.1 U15933 Nicotiana tabacum
DESCRIPTION: reduction of hydrogen peroxide. ascorbate peroxidase. APX.

10 CAA84406.1 Z34934 Zea mays
DESCRIPTION: cytosolic ascorbate peroxidase. apx.

15 CAA43992.1 X62077 Pisum sativum
DESCRIPTION: L-ascorbate peroxidase. AppxI.

20 AAA33645.1 M93051 Pisum sativum
DESCRIPTION: hydrogen peroxide removal; oxidative stress. ascorbate
peroxidase. ApxI.

25 AAB01221.1 U56634 Glycine max
DESCRIPTION: ascorbate peroxidase 2. APx2.

30 AAA61779.1 L10292 Glycine max
DESCRIPTION: ascorbate peroxidase. Automated Edman sequencing of the
N-terminal amino acids confirmed that the protein was authentic ascorbate
peroxidase; putative.

35 BAB20889.1 AB053297 Oryza sativa
DESCRIPTION: L-ascorbate peroxidase. APXb.

40 CAA72247.1 Y11461 Brassica napus
DESCRIPTION: L-ascorbate peroxidase. APX.

45 BAB17666.1 AB050724 Oryza sativa subsp. japonica
DESCRIPTION: ascorbate peroxidase. APXb.

45 AAD20022.1 AF127804 Glycine max
DESCRIPTION: ascorbate peroxidase. apx1. AsPOX; cytosolic.

- 5 AAB94927.1 AF038839 Brassica juncea
DESCRIPTION: ascorbate peroxidase.
103
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- 10 AAA74900.1 L34343 Ruta graveolens
DESCRIPTION: anthranilate synthase alpha subunit.
- 15 AAA74901.1 L34344 Ruta graveolens
DESCRIPTION: anthranilate synthase alpha subunit.
- 20 AAC27795.1 AF079168 Nicotiana tabacum
DESCRIPTION: feedback-insensitive anthranilate synthase alpha-2 chain.
ASA2.
- 25 BAA82095.1 AB022603 Oryza sativa
DESCRIPTION: anthranilate synthase alpha 2 subunit. OsASA2.
- 30 BAA82094.1 AB022602 Oryza sativa
DESCRIPTION: anthranilate synthase alpha 1 subunit. OsASA1.
- 35 CAC29060.1 AJ250008 Catharanthus roseus
DESCRIPTION: enzyme in tryptophan biosynthesis. anthranilate synthase
alpha subunit. asa.
- CAA06837.1 AJ006065 Catharanthus roseus
DESCRIPTION: isochorismate synthase.
104
-
- 40 CAA57724.1 X82273 Brassica oleracea
DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase.
- 45 CAA51227.1 X72676 Brassica juncea
DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase. MACC.

- AAC83147.1 AF057563 *Nicotiana glutinosa*
DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase. ACS2. ACC synthase.
- 5 CAB60722.1 AJ012551 *Citrus sinensis*
DESCRIPTION: ACC synthase. acs1.
- 10 CAB60721.1 AJ012550 *Citrus sinensis*
DESCRIPTION: ACC synthase. acs1.
- 15 CAA06288.1 AJ005002 *Nicotiana tabacum*
DESCRIPTION: 1-cyclopropane-1-carboxylate synthase. acs2.
- 20 CAB65314.1 AJ131836 *Nicotiana tabacum*
DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase. acs2.
- 25 BAA78333.1 AB015625 *Pyrus pyrifolia*
DESCRIPTION: 1-aminocyclopropane-1-carboxylic acid synthase. pPPACS3.
- 30 AAB17279.1 U72390 *Lycopersicon esculentum*
DESCRIPTION: converts S-adenosylmethionine to
1-aminocyclopropane-1-carboxylate hormone biosynthesis.
1-aminocyclopropane-1-carboxylate synthase. LE-ACS1B.
- 35 AAF97614.1 U18056 *Lycopersicon esculentum*
DESCRIPTION: converts SAM to ACC; plant hormone biosynthesis.
1-amino-cyclopropane-1-carboxylate synthase. LE-ACS1A. ACC synthase;
direct precursor of ethylene; one member of a multigene family.
- 40 AAF97615.1 U18057 *Lycopersicon esculentum*
DESCRIPTION: converts SAM to ACC; plant hormone biosynthesis.
1-amino-cyclopropane-1-carboxylate synthase. LE-ACS1B. ACC synthase;
direct precursor of ethylene; one member of a multigene family.
- 45 AAB17278.1 U72389 *Lycopersicon esculentum*
DESCRIPTION: converts S-adenosylmethionine to
1-aminocyclopropane-1-carboxylate hormone biosynthesis.

1-aminocyclopropane-1-carboxylate synthase. LE-ACS1A.

CAA46797.1 X65982 Nicotiana tabacum
5 DESCRIPTION: 1-aminocyclopropane 1-carboxylate synthase.

BAA06464.1 D30805 Cucumis melo
10 DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase.

AAB06724.1 U64804 Petunia x hybrida
15 DESCRIPTION: ethylene biosynthesis enzyme.
1-aminocyclopropane-1-carboxylate synthase. PH-ACS1.

CAA79478.1 Z18953 Petunia x hybrida
20 DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase.

BAA94599.1 AB033502 Populus euphratica
DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase. peacs-1.

CAA67118.1 X98492 Nicotiana tabacum
25 DESCRIPTION: ACC synthase. ACCS2.

CAA79477.1 Z18952 Dianthus caryophyllus
30 DESCRIPTION: 1-aminocyclopropane 1-carboxylate synthase.

AAA33275.1 M66619 Dianthus caryophyllus
35 DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase. CARACC.

BAA83618.1 AB025906 Cucumis melo
40 DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase. CMe-ACS1
(ME-ACS1).

BAA34923.1 AB013100 Lycopersicon esculentum
45 DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase. LE-ACS6. ACC
synthase.

- BAA25916.1 AB013346 *Lycopersicon esculentum*
DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase.
- 5 CAB60831.1 AJ012696 *Citrus sinensis*
DESCRIPTION: ACC synthase. acs2.
- 10 CAA41855.1 X59139 *Lycopersicon esculentum*
DESCRIPTION: 1-aminocyclopropane 1-carboxylate synthase. LE-Acc2.
- 15 CAA44397.1 X62536 *Lycopersicon esculentum*
DESCRIPTION: 1-aminocyclopropane 1-carboxylate synthase.
- 20 CAA41856.1 X59145 *Lycopersicon esculentum*
DESCRIPTION: 1-aminocyclopropane 1-carboxylate synthase. LE-ACC2.
- 25 AAA81580.1 M34289 *Lycopersicon esculentum*
DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase.
- 30 AAC98809.1 U68216 *Carica papaya*
DESCRIPTION: ACC synthase. fruit specific; ripening related.
- 35 BAA92350.1 AB034992 *Malus x domestica*
DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase. MdACS-5A.
- BAA92351.1 AB034993 *Malus x domestica*
DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase. MdACS-5B.
- 40 BAA94600.1 AB033503 *Populus euramericana*
DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase. peacs-2.
- 45 CAA77688.1 Z11613 *Vigna radiata*
DESCRIPTION: 1-aminocyclopropane 1-carboxylate synthase.
- CAA47474.1 X67100 *Glycine max*
DESCRIPTION: 1-aminocyclopropane 1-carboxylate synthase.

- 5 AAB70885.1 U88971 *Pelargonium x hortorum*
DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase. GACS2. similar
to *Pelargonium hortorum* clone pGAC-2, Genbank Accession Number U17231.
- 10 AAD04199.1 AF016459 *Pisum sativum*
DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase. ACS2. ACC
synthase.
- 15 BAB18464.1 D86242 *Cucumis melo*
DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase. CMe-ACS2
(ME-ACS2).
- 20 BAA93713.1 AB032936 *Cucumis melo*
DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase. CMe-ACS2.
- 25 BAA93715.1 AB032938 *Cucumis sativus*
DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase. CS-ACS2.
- 30 BAA33375.1 AB006804 *Cucumis sativus*
DESCRIPTION: ACC synthase. CS-ACS2.
- 35 BAB16433.1 AB041521 *Solanum tuberosum*
DESCRIPTION: ACC synthase. ppACS1.
- AAC15777.1 AF061605 *Nicotiana glutinosa*
DESCRIPTION: ACC synthase. ACS3.
- 40 CAA72191.1 Y11357 *Carica papaya*
DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase.
- 45 BAA96743.1 AB044662 *Prunus persica*
DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase. PP-ACS1.
- BAA90549.1 AB031026 *Prunus mume*

DESCRIPTION: ACC synthase. PM-ACS1. 1-aminocyclopropane-1-carboxylic acid synthase.

5

BAA93712.1 AB032935 Cucumis melo
DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase. CMe-ACS1.

10

AAF22109.1 AF119411 Lupinus albus
DESCRIPTION: ethylene biosynthesis enzyme.
1-aminocyclopropane-1-carboxylate synthase 1. ACS1. ACC synthase;
S-adenosyl-L-methionine methylthioadenosine-lyase.

15

AAC83146.1 AF057562 Nicotiana glutinosa
DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase. ACS1. ACC synthase.

20

CAA09477.1 AJ011095 Citrus sinensis
DESCRIPTION: ACC synthase. acs-1.

25

BAA93714.1 AB032937 Cucumis sativus
DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase. CS-ACS1.

106

30

AAF63205.1 AF245119 Mesembryanthemum crystallinum
DESCRIPTION: AP2-related transcription factor. CDBP. stress induced transcription factor.

35

BAA97122.1 AB016264 Nicotiana sylvestris
DESCRIPTION: ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf2.

40

AAC50047.1 U89255 Lycopersicon esculentum
DESCRIPTION: binds the GCC box pathogenesis-related promoter element DNA-binding protein. Pti4.

45

BAA07321.1 D38123 Nicotiana tabacum

DESCRIPTION: ERF1. ethylene-responsive transcription factor.

- 5 AAC62619.1 AF057373 *Nicotiana tabacum*
DESCRIPTION: transcription factor. ethylene response element binding protein 1. EREBP1.
- 10 BAA87068.1 AB035270 *Matricaria chamomilla*
DESCRIPTION: ethylene-responsive element binding protein1 homolog. McEREBP1.
- 15 AAC49740.1 U89256 *Lycopersicon esculentum*
DESCRIPTION: binds the GCC box pathogenesis-related promoter element DNA-binding protein. Pti5.
- 20 AAG43545.1 AF211527 *Nicotiana tabacum*
DESCRIPTION: Avr9/Cf-9 rapidly elicited protein 1. ACRE1. similar to EREBP transcription factors.
- 25 BAA97124.1 AB016266 *Nicotiana sylvestris*
DESCRIPTION: ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf4.
- 30 CAB96900.1 AJ251250 *Catharanthus roseus*
DESCRIPTION: transcription factor. AP2-domain DNA-binding protein. orca3.
- 35 CAB96899.1 AJ251249 *Catharanthus roseus*
DESCRIPTION: transcription factor. AP2-domain DNA-binding protein. orca3.
- 40 AAB38748.1 U81157 *Nicotiana tabacum*
DESCRIPTION: S25-XP1 DNA binding protein.
- 45 AAG60182.1 AC084763 *Oryza sativa*
DESCRIPTION: putative ethylene-responsive element binding protein. OSJNBa0027P10.12.

AAK31279.1 AC079890 *Oryza sativa*

DESCRIPTION: putative ethylene-responsive element binding protein.
OSJNBb0089A17.16.

5

CAB93940.1 AJ238740 *Catharanthus roseus*

DESCRIPTION: putative transcription factor. AP2-domain DNA-binding
protein. orca2.

10

AAC49741.1 U89257 *Lycopersicon esculentum*

DESCRIPTION: DNA-binding protein binds the GCC box pathogenesis-related
promoter element. Pti6.

15

CAC12822.1 AJ299252 *Nicotiana tabacum*

DESCRIPTION: AP2 domain-containing transcription factor. ap2.

20

BAB03248.1 AB037183 *Oryza sativa*

DESCRIPTION: ERF protein transcriptional repressor. ethylene responsive
element binding factor3. osERF3.

25

AAC14323.1 AF058827 *Nicotiana tabacum*

DESCRIPTION: TSI1. Tsi1. contains putative AP2 DNA-binding domain;
similar to Pti6.

30

BAA97123.1 AB016265 *Nicotiana sylvestris*

DESCRIPTION: ERF (EREBP); ethylene-responsive element binding factor for
basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive
element binding factor. nserf3.

35

AAD00708.1 U91857 *Stylosanthes hamata*

DESCRIPTION: ethylene-responsive element binding protein homolog. similar
to EREBP1, -2, -3 and -4 proteins encoded by GenBank Accession Numbers
D38123, D38126, D38124, and D38125 respectively.

40

AAF05606.1 AF190770 *Oryza sativa*

DESCRIPTION: EREBP-like protein. tsh1. TSH1; induced by ethylene.

45

BAA76734.1 AB024575 *Nicotiana tabacum*

DESCRIPTION: ethylene responsive element binding factor.

5 AAC29516.1 U77655 Solanum tuberosum
DESCRIPTION: DNA binding protein homolog. STWAAEIRD.

10 AAF23899.1 AF193803 Oryza sativa
DESCRIPTION: transcription factor EREBP1. EREBP/AP2-like transcription factor.

15 CAB93939.1 AJ238739 Catharanthus roseus
DESCRIPTION: putative transcription factor. AP2-domain DNA-binding protein. orca1.

20 AAD45623.1 AF084185 Brassica napus
DESCRIPTION: dehydration responsive element binding protein. DNA binding protein; DRE binding protein.

25 AAK31271.1 AC079890 Oryza sativa
DESCRIPTION: putative transcriptional factor. OSJNBb0089A17.22.

30 AAG43548.1 AF211530 Nicotiana tabacum
DESCRIPTION: Avr9/Cf-9 rapidly elicited protein 111A. ACRE111A. similar to EREBP transcription factors.

35 BAB21218.1 AP002913 Oryza sativa
DESCRIPTION: putative DNA binding protein RAV2. P0480E02.24.

AAG43549.1 AF211531 Nicotiana tabacum
DESCRIPTION: Avr9/Cf-9 rapidly elicited protein 111B. ACRE111B. similar to EREBP transcription factors.

40 BAB21211.1 AP002913 Oryza sativa
DESCRIPTION: putative DNA binding protein RAV2. P0480E02.17.

45 AAK01088.1 AF298230 Hordeum vulgare

DESCRIPTION: CBF1-like protein BCBF1. BCBF1. AP2 domain protein;
putative
DRE binding factor.

5

AAK01089.1 AF298231 *Hordeum vulgare*
DESCRIPTION: CBF3-like protein BCBF3. BCBF3. AP2 domain protein; DRE
binding factor.

10 107

AAF63205.1 AF245119 *Mesembryanthemum crystallinum*
DESCRIPTION: AP2-related transcription factor. CDBP. stress induced
transcription factor.

15

AAC50047.1 U89255 *Lycopersicon esculentum*
DESCRIPTION: binds the GCC box pathogenesis-related promoter element
DNA-binding protein. Pti4.

20

BAA97122.1 AB016264 *Nicotiana sylvestris*
DESCRIPTION: ERF (EREBP); ethylene-responsive element binding factor for
basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive
element binding factor. nserf2.

25

BAA07321.1 D38123 *Nicotiana tabacum*
DESCRIPTION: ERF1. ethylene-responsive transcription factor.

30

AAC62619.1 AF057373 *Nicotiana tabacum*
DESCRIPTION: transcription factor. ethylene response element binding
protein 1. EREBP1.

35

BAA87068.1 AB035270 *Matricaria chamomilla*
DESCRIPTION: ethylene-responsive element binding protein1 homolog.
McEREBP1.

40

CAB96899.1 AJ251249 *Catharanthus roseus*
DESCRIPTION: transcription factor. AP2-domain DNA-binding protein. orca3.

45

CAB96900.1 AJ251250 *Catharanthus roseus*

DESCRIPTION: transcription factor. AP2-domain DNA-binding protein. orca3.

5 AAB38748.1 U81157 *Nicotiana tabacum*
DESCRIPTION: S25-XP1 DNA binding protein.

10 AAC49740.1 U89256 *Lycopersicon esculentum*
DESCRIPTION: binds the GCC box pathogenesis-related promoter element
DNA-binding protein. Pti5.

15 CAB93940.1 AJ238740 *Catharanthus roseus*
DESCRIPTION: putative transcription factor. AP2-domain DNA-binding
protein. orca2.

20 AAG43545.1 AF211527 *Nicotiana tabacum*
DESCRIPTION: Avr9/Cf-9 rapidly elicited protein 1. ACRE1. similar to
EREBP transcription factors.

25 BAA97124.1 AB016266 *Nicotiana sylvestris*
DESCRIPTION: ERF (EREBP); ethylene-responsive element binding factor for
basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive
element binding factor. nserf4.

30 AAG60182.1 AC084763 *Oryza sativa*
DESCRIPTION: putative ethylene-responsive element binding protein.
OSJNBa0027P10.12.

35 AAK31279.1 AC079890 *Oryza sativa*
DESCRIPTION: putative ethylene-responsive element binding protein.
OSJNBb0089A17.16.

40 BAA97123.1 AB016265 *Nicotiana sylvestris*
DESCRIPTION: ERF (EREBP); ethylene-responsive element binding factor for
basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive
element binding factor. nserf3.

45 AAD00708.1 U91857 *Stylosanthes hamata*
DESCRIPTION: ethylene-responsive element binding protein homolog. similar

to EREBP1, -2, -3 and -4 proteins encoded by GenBank Accession Numbers D38123, D38126, D38124, and D38125 respectively.

- 5 AAC14323.1 AF058827 *Nicotiana tabacum*
DESCRIPTION: TSI1. Tsi1. contains putative AP2 DNA-binding domain;
similar to Pti6.
- 10 CAC12822.1 AJ299252 *Nicotiana tabacum*
DESCRIPTION: AP2 domain-containing transcription factor. ap2.
- 15 BAB03248.1 AB037183 *Oryza sativa*
DESCRIPTION: ERF protein transcriptional repressor. ethylene responsive
element binding factor3. osERF3.
- 20 AAF05606.1 AF190770 *Oryza sativa*
DESCRIPTION: EREBP-like protein. tsh1. TSH1; induced by ethylene.
- 25 BAA76734.1 AB024575 *Nicotiana tabacum*
DESCRIPTION: ethylene responsive element binding factor.
- 30 AAC49741.1 U89257 *Lycopersicon esculentum*
DESCRIPTION: DNA-binding protein binds the GCC box pathogenesis-related
promoter element. Pti6.
- 35 AAF23899.1 AF193803 *Oryza sativa*
DESCRIPTION: transcription factor EREBP1. EREBP/AP2-like transcription
factor.
- 40 AAC29516.1 U77655 *Solanum tuberosum*
DESCRIPTION: DNA binding protein homolog. STWAAEIRD.
- 45 CAB93939.1 AJ238739 *Catharanthus roseus*
DESCRIPTION: putative transcription factor. AP2-domain DNA-binding
protein. orcal.
- BAA78738.1 AB023482 *Oryza sativa*

DESCRIPTION: EST AU055776(S20048) corresponds to a region of the predicted gene.; Similar to Arabidopsis thaliana AP2 domain containing protein RAP2.10 mRNA, partial cds.(AF003103).

5

AAD45623.1 AF084185 Brassica napus
DESCRIPTION: dehydration responsive element binding protein. DNA binding protein; DRE binding protein.

10

AAG43548.1 AF211530 Nicotiana tabacum
DESCRIPTION: Avr9/Cf-9 rapidly elicited protein 111A. ACRE111A. similar to EREBP transcription factors.

15

AAG43549.1 AF211531 Nicotiana tabacum
DESCRIPTION: Avr9/Cf-9 rapidly elicited protein 111B. ACRE111B. similar to EREBP transcription factors.

20

BAA99376.1 AP002526 Oryza sativa
DESCRIPTION: ESTs AU093391(E60370),AU091593(C60458), AU093392(E60370) correspond to a region of the predicted gene. Similar to Arabidopsis thaliana BAC F21J9; AP2 domain protein. (AC000103).

25

BAB21218.1 AP002913 Oryza sativa
DESCRIPTION: putative DNA binding protein RAV2. P0480E02.24.

30

AAK31271.1 AC079890 Oryza sativa
DESCRIPTION: putative transcriptional factor. OSJNBb0089A17.22.

35

BAB21211.1 AP002913 Oryza sativa
DESCRIPTION: putative DNA binding protein RAV2. P0480E02.17.

40

AAK01088.1 AF298230 Hordeum vulgare
DESCRIPTION: CBF1-like protein BCBF1. BCBF1. AP2 domain protein; putative DRE binding factor.

45

AAG59618.1 AF239616 Hordeum vulgare

DESCRIPTION: CRT/DRE-binding factor. CBF.

- 5 AAK01089.1 AF298231 *Hordeum vulgare*
DESCRIPTION: CBF3-like protein BCBF3. BCBF3. AP2 domain protein; DRE binding factor.

109

- 10 BAA97124.1 AB016266 *Nicotiana sylvestris*
DESCRIPTION: ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf4.

- 15 AAG43545.1 AF211527 *Nicotiana tabacum*
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- 20 AAK31279.1 AC079890 *Oryza sativa*
DESCRIPTION: putative ethylene-responsive element binding protein. OSJNBb0089A17.16.

- 25 AAG60182.1 AC084763 *Oryza sativa*
DESCRIPTION: putative ethylene-responsive element binding protein. OSJNBa0027P10.12.

- 30 BAA87068.1 AB035270 *Matricaria chamomilla*
DESCRIPTION: ethylene-responsive element binding protein1 homolog. McEREBP1.

- 35 AAF63205.1 AF245119 *Mesembryanthemum crystallinum*
DESCRIPTION: AP2-related transcription factor. CDBP. stress induced transcription factor.

- 40 AAC50047.1 U89255 *Lycopersicon esculentum*
DESCRIPTION: binds the GCC box pathogenesis-related promoter element DNA-binding protein. Pti4.

- 45 BAA97122.1 AB016264 *Nicotiana sylvestris*

DESCRIPTION: ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf2.

5

BAA07321.1 D38123 *Nicotiana tabacum*

DESCRIPTION: ERF1. ethylene-responsive transcription factor.

10

CAB93940.1 AJ238740 *Catharanthus roseus*

DESCRIPTION: putative transcription factor. AP2-domain DNA-binding protein. orca2.

15

AAC49740.1 U89256 *Lycopersicon esculentum*

DESCRIPTION: binds the GCC box pathogenesis-related promoter element DNA-binding protein. Pti5.

20

AAC62619.1 AF057373 *Nicotiana tabacum*

DESCRIPTION: transcription factor. ethylene response element binding protein 1. EREBP1.

25

AAB38748.1 U81157 *Nicotiana tabacum*

DESCRIPTION: S25-XP1 DNA binding protein.

30

CAC12822.1 AJ299252 *Nicotiana tabacum*

DESCRIPTION: AP2 domain-containing transcription factor. ap2.

35

CAB96900.1 AJ251250 *Catharanthus roseus*

DESCRIPTION: transcription factor. AP2-domain DNA-binding protein. orca3.

40

CAB96899.1 AJ251249 *Catharanthus roseus*

DESCRIPTION: transcription factor. AP2-domain DNA-binding protein. orca3.

45

BAA97123.1 AB016265 *Nicotiana glauca*

DESCRIPTION: ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf3.

- BAB03248.1 AB037183 *Oryza sativa*
DESCRIPTION: ERF protein transcriptional repressor. ethylene responsive element binding factor3. osERF3.
- 5 AAD00708.1 U91857 *Stylosanthes hamata*
DESCRIPTION: ethylene-responsive element binding protein homolog. similar to EREBP1, -2, -3 and -4 proteins encoded by GenBank Accession Numbers D38123, D38126, D38124, and D38125 respectively.
- 10 AAC14323.1 AF058827 *Nicotiana tabacum*
DESCRIPTION: TSI1. Tsi1. contains putative AP2 DNA-binding domain; similar to Pti6.
- 15 AAC49741.1 U89257 *Lycopersicon esculentum*
DESCRIPTION: DNA-binding protein binds the GCC box pathogenesis-related promoter element. Pti6.
- 20 AAC29516.1 U77655 *Solanum tuberosum*
DESCRIPTION: DNA binding protein homolog. STWAAEIRD.
- 25 AAF05606.1 AF190770 *Oryza sativa*
DESCRIPTION: EREBP-like protein. tsh1. TSH1; induced by ethylene.
- 30 BAA76734.1 AB024575 *Nicotiana tabacum*
DESCRIPTION: ethylene responsive element binding factor.
- 35 AAF23899.1 AF193803 *Oryza sativa*
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- 40 BAA78738.1 AB023482 *Oryza sativa*
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DESCRIPTION: putative transcription factor. AP2-domain DNA-binding

protein. orcal.

- 5 AAD45623.1 AF084185 Brassica napus
DESCRIPTION: dehydration responsive element binding protein. DNA binding protein; DRE binding protein.
- 10 AAG43549.1 AF211531 Nicotiana tabacum
DESCRIPTION: Avr9/Cf-9 rapidly elicited protein 111B. ACRE111B. similar to EREBP transcription factors.
- 15 AAG43548.1 AF211530 Nicotiana tabacum
DESCRIPTION: Avr9/Cf-9 rapidly elicited protein 111A. ACRE111A. similar to EREBP transcription factors.
- 20 AAK31271.1 AC079890 Oryza sativa
DESCRIPTION: putative transcriptional factor. OSJNBb0089A17.22.
- 25 AAK01088.1 AF298230 Hordeum vulgare
DESCRIPTION: CBF1-like protein BCBF1. BCBF1. AP2 domain protein; putative DRE binding factor.
- 30 BAA99376.1 AP002526 Oryza sativa
DESCRIPTION: ESTs AU093391(E60370),AU091593(C60458), AU093392(E60370) correspond to a region of the predicted gene. Similar to Arabidopsis thaliana BAC F21J9; AP2 domain protein. (AC000103).
- 35 AAG59619.1 AF243384 Oryza sativa
DESCRIPTION: CRT/DRE binding factor. CBF. DREB.
- 40 BAB21218.1 AP002913 Oryza sativa
DESCRIPTION: putative DNA binding protein RAV2. P0480E02.24.
- 45 AAG32659.1 AF253971 Picea abies
DESCRIPTION: APETALA2-related transcription factor 2. AP2L2. PaAP2L2.

AAC49567.1 U41466 Zea mays
DESCRIPTION: Glossy15. Glossy15. AP2 DNA-binding domain protein;
similar
5 to the Arabidopsis floral homeotic gene APETALA2; maize AP2-domain
regulator of leaf epidermal traits; homeotic regulator of leaf epidermal
cell identity; allele: W64A; putative transcription factor.

110
10 -----

AAG43545.1 AF211527 Nicotiana tabacum
DESCRIPTION: Avr9/Cf-9 rapidly elicited protein 1. ACRE1. similar to
EREBP transcription factors.

15 BAA97124.1 AB016266 Nicotiana sylvestris
DESCRIPTION: ERF (EREBP); ethylene-responsive element binding factor for
basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive
element binding factor. nserf4.

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DESCRIPTION: putative ethylene-responsive element binding protein.
OSJNBb0089A17.16.

25 AAG60182.1 AC084763 Oryza sativa
DESCRIPTION: putative ethylene-responsive element binding protein.
OSJNBa0027P10.12.

30 AAF63205.1 AF245119 Mesembryanthemum crystallinum
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transcription factor.

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element binding factor. nserf2.

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45 McEREBP1.

AAC50047.1 U89255 Lycopersicon esculentum
DESCRIPTION: binds the GCC box pathogenesis-related promoter element
DNA-binding protein. Pti4.

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DNA-binding protein. Pti5.

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CAB96899.1 AJ251249 Catharanthus roseus
DESCRIPTION: transcription factor. AP2-domain DNA-binding protein. orca3.

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DESCRIPTION: transcription factor. AP2-domain DNA-binding protein. orca3.

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DESCRIPTION: S25-XP1 DNA binding protein.

40

CAC12822.1 AJ299252 Nicotiana tabacum
DESCRIPTION: AP2 domain-containing transcription factor. ap2.

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AAF05606.1 AF190770 Oryza sativa
DESCRIPTION: EREBP-like protein. tsh1. TSH1; induced by ethylene.

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DESCRIPTION: DNA binding protein homolog. STWAAEIRD.

- 5 AAF23899.1 AF193803 *Oryza sativa*
DESCRIPTION: transcription factor EREBP1. EREBP/AP2-like transcription factor.
- 10 BAB03248.1 AB037183 *Oryza sativa*
DESCRIPTION: ERF protein transcriptional repressor. ethylene responsive element binding factor3. osERF3.
- 15 BAA97123.1 AB016265 *Nicotiana sylvestris*
DESCRIPTION: ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf3.
- 20 BAA76734.1 AB024575 *Nicotiana tabacum*
DESCRIPTION: ethylene responsive element binding factor.
- 25 AAD00708.1 U91857 *Stylosanthes hamata*
DESCRIPTION: ethylene-responsive element binding protein homolog. similar to EREBP1, -2, -3 and -4 proteins encoded by GenBank Accession Numbers D38123, D38126, D38124, and D38125 respectively.
- 30 AAC49741.1 U89257 *Lycopersicon esculentum*
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- 35 AAC14323.1 AF058827 *Nicotiana tabacum*
DESCRIPTION: TSI1. Tsi1. contains putative AP2 DNA-binding domain; similar to Pti6.
- 40 CAB93939.1 AJ238739 *Catharanthus roseus*
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AAK31271.1 AC079890 *Oryza sativa*

15 DESCRIPTION: putative transcriptional factor. OSJNBb0089A17.22.

BAB21218.1 AP002913 *Oryza sativa*

20 DESCRIPTION: putative DNA binding protein RAV2. P0480E02.24.

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AAG59619.1 AF243384 *Oryza sativa*

30 DESCRIPTION: CRT/DRE binding factor. CBF. DREB.

BAB21211.1 AP002913 *Oryza sativa*

35 DESCRIPTION: putative DNA binding protein RAV2. P0480E02.17.

AAK01089.1 AF298231 *Hordeum vulgare*

DESCRIPTION: CBF3-like protein BCBF3. BCBF3. AP2 domain protein; DRE binding factor.

40 111

AAF87216.1 AF231351 *Nicotiana tabacum*

DESCRIPTION: plastidic glucose 6-phosphate dehydrogenase. G6PDHP2.

45

CAA67782.1 X99405 *Nicotiana tabacum*

DESCRIPTION: glucose-6-phosphate dehydrogenase. G6PD.

AAB69317.1 AF012861 *Petroselinum crispum*

5 DESCRIPTION: plastidic glucose-6-phosphate dehydrogenase. pG6PDH.

CAB52708.1 AJ010712 *Solanum tuberosum*

10 DESCRIPTION: glucose-6-phosphate 1-dehydrogenase. g6pd.

CAB52685.1 AJ132346 *Dunaliella bioculata*

DESCRIPTION: plastidic glucose-6-phosphate dehydrogenase. g6PD.

15 CAA04994.1 AJ001772 *Nicotiana tabacum*

DESCRIPTION: glucose-6-phosphate dehydrogenase. TCG18.

20 CAA58775.1 X83923 *Solanum tuberosum*

DESCRIPTION: glucose-6-phosphate dehydrogenase.

CAA03941.1 AJ000184 *Spinacia oleracea*

25 DESCRIPTION: Glucose-6-phosphate dehydrogenase. G6PD.

CAA03939.1 AJ000182 *Spinacia oleracea*

30 DESCRIPTION: Glucose-6-phosphate dehydrogenase. G6PD.

CAA03940.1 AJ000183 *Spinacia oleracea*

DESCRIPTION: Glucose-6-phosphate dehydrogenase. G6PD.

35 AAB41552.1 U18238 *Medicago sativa* subsp. *sativa*
DESCRIPTION: glucose-6-phosphate dehydrogenase.

40 AAD11426.1 AF097663 *Mesembryanthemum crystallinum*

DESCRIPTION: cytoplasmic glucose-6-phosphate 1-dehydrogenase. G6PD.

AAB69319.1 AF012863 *Petroselinum crispum*

45 DESCRIPTION: cytosolic glucose-6-phosphate dehydrogenase 2. cG6PDH2.

- CAA52442.1 X74421 *Solanum tuberosum*
DESCRIPTION: glucose-6-phosphate 1-dehydrogenase. g6pdh. homotetramer.
- 5 AAB69318.1 AF012862 *Petroselinum crispum*
DESCRIPTION: cytosolic glucose-6-phosphate dehydrogenase 1. cG6PDH1.
- 10 BAA97662.1 AB029454 *Triticum aestivum*
DESCRIPTION: glucose-6-phosphate dehydrogenase. g6pdh.
- BAA97663.1 AB029455 *Triticum aestivum*
15 DESCRIPTION: glucose-6-phosphate dehydrogenase. g6pdh.
- CAA04993.1 AJ001770 *Nicotiana tabacum*
DESCRIPTION: glucose-6-phosphate dehydrogenase. TCG9.
20
- CAA04992.1 AJ001769 *Nicotiana tabacum*
DESCRIPTION: glucose-6-phosphate dehydrogenase. TCG6.
- 25 BAA97664.1 AB029456 *Triticum aestivum*
DESCRIPTION: glucose-6-phosphate dehydrogenase. g6pdh.
- 30 AAG23802.1 AF260736 *Cucurbita pepo*
DESCRIPTION: plastidic glucose-6-phosphate dehydrogenase.
- CAB66330.1 AJ279688 *Betula pendula*
35 DESCRIPTION: glucose-6-phosphate dehydrogenase. g6pd.
- BAA82155.1 AB011441 *Triticum aestivum*
DESCRIPTION: glucose-6-phosphate dehydrogenase. WESR5. salt-stress
40 responding gene.
- CAA06200.1 AJ004900 *Glycine max*
DESCRIPTION: pentose phosphate pathway oxidoreductase generating
45 NADPH.
glucose-6-phosphate-dehydrogenase.

- CAA48611.1 X68652 *Raphanus sativus*
5 DESCRIPTION: hydroxymethylglutaryl-CoA reductase (NADPH). HMG2.
- CAA48610.1 X68651 *Raphanus sativus*
10 DESCRIPTION: hydroxymethylglutaryl-CoA reductase (NADPH). HMG1.
- AAC05089.1 AF038046 *Gossypium hirsutum*
15 DESCRIPTION: catalyzes the synthesis of mevalonate from hmg-coA.
3-hydroxy-3-methylglutaryl-coenzyme A reductase 2. hmg2. hmg-coA reductase
2; HMGR2.
- AAA33108.1 M96068 *Catharanthus roseus*
20 DESCRIPTION: hydroxymethylglutaryl-CoA reductase. HMGR.
- BAA36291.1 AB021862 *Cucumis melo*
25 DESCRIPTION: HMG-CoA reductase. Cm-HMGR. putative.
- AAB52551.1 U51985 *Solanum tuberosum*
DESCRIPTION: HMG-CoA reductase.
- 30 AAA93498.1 L01400 *Solanum tuberosum*
DESCRIPTION: convert HMG-CoA into mevalonate. hydroxymethylglutaryl
coenzyme A reductase. hmgr. putative.
- 35 AAB87727.1 U60452 *Nicotiana tabacum*
DESCRIPTION: hydroxy-methylglutaryl-coenzyme A reductase. HMGR1.
- CAA70440.1 Y09238 *Zea mays*
40 DESCRIPTION: 3-hydroxy-3-methylglutaryl coenzyme A reductase.
- CAA45181.1 X63649 *Nicotiana glauca*
45 DESCRIPTION: catalyzes synthesis of mevalonate.
3-hydroxy-3-methylglutaryl-coenzyme A reductase. HMGR. endoplasmic
reticulum location.

- AAD28179.1 AF110383 *Capsicum annuum*
 DESCRIPTION: 3-hydroxy-3-methylglutaryl-coenzyme A reductase.
 5 HMGR2M.
 HMGR.
- AAB52552.1 U51986 *Solanum tuberosum*
 10 DESCRIPTION: HMG-CoA reductase.
- BAA93631.1 AB022690 *Solanum tuberosum*
 15 DESCRIPTION: 3-hydroxy-3-methylglutaryl coenzyme A reductase.HMG3.
- AAB62581.1 U68072 *Lycopersicon esculentum*
 DESCRIPTION: 3-hydroxy-3-methylglutaryl CoA reductase 2. HMG2.
 20
- AAB69726.1 U72145 *Camptotheca acuminata*
 DESCRIPTION: converts HMGC_oA to mevalonate. 3-hydroxy-3-methylglutaryl
 coenzyme a reductase. hmg3. HMGR.
 25
- AAB53748.1 U95816 *Oryza sativa*
 DESCRIPTION: 3-hydroxy-3-methylglutaryl-CoA reductase. HMGR.
- 30 BAB20771.1 AB041031 *Solanum tuberosum*
 DESCRIPTION: 3-hydroxy-3-methylglutaryl coenzyme A reductase. HMG2.
- AAB69727.1 U72146 *Camptotheca acuminata*
 35 DESCRIPTION: 3-hydroxy-3-methylglutaryl coenzyme A reductase. converts
 HMGC_oA in mevalonate precursor for isoprenoid compounds; HMGR; hmg2;
 similar to protein encoded by GenBank Accession Number L10390.
- 40 AAD47596.1 AF142473 *Artemisia annua*
 DESCRIPTION: HMG-CoA reductase. HMGR1.
- AAA34169.1 M63642 *Lycopersicon esculentum*
 45 DESCRIPTION: 3-hydroxy-3-methylglutaryl coenzyme A reductase. hmg2.

- AAA68966.1 U14625 *Artemisia annua*
DESCRIPTION: 3-hydroxy-3-methylglutaryl coenzyme A reductase. AHM4.
- 5 AAA33358.1 M74798 *Hevea brasiliensis*
DESCRIPTION: 3-hydroxy-3-methylglutaryl-coenzyme A reductase. hmgr3.
- 10 AAA68965.1 U14624 *Artemisia annua*
DESCRIPTION: 3-hydroxy-3-methylglutaryl coenzyme A reductase. AHM1.
- 15 AAD08820.1 U43961 *Oryza sativa*
DESCRIPTION: 3-hydroxy-3-methylglutaryl-CoA reductase. HMGR.
- 20 AAA33360.1 M74800 *Hevea brasiliensis*
DESCRIPTION: 3-hydroxy-3-methylglutaryl-coenzyme A reductase. hmgr3.
- 25 CAA92821.1 Z68504 *Oryza sativa*
DESCRIPTION: 3-hydroxy-3-methylglutaryl-CoA reductase.
- 30 AAC05088.1 AF038045 *Gossypium hirsutum*
DESCRIPTION: catalyzes the synthesis of mevalonate from hmg-coA.
3-hydroxy-3-methylglutaryl-coenzyme A reductase 1. hmg1. hmg-coA reductase
1; HMGR1.
- 35 AAC15475.1 AF034760 *Tagetes erecta*
DESCRIPTION: 3-hydroxy-3-methylglutaryl coenzyme A reductase.
- 40 CAA38469.1 X54659 *Hevea brasiliensis*
DESCRIPTION: hydroxymethylglutaryl-CoA reductase. HMGR1.
- 45 CAA38467.1 X54657 *Hevea brasiliensis*
DESCRIPTION: hydroxymethylglutaryl-CoA reductase. HMGR1.

- 5 AAD38873.1 AF110382 *Oryza sativa*
DESCRIPTION: 3-hydroxy-3-methylglutaryl-coenzyme A reductase. HMGR3G.
HMG-CoA reductase.
- 10 AAA33040.1 L10390 *Camptotheca acuminata*
DESCRIPTION: 3-hydroxy-3-methylglutaryl coA reductase.
- 15 AAD03789.1 U43711 *Morus alba*
DESCRIPTION: catalyzes the final step in mevalonate pathway.
3-hydroxy-3-methylglutaryl-coenzyme A reductase. HMGR.
- 20 AAA21720.1 L28995 *Oryza sativa*
DESCRIPTION: conversion of hydroxymethylglutaryl coenzyme A to
mevalonate. 3-hydroxy-3-methylglutaryl coenzyme A reductase. putative.
- 25 AAC72378.1 AF096838 *Solanum tuberosum*
DESCRIPTION: 3-hydroxy-3-methylglutaryl coenzyme A reductase.
- 30 AAB04043.1 L40938 *Lycopersicon esculentum*
DESCRIPTION: HMGR CoA reductase. HMGR1.
- 35 CAA38468.1 X54658 *Hevea brasiliensis*
DESCRIPTION: hydroxymethylglutaryl-CoA reductase. HMGR2.
- 40 CAA52787.1 X74783 *Lithospermum erythrorhizon*
DESCRIPTION: 3-hydroxy-3-methyl glutaryl coenzyme A reductase. Lehmgr1.
- 45 AAD09278.1 U97683 *Glycine max*
DESCRIPTION: catalyzes the synthesis of mevalonate, the specific
precursor of all isoprenoid compounds present in plants.
3-hydroxy-3-methylglutaryl-coenzyme A reductase. HMG-CoA reductase.
- AAG43469.1 AF196964 *Bixa orellana*
DESCRIPTION: catalyzes mevalonate synthesis from hmg-CoA.
3-hydroxy-3-methylglutaryl-coenzyme A reductase.

BAA09705.1 D63389 Cucumis sativus
DESCRIPTION: 3-hydroxy-3-methylglutaryl CoA reductase.

5

AAB47161.1 S82272 Gossypium barbadense
DESCRIPTION: 3-hydroxy-3-methylglutaryl coenzyme A reductase.
/gene="3-hydroxy-3-methylglutaryl coenzyme A reductase,. This
sequence comes from Fig. 2; 3-hydroxy-3-methylglutaryl CoA reductase;
HMGR.

10

AAA33359.1 M74799 Hevea brasiliensis
DESCRIPTION: 3-hydroxy-3-methylglutaryl-coenzyme A reductase. hmgr3.

15

AAC37432.1 L34825 Solanum tuberosum
DESCRIPTION: HMG-CoA reductase. hmg1 gene family.

20

AAC37434.1 L34827 Solanum tuberosum
DESCRIPTION: HMG-CoA reductase. hmg1 gene family.

25

AAC37431.1 L34823 Solanum tuberosum
DESCRIPTION: HMG-CoA reductase. hmg1 gene family.

30

AAC37433.1 L34826 Solanum tuberosum
DESCRIPTION: HMG-CoA reductase. hmg1 gene family.

35

AAC37435.1 L34828 Solanum tuberosum
DESCRIPTION: HMG-CoA reductase. hmg1 gene family.

40

AAC37436.1 L34829 Solanum tuberosum
DESCRIPTION: HMG-CoA reductase. hmg1 gene family.

45

AAC49676.1 U77345 Zea mays
DESCRIPTION: lethal leaf-spot 1. lls1. Allele: wild-type; LLS1; similar
to bacterial ring-hydroxylating dioxygenase.

AAG03051.1 AF284781 *Oryza sativa*
DESCRIPTION: LLS1 protein. Lls1.

115

5

BAA82379.1 AP000367 *Oryza sativa*
DESCRIPTION: Similar to putative receptor kinase. (AC002332).

10

BAA87853.1 AP000816 *Oryza sativa*
DESCRIPTION: EST AU030604(E51294) corresponds to a region of the
predicted gene. Similar to putative NAK-like Ser/Thr protein kinase.
(AF001308).

15

AAG25966.1 AF302082 *Nicotiana tabacum*
DESCRIPTION: cytokinin-regulated kinase 1. CRK1. protein kinase;
transcript abundance decreases rapidly after cytokinin treatment.

20

BAB39873.1 AP002882 *Oryza sativa*
DESCRIPTION: putative protein kinase. P0439B06.8. contains ESTs
AU056701(S20808),AU056702(S20808).

25

AAC27894.1 AF023164 *Zea mays*
DESCRIPTION: leucine-rich repeat transmembrane protein kinase 1. ltk1.

30

AAC27895.1 AF023165 *Zea mays*
DESCRIPTION: leucine-rich repeat transmembrane protein kinase 2. ltk2.

35

BAB21240.1 AP002953 *Oryza sativa*
DESCRIPTION: Putative protein kinase. P0426D06.20. contains ESTs
C22359(C11461),C22360(C11461).

40

BAB16871.1 AP002537 *Oryza sativa*
DESCRIPTION: putative protein kinase APK1A*Arabidopsis thaliana*.
P0001B06.24. contains ESTs C22608(R3192),D25110(R3192).

45

BAB39409.1 AP002901 *Oryza sativa*
DESCRIPTION: putative protein kinase. P0456F08.9. contains EST
C23560(R0290).

- 5 AAF66615.1 AF142596 *Nicotiana tabacum*
DESCRIPTION: LRR receptor-like protein kinase.
- CAB41878.1 Y18259 *Brassica oleracea*
DESCRIPTION: SRK5 protein. SRK5. receptor-like kinase.
- 10 AAG59657.1 AC084319 *Oryza sativa*
DESCRIPTION: putative protein kinase. OSJNBa0004B24.20.
- 15 BAB03429.1 AP002817 *Oryza sativa*
DESCRIPTION: EST C22619(S11214) corresponds to a region of the predicted gene. Similar to *Arabidopsis thaliana* chromosome 2, BAC clone T17D12; putative protein kinase (AC006587).
- 20 BAB07999.1 AP002525 *Oryza sativa*
DESCRIPTION: putative protein kinase. P0462H08.22. contains EST C22619(S11214).
- 25 AAK00425.1 AC069324 *Oryza sativa*
DESCRIPTION: Putative protein kinase. OSJNBa0071K19.11.
- 30 CAB41879.1 Y18260 *Brassica oleracea*
DESCRIPTION: SRK15 protein. SRK15. receptor-like kinase.
- 35 AAK21965.1 AY028699 *Brassica napus*
DESCRIPTION: receptor protein kinase PERK1.
- 40 AAD21872.1 AF078082 *Phaseolus vulgaris*
DESCRIPTION: receptor-like protein kinase homolog RK20-1.
- 45 CAA97692.1 Z73295 *Catharanthus roseus*
DESCRIPTION: receptor-like protein kinase. CRPK1. Autophosphorylation predominantly on Thr, less on Ser. Mechanism: autophosphorylation in cis.

CAA74661.1 Y14285 Brassica oleracea
DESCRIPTION: SFR1. extracellular S domain: 8-1342; transmembrane domain:
1343-1411; intracellular kinase domain: 1412-2554.

5

AAC23542.1 U20948 Ipomoea trifida
DESCRIPTION: receptor protein kinase. IRK1.

10

AAG16628.1 AY007545 Brassica napus
DESCRIPTION: protein serine/threonine kinase BNK1.

15

BAA94509.1 AB041503 Populus nigra
DESCRIPTION: protein kinase 1. PnPK1.

20

BAA23676.1 AB000970 Brassica rapa
DESCRIPTION: receptor kinase 1. BcRK1.

25

CAA47962.1 X67733 Zea mays
DESCRIPTION: receptor-like protein kinase. PK1.

30

AAB09771.1 U67422 Zea mays
DESCRIPTION: CRINKLY4 precursor. cr4. receptor kinase homolog.

35

CAA74662.1 Y14286 Brassica oleracea
DESCRIPTION: SFR3. extracellular S domain: 123-1346; transmembrane
domain: 1347-1412; intracellular kinase domain: from 1413.

40

BAA94510.1 AB041504 Populus nigra
DESCRIPTION: protein kinase 2. PnPK2.

45

AAB93834.1 U82481 Zea mays
DESCRIPTION: KI domain interacting kinase 1. KIK1. receptor-like protein
kinase; serine/threonine protein kinase.

- CAA73133.1 Y12530 *Brassica oleracea*
DESCRIPTION: serine /threonine kinase. ARLK.
- 5 BAA06538.1 D31737 *Nicotiana tabacum*
DESCRIPTION: protein-serine/threonine kinase.
- 10 AAF43496.1 AF131222 *Lophopyrum elongatum*
DESCRIPTION: protein serine/threonine kinase. ESI47. induced in roots by salt stress, osmotic stress, and ABA treatment.
- 15 AAK11674.1 AF339747 *Lophopyrum elongatum*
DESCRIPTION: protein kinase. ESI47.
- 20 BAB21001.1 AB054061 *Brassica rapa*
DESCRIPTION: S locus receptor kinase. SRK22.
- 25 CAB51480.1 Y14600 *Sorghum bicolor*
DESCRIPTION: putative protein serine /threonine kinase. RLK1. accumulates in mesophyll cells.
- 30 BAA87852.1 AP000816 *Oryza sativa*
DESCRIPTION: Similar to putative Ser/Thr protein kinase. (AC004218).
- 35 BAA92221.1 AP001278 *Oryza sativa*
DESCRIPTION: Similar to *Arabidopsis thaliana* chromosome II BAC F12L6 genomic sequence, putative protein kinase. (AC004218).
- 40 BAA78764.1 AB023482 *Oryza sativa*
DESCRIPTION: ESTs C98382(C2985),D22444(C11129) correspond to a region of the predicted gene.; Similar to *Arabidopsis thaliana* APK1 gene for protein tyrosine-serine-threonine kinase.(D12522).
- 45 BAA90808.1 AP001168 *Oryza sativa*
DESCRIPTION: Similar to putative receptor-like protein kinase (AL035679).

- 5 BAA07576.1 D38563 Brassica rapa
DESCRIPTION: receptor protein kinase SRK8.
- 10 AAB47422.1 U59318 Lycopersicon esculentum
DESCRIPTION: serine/threonine protein kinase Fen. fen. allele of Fen,
fenthion sensitivity gene from tomato.
- 117
15 -----
AAA34002.1 M67449 Glycine max
DESCRIPTION: protein kinase. PK6.
- 20 AAG31141.1 AF305911 Oryza sativa
DESCRIPTION: EDR1. EDR1. MAP kinase kinase kinase; similar to
Arabidopsis
thaliana EDR1.
- 25 AAG31142.1 AF305912 Hordeum vulgare
DESCRIPTION: EDR1. EDR1. MAP kinase kinase kinase; similar to
Arabidopsis
thaliana EDR1.
- 30 CAC09580.1 AJ298992 Fagus sylvatica
DESCRIPTION: Absciscic acid (ABA) and calcium induced protein kinase.
protein kinase (PK). pk1.
- 35 CAA06334.1 AJ005077 Lycopersicon esculentum
DESCRIPTION: protein kinase. TCTR2 protein. TCTR2.
- 40 AAD10057.1 AF110519 Lycopersicon esculentum
DESCRIPTION: ethylene-inducible CTR1-like protein kinase. protein kinase
homolog; ethylene and fruit ripening inducible CTR1-like protein kinase;
TCTR1v.
- 45

DESCRIPTION: protein kinase PK4. ZmPK4.

5 BAA87852.1 AP000816 Oryza sativa
DESCRIPTION: Similar to putative Ser/Thr protein kinase. (AC004218).

10 BAA92221.1 AP001278 Oryza sativa
DESCRIPTION: Similar to Arabidopsis thaliana chromosome II BAC F12L6
genomic sequence, putative protein kinase. (AC004218).

15 AAF91323.1 AF244889 Glycine max
DESCRIPTION: receptor-like protein kinase 2. RLK2. GmRLK2.

20 BAB40094.1 AP003210 Oryza sativa
DESCRIPTION: putative receptor protein kinase. OSJNBa0010K01.7.

AAF91324.1 AF244890 Glycine max
DESCRIPTION: receptor-like protein kinase 3. RLK3. GmRLK3.

25 BAA34675.1 AB011670 Triticum aestivum
DESCRIPTION: wpk4 protein kinase. wpk4.

30 BAA92970.1 AP001551 Oryza sativa
DESCRIPTION: Similar to Arabidopsis thaliana chromosome 4 BAC clone
F28A21 ; putative protein kinase. (AL035526).

35 AAF91322.1 AF244888 Glycine max
DESCRIPTION: receptor-like protein kinase 1. RLK1. GmRLK1.

40 BAB07999.1 AP002525 Oryza sativa
DESCRIPTION: putative protein kinase. P0462H08.22. contains EST
C22619(S11214).

45 BAB03429.1 AP002817 Oryza sativa
DESCRIPTION: EST C22619(S11214) corresponds to a region of the predicted
gene. Similar to Arabidopsis thaliana chromosome 2, BAC clone T17D12;
putative protein kinase (AC006587).

- 5 CAA73067.1 Y12464 Sorghum bicolor
DESCRIPTION: serine/threonine kinase. SNFL1.
- 10 AAF59906.1 AF197947 Glycine max
DESCRIPTION: receptor protein kinase-like protein. CLV1B.
- 15 AAF59905.1 AF197946 Glycine max
DESCRIPTION: receptor protein kinase-like protein. CLV1A.
- 20 BAB16918.1 AP002863 Oryza sativa
DESCRIPTION: putative protein kinase. P0005A05.22.
- 25 AAC36318.1 AF053127 Malus x domestica
DESCRIPTION: leucine-rich receptor-like protein kinase. LRPKm1.
- 30 BAA83689.1 AB011968 Oryza sativa
DESCRIPTION: OsPK7. OsPK7. protein kinase.
- 35 CAA74646.1 Y14274 Sorghum bicolor
DESCRIPTION: putative serine/threonine protein kinase. SNFL3.
- 40 BAA95893.1 AP002071 Oryza sativa
DESCRIPTION: Similar to Arabidopsis thaliana wak4 gene; wall-associated kinase 4. (AJ009695).
- 45 BAA92954.1 AP001551 Oryza sativa
DESCRIPTION: Similar to Oryza sativa protein kinase (OSPK10) mRNA. (L27821).
- 50 AAC83393.1 U83625 Zea mays
DESCRIPTION: protein kinase ZmMEK1. mitogen-activated; ERK-activating protein kinase (MEK) homolog.
- 55 BAA92972.1 AP001551 Oryza sativa

DESCRIPTION: ESTs AU056183(S20356),AU056881(S20950) correspond to a region of the predicted gene. Similar to Arabidopsis thaliana chromosome 4 BAC clone F6I18 ; putative protein kinase. (AL022198).

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BAB18292.1 AP002860 Oryza sativa

DESCRIPTION: putative receptor-like protein kinase. P0409B08.19.

10

BAB40015.1 AP003021 Oryza sativa

DESCRIPTION: putative wall-associated kinase 1. P0503E05.18.

15

BAA05648.1 D26601 Nicotiana tabacum

DESCRIPTION: protein kinase.

20

AAC27489.1 AF077130 Oryza sativa

DESCRIPTION: receptor-like protein kinase.

25

AAC02535.1 AF044260 Oryza sativa

DESCRIPTION: receptor serine/threonine kinase. protein kinase.

30

AAG40578.1 AF216314 Oryza sativa

DESCRIPTION: MAP kinase kinase 1. protein kinase; MEK1.

CAA08997.1 AJ010093 Brassica napus

DESCRIPTION: MAP3K beta 1 protein kinase. MAP3K beta 1.

118

35

AAD21199.1 AF127797 Capsicum chinense

DESCRIPTION: putative bZIP DNA-binding protein.

40

CAC00658.1 AJ292745 Petroselinum crispum

DESCRIPTION: bZIP type transcription factor. common plant regulatory factor 7. cprf7.

45

CAC00657.1 AJ292744 Petroselinum crispum

DESCRIPTION: bZIP type transcription factor. common plant regulatory factor 6. cprf6.

- CAA41453.1 X58577 *Petroselinum crispum*
DESCRIPTION: DNA-binding protein; bZIP type. CPRF2.
- 5 CAA71768.1 Y10809 *Petroselinum crispum*
DESCRIPTION: bZIP DNA-binding protein. CPRF4a.
- 10 AAD42938.1 AF084972 *Catharanthus roseus*
DESCRIPTION: G-Box binding protein 2. GBF2. basic leucine zipper;
trans-regulatory factor.
- 15 AAC49556.1 U04295 *Oryza sativa*
DESCRIPTION: DNA-binding factor of bZIP class. osZIP-1a.
- 20 BAA07289.1 D38111 *Triticum aestivum*
DESCRIPTION: transcription factor HBP-1a(17).
- 25 CAA71795.1 Y10834 *Hordeum vulgare*
DESCRIPTION: bZIP transcription factor 2. Blz2.
- CAA70216.1 Y09013 *Triticum aestivum*
DESCRIPTION: transcriptional activator. SPA.
- 30 CAA40101.1 X56781 *Triticum aestivum*
DESCRIPTION: transcription factor. HBP-1a. la-17.
- 35 AAA80169.1 U10270 *Zea mays*
DESCRIPTION: G-box binding factor 1. GBF1.
- 40 CAA11499.1 AJ223624 *Spinacia oleracea*
DESCRIPTION: basic leucine zipper protein. bZIP.
- 45 AAC49474.1 U41817 *Phaseolus vulgaris*
DESCRIPTION: regulator of MAT2. ROM2. Repressor of seed-specific lectin
(phytohemagglutinin) gene; bZIP transcriptional repressor.

AAB40291.1 U42208 *Oryza sativa*
DESCRIPTION: OSBZ8. G-box binding protein; GBF type bZIP protein.

5 BAA02304.1 D12920 *Triticum aestivum*
DESCRIPTION: transcription factor HBP-1a(c14).

119

10 BAA96200.1 AP002093 *Oryza sativa*
DESCRIPTION: EST D40368(S2303) corresponds to a region of the predicted
gene. Similar to *Arabidopsis thaliana* chromosome II putative cytochrome
P450 (AC004077).

15 BAA96158.1 AP002092 *Oryza sativa*
DESCRIPTION: EST D40368(S2303) corresponds to a region of the predicted
gene. Similar to *Arabidopsis thaliana* chromosome II BAC T31E10; putative
cytochrome P450 (AC004077).

20

BAA96196.1 AP002093 *Oryza sativa*
DESCRIPTION: ESTs AU086027(S2303),D40339(S2251) correspond to a
region of
25 the predicted gene. Similar to *Arabidopsis thaliana* chromosome II BAC
T31E10; putative cytochrome P450 (AC004077).

BAA96154.1 AP002092 *Oryza sativa*
30 DESCRIPTION: ESTs AU086027(S2303),D40339(S2251) correspond to a
region of
the predicted gene. Similar to *Arabidopsis thaliana* chromosome II BAC
T31E10; putative cytochrome P450 (AC004077).

35

BAA96193.1 AP002093 *Oryza sativa*
DESCRIPTION: Similar to *Arabidopsis thaliana* chromosome II BAC T31E10;
putative cytochrome P450 (AC004077).

40

BAA96151.1 AP002092 *Oryza sativa*
DESCRIPTION: Similar to *Arabidopsis thaliana* chromosome II BAC T31E10;
putative cytochrome P450 (AC004077).

45

BAA96194.1 AP002093 *Oryza sativa*

DESCRIPTION: Similar to *Arabidopsis thaliana* chromosome II BAC T31E10; putative cytochrome P450 (AC004077).

5 BAA96152.1 AP002092 *Oryza sativa*

DESCRIPTION: Similar to *Arabidopsis thaliana* chromosome II BAC T31E10; putative cytochrome P450 (AC004077).

10 AAG41777.1 AF212991 *Cucurbita maxima*

DESCRIPTION: ent-kaurene oxidase. CYP88A2. cytochrome P450; similar to maize Dwarf3 protein.

15 AAK11616.1 AF326277 *Hordeum vulgare*

DESCRIPTION: ent-kaurenoic acid oxidase. KAO1. cytochrome P450; CYP88A; HvKAO1.

20

AAK00946.1 AF318211 *Taxus cuspidata*

DESCRIPTION: 5-alpha-taxadienol-10-beta-hydroxylase. cytochrome P450-like protein.

25

AAC49659.1 U74319 *Sorghum bicolor*

DESCRIPTION: obtusifolios 14-alpha demethylase CYP51. CYP51. cytochrome P450 catalyzing the 14-alpha demethylation of obtusifolios in plants.

30

AAA17746.1 L19075 *Catharanthus roseus*

DESCRIPTION: cytochrome P450. CYP72C. putative.

35 AAA33106.1 L10081 *Catharanthus roseus*

DESCRIPTION: cytochrome P-450 protein. CYP72. putative; CYP72 protein.

40 AAA17732.1 L19074 *Catharanthus roseus*

DESCRIPTION: cytochrome P450. CYP72B.

45 CAB56503.1 AJ238612 *Catharanthus roseus*

DESCRIPTION: cytochrome P450.

- AAB17070.1 U54770 *Lycopersicon esculentum*
DESCRIPTION: cytochrome P450 homolog. dwarf.
- 5 CAB41490.1 AJ238439 *Cicer arietinum*
DESCRIPTION: cytochrome P450 monooxygenase. cyp81E3v2.
- 10 BAB19089.1 AP002744 *Oryza sativa*
DESCRIPTION: putative cytochrome P450. P0006C01.31. contains ESTs
D24685(R2374),AU031882(R2374).
- 15 AAD44150.1 AF124815 *Mentha spicata*
DESCRIPTION: cytochrome p450.
- 20 BAB19110.1 AP002839 *Oryza sativa*
DESCRIPTION: putative cytochrome P450. P0688A04.16. contains ESTs
D24685(R2374),AU031882(R2374).
- 25 BAA74465.1 AB022732 *Glycyrrhiza echinata*
DESCRIPTION: cytochrome P450. CYP Ge-31.
- 30 BAA22422.1 AB001379 *Glycyrrhiza echinata*
DESCRIPTION: cytochrome P450. CYP81E1.
- CAA10067.1 AJ012581 *Cicer arietinum*
DESCRIPTION: cytochrome P450. cyp81E3.
- 35 BAB40322.1 AB036772 *Triticum aestivum*
DESCRIPTION: cytochrome P450. N-1.
- 40 CAB43505.1 AJ239051 *Cicer arietinum*
DESCRIPTION: cytochrome P450. cyp81E2.
- 45 CAB56742.1 AJ249800 *Cicer arietinum*
DESCRIPTION: cytochrome P450 monooxygenase. cyp81E5.

AAF89209.1 AF279252 *Vigna radiata*
DESCRIPTION: cytochrome P450. CipCYP.

5 BAA93634.1 AB025016 *Lotus japonicus*
DESCRIPTION: cytochrome P450.

BAB19107.1 AP002839 *Oryza sativa*
10 DESCRIPTION: putative cytochrome P450. P0688A04.13. contains ESTs
AU100635(C10787),D22354(C10787).

BAB19086.1 AP002744 *Oryza sativa*
15 DESCRIPTION: putative cytochrome P450. P0006C01.28. contains ESTs
AU100635(C10787),D22354(C10787).

CAA04116.1 AJ000477 *Helianthus tuberosus*
20 DESCRIPTION: fatty acid in-chain hydroxylase. cytochrome P450. CYP81B1c.

CAA04117.1 AJ000478 *Helianthus tuberosus*
25 DESCRIPTION: fatty acid in-chain hydroxylase. cytochrome P450. CYP81B1.
chimeric sequence (from 5'-race).

CAA71517.1 Y10493 *Glycine max*
30 DESCRIPTION: putative cytochrome P450.

BAB21156.1 AP002899 *Oryza sativa*
DESCRIPTION: putative cytochrome P450. P0456A01.12.

35 AAG13498.1 AC068924 *Oryza sativa*
DESCRIPTION: putative cytochrome P450. OSJNBa0026L12.20.

40 AAF34534.1 AF195813 *Lupinus albus*
DESCRIPTION: isoflavone synthase 1. ifs1. cytochrome P450.

CAA83941.1 Z33875 *Mentha x piperita*
45 DESCRIPTION: cytochrome P-450 oxidase.

AAF34533.1 AF195812 Pisum sativum
DESCRIPTION: isoflavone synthase 1. ifs1. cytochrome P450.

5

AAF45142.1 AF195818 Glycine max
DESCRIPTION: isoflavone synthase 1. ifs1. cytochrome P450.

120

10

CAB42052.1 AJ242045 Lycopersicon esculentum
DESCRIPTION: nicotianamine synthase. chln.

15

BAA74581.1 AB011264 Hordeum vulgare
DESCRIPTION: nicochianamine synthase 3. hvnas3.

20

AAD32651.1 AF136942 Hordeum vulgare
DESCRIPTION: nicotianamine synthase 2. nashor2.

25

BAA74582.1 AB011265 Hordeum vulgare
DESCRIPTION: nicochianamine synthase 2. hvnas2.

30

BAB17824.1 AB023819 Oryza sativa
DESCRIPTION: nicotianamine synthase 3. osnas3.

35

BAA74583.1 AB011266 Hordeum vulgare
DESCRIPTION: nicotianamine Synthase 4. hvnas4.

40

BAA74586.1 AB011269 Hordeum vulgare
DESCRIPTION: nicotianamine Synthase 6. hvnas6.

45

BAA74587.1 AB019525 Hordeum vulgare
DESCRIPTION: nicotianamine synthase 7. hvnas7.

BAB17826.1 AB046401 Oryza sativa
DESCRIPTION: nicotianamine synthase 2. OsNAS2.

5 BAB17823.1 AB023818 Oryza sativa
DESCRIPTION: nicotianamine synthase 2. osnas2.

10 BAB17825.1 AB046401 Oryza sativa
DESCRIPTION: nicotianamine synthase 1. OsNAS1.

15 BAA74588.2 AB021746 Oryza sativa
DESCRIPTION: nicotianamine synthase 1. osnas1.

20 BAA74580.1 AB010086 Hordeum vulgare
DESCRIPTION: nicotianamine synthase 1. hvnas1.

BAA74585.1 AB011268 Hordeum vulgare
DESCRIPTION: nicotianamine Synthase 5-2. hvnas5-2.

25 BAA74584.1 AB011267 Hordeum vulgare
DESCRIPTION: nicotianamine synthase 5-1. hvnas5-1.

122

30 AAD01804.1 AF026480 Dianthus caryophyllus
DESCRIPTION: lipase. lipid-protein-particle associated.

35 BAB39417.1 AP002901 Oryza sativa
DESCRIPTION: putative lipase. P0456F08.17. contains ESTs
C99390(E11001),AU101109(E0858),AU101332(E11001).

40 AAB07724.1 U55867 Ipomoea nil
DESCRIPTION: Pn47p. lipase-like protein.

45 AAK31273.1 AC079890 Oryza sativa
DESCRIPTION: putative lipase. OSJNBb0089A17.13.

123

DESCRIPTION: C2H2 zinc-finger protein ZPT3-3. ZPT3-3.

5 BAA21927.1 AB006605 Petunia x hybrida
DESCRIPTION: ZPT3-3. C2H2 zinc finger protein, 3 finger.

10 BAA96070.1 AB035132 Petunia x hybrida
DESCRIPTION: C2H2 zinc-finger protein ZPT2-10. PETHy;ZPT2-10.

15 BAA21919.1 AB006597 Petunia x hybrida
DESCRIPTION: ZPT2-10. C2H2 zinc finger protein, 2 finger.

AAK01713.1 AF332876 Oryza sativa
DESCRIPTION: zinc finger transcription factor ZF1.

20 AAC06243.1 AF053077 Nicotiana tabacum
DESCRIPTION: transcription factor. osmotic stress-induced zinc-finger
protein. zfp.

25 BAA05079.1 D26086 Petunia x hybrida
DESCRIPTION: zinc-finger protein.

30 BAA05078.1 D26085 Petunia x hybrida
DESCRIPTION: zinc-finger DNA binding protein.

35 AAB39638.1 U68763 Glycine max
DESCRIPTION: putative transcription factor. SCOF-1. scof-1. zinc-finger
protein.

40 BAA05076.1 D26083 Petunia x hybrida
DESCRIPTION: zinc-finger DNA binding protein.

BAA05077.1 D26084 Petunia x hybrida
DESCRIPTION: zinc-finger DNA binding protein.

45 BAA21928.1 AB006606 Petunia x hybrida

DESCRIPTION: ZPT4-4. C2H2 zinc finger protein, 4 finger.

5 BAA19114.1 AB000455 Petunia x hybrida
DESCRIPTION: PETHy;ZPT4-1. Cys(2) His(2) zinc finger protein, 4 fingers.

AAD26942.1 AF119050 Datisca glomerata
DESCRIPTION: zinc-finger protein 1. zfp1. DgZFP1.
10

BAA19112.1 AB000453 Petunia x hybrida
DESCRIPTION: PETHy;ZPT3-1. Cys(2) His(2) zinc finger protein, 3 fingers.
15

AAB53260.1 U76554 Brassica rapa
DESCRIPTION: transcription factor. zinc-finger protein-1. BR42.

20 AAB53261.1 U76555 Brassica rapa
DESCRIPTION: zinc-finger protein BcZFP1. BcZFP1(3-2z).

BAA19926.1 AB000456 Petunia x hybrida
DESCRIPTION: PETHy; ZPT4-2. C2H2 zinc finger protein, 4 finger.
25

126

30 CAA10134.1 AJ012693 Cicer arietinum
DESCRIPTION: basic blue copper protein.

CAB65280.1 AJ248323 Medicago sativa subsp. x varia
DESCRIPTION: basic blue protein. babl.
35

AAC32448.1 U76296 Spinacia oleracea
DESCRIPTION: plantacyanin. member of a strictly plant-specific family of
mononuclear blue copper proteins known as phytoeyanins, which are further
40 classified into three distinct subfamilies: Uclacyanins, Stellacyanins,
and Plantacyanins; member of the subfamily of Plantacyanins;
non-glycosylated.

45 AAF66243.1 AF243181 Lycopersicon esculentum
DESCRIPTION: plantacyanin. naturally occurring cupredoxin with a Val

residue in the position of the axial ligand Met; member of the plantacyanin subfamily of a strictly plant-specific family of mononuclear blue copper proteins known as phytoeyanins.

5

AAD10251.1 AF031195 *Triticum aestivum*
DESCRIPTION: blue copper-binding protein homolog. S85.

10

AAF66242.1 AF243180 *Lycopersicon esculentum*
DESCRIPTION: dicyanin. binuclear blue copper protein; contains two stellacyanins linked together.

15

CAA80963.1 Z25471 *Pisum sativum*
DESCRIPTION: blue copper protein.

20

AAC64163.1 AF093537 *Zea mays*
DESCRIPTION: blue copper protein. similar to pea blue copper protein in GenBank Accession Number Z25471.

25

AAC32421.1 U65511 *Cucumis sativus*
DESCRIPTION: putative oxygen activation and/or lignin formation. stellacyanin. member of a strictly plant-specific family of mononuclear blue copper proteins known as phytoeyanins, which are further classified into three distinct subfamilies: Uclacyanins, Stellacyanins, and Plantacyanins; member of the subfamily of Stellacyanins; similar to *Rhus vernicifera* stellacyanin: SwissProt Accession Number P00302; similar to umecyanin: SwissProt Accession Number P42849; similar to mavicyanin: SwissProt Accession Number P80728; similar to BCB encoded by GenBank Accession Number Z15058; similar to F18A8.9, encoded by GenBank Accession Number AC003105; similar to F7F1.27 encoded by GenBank Accession Number AC004669; similar to F9D12.16 encoded by GenBank Accession Number AF077407; glycoprotein.

30

35

127

40

AAA17000.1 L08632 *Glycine max*
DESCRIPTION: pyruvate kinase.

45

CAA37727.1 X53688 *Solanum tuberosum*
DESCRIPTION: pyruvate kinase.

- CAA82628.1 Z29492 *Nicotiana tabacum*
DESCRIPTION: glycolytic enzyme. pyruvate kinase.
- 5 AAF44707.1 AF242871 *Lilium longiflorum*
DESCRIPTION: cytosolic pyruvate kinase.
- 10 BAA88185.1 AP000836 *Oryza sativa*
DESCRIPTION: ESTs AU081247(C50004),AU068940(C51113) correspond to
a region of the predicted gene. Similar to pyruvate kinase (Q42954).
- 15 BAA76433.1 AB025005 *Cicer arietinum*
DESCRIPTION: pyruvate kinase.
- 20 CAA49996.1 X70653 *Nicotiana tabacum*
DESCRIPTION: pyruvate kinase. PKTL7. monomer.
- 25 CAA82223.1 Z28374 *Nicotiana tabacum*
DESCRIPTION: glycolytic enzyme. Pyruvate kinase; plastid isozyme.
- 30 CAA82222.1 Z28373 *Nicotiana tabacum*
DESCRIPTION: Glycolytic enzyme. pyruvate kinase; plastid isozyme.
- 35 AAA33871.1 M64737 *Ricinus communis*
DESCRIPTION: ATP:pyruvate phosphotransferase.
- AAA33870.1 M64736 *Ricinus communis*
DESCRIPTION: ATP:pyruvate phosphotransferase.
- 129
40 -----
BAB12433.1 AB025030 *Coptis japonica*
DESCRIPTION: p450.
- 45 AAF05621.1 AF191772 *Papaver somniferum*
DESCRIPTION: hydroxylase involved in benzylisoquinoline alkaloid

biosynthesis. (S)-N-methylcoclaurine 3'-hydroxylase. CYP80B1. cytochrome P450-dependent monooxygenase.

5 AAC39452.1 AF014800 *Eschscholzia californica*
DESCRIPTION: hydroxylase involved in the biosynthesis of
tetrahydrobenzylisoquinoline alkaloids in plants. (S)-N-methylcoclaurine
3'-hydroxylase. CYP80B1. cytochrome P-450-dependent monooxygenase;
CYP80B1v1.

10

AAC39453.1 AF014801 *Eschscholzia californica*
DESCRIPTION: hydroxylase involved in the biosynthesis of
tetrahydrobenzylisoquinoline alkaloids in plants. (S)-N-methylcoclaurine
15 3'-hydroxylase. CYP80B1. cytochrome P-450-dependent monooxygenase;
CYP80B1v2.

20 AAA32913.1 M32885 *Persea americana*
DESCRIPTION: cytochrome P-450LXXIA1 (cyp71A1).

25 AAA19701.1 L24438 *Thlaspi arvense*
DESCRIPTION: cytochrome P450.

CAA50648.1 X71657 *Solanum melongena*
DESCRIPTION: P450 hydroxylase.

30 AAG34695.1 AF313492 *Matthiola incana*
DESCRIPTION: putative cytochrome P450.

35 AAG44132.1 AF218296 *Pisum sativum*
DESCRIPTION: cytochrome P450. P450 isolog.

40 BAA12159.1 D83968 *Glycine max*
DESCRIPTION: Cytochrome P-450 (CYP93A1).

45 AAC48987.1 U09610 *Berberis stolonifera*
DESCRIPTION: cytochrome P-450 CYP80.

- AAD56282.1 AF155332 *Petunia x hybrida*
DESCRIPTION: flavonoid 3'-hydroxylase. Ht1. cytochrome P450; CYP75B2.
- 5 AAC32274.1 AF081575 *Petunia x hybrida*
DESCRIPTION: flavonoid 3',5'-hydroxylase. Hf1. P450 enzyme.
- 10 AAB17562.1 U72654 *Eustoma grandiflorum*
DESCRIPTION: flavonoid 3'5'-hydroxylase. F3'5'H. cytochrome P450; CYP75.
- 15 BAA84916.1 AB032833 *Cicer arietinum*
DESCRIPTION: cytochrome P450. CYP76D1.
- AAB94588.1 AF022459 *Glycine max*
DESCRIPTION: CYP71D10p. CYP71D10. cytochrome P450 monooxygenase.
- 20 BAB40324.1 AB037245 *Asparagus officinalis*
DESCRIPTION: cytochrome P450. ASPI-2.
- 25 BAB40323.1 AB037244 *Asparagus officinalis*
DESCRIPTION: cytochrome P450. ASPI-1.
- 30 CAA50155.1 X70824 *Solanum melongena*
DESCRIPTION: flavonoid hydroxylase (P450). CYP75.
- 35 AAC39318.1 AF029858 *Sorghum bicolor*
DESCRIPTION: second multifunctional cytochrome P450 in the biosynthetic pathway of the cyanogenic glucoside dhurrin. Catalyzes the conversion of p-hydroxyphenylacetaldoxime to p-hydroxymandelonitrile. cytochrome P450 CYP71E1. CYP71E1. No EST#s identified.
- 40 CAB56503.1 AJ238612 *Catharanthus roseus*
DESCRIPTION: cytochrome P450.
- 45 CAA71514.1 Y10490 *Glycine max*
DESCRIPTION: putative cytochrome P450.

BAA84071.1 AB028151 *Antirrhinum majus*
DESCRIPTION: flavone synthase II. cytochrome P450. AFNS2.

5

CAA70575.1 Y09423 *Nepeta racemosa*
DESCRIPTION: cytochrome P450. CYP71A5.

10

CAA70576.1 Y09424 *Nepeta racemosa*
DESCRIPTION: cytochrome P450. CYP71A6.

15

CAA71513.1 Y10489 *Glycine max*
DESCRIPTION: putative cytochrome P450.

20

BAA84072.1 AB028152 *Torenia hybrida*
DESCRIPTION: flavone synthase II. cytochrome P450. TFNS5.

25

CAA71516.1 Y10492 *Glycine max*
DESCRIPTION: putative cytochrome P450.

30

BAA13076.1 D86351 *Glycine max*
DESCRIPTION: cytochrome P-450 (CYP93A2).

132

35

CAB55396.1 AL117264 *Oryza sativa*
DESCRIPTION: zwh12.1. similar to Arabidopsis putative
UDP-galactase-4-epimerase (AC007060); Method: conceptual translation with
partial peptide sequencing.

40

133

AAG43835.1 AF213455 *Zea mays*
DESCRIPTION: protein phosphatase type-2C. pp2c-1. PP2C-1.

45

AAG13599.1 AC051633 *Oryza sativa*

DESCRIPTION: putative protein phosphatase-2C. OSJNBb0015I11.26.

AAG46118.1 AC073166 *Oryza sativa*

5 DESCRIPTION: putative protein phosphatase-2C. OSJNBb0064P21.12. tRNA-Lys.

BAB12036.1 AP002820 *Oryza sativa*

10 DESCRIPTION: putative protein phosphatase. P0702D12.18.

AAC36698.1 AF075580 *Mesembryanthemum crystallinum*

15 DESCRIPTION: protein phosphatase-2C. PP2C.

CAC10359.1 AJ277087 *Nicotiana tabacum*

20 DESCRIPTION: protein phosphatase 2C. PP2C2.

CAB90633.1 AJ277743 *Fagus sylvatica*

DESCRIPTION: protein phpsphatase 2C (PP2C). pp2C1. ABA-induced protein.

25 CAC10358.1 AJ277086 *Nicotiana tabacum*

DESCRIPTION: protein phosphatase 2C. PP2C1.

CAA72341.1 Y11607 *Medicago sativa*

30 DESCRIPTION: protein phosphatase 2C. MP2C.

AAC36697.1 AF075579 *Mesembryanthemum crystallinum*

35 DESCRIPTION: protein phosphatase-2C. PP2C.

CAB61839.1 AJ242803 *Sporobolus stapfianus*

DESCRIPTION: putative serine/threonine phosphatase type 2c.

40

AAC36700.1 AF075582 *Mesembryanthemum crystallinum*

DESCRIPTION: protein phosphatase-2C. PP2C.

45 AAD17804.1 AF092431 *Lotus japonicus*

DESCRIPTION: nodule-enhanced protein phosphatase type 2C. NPP2C1.

- 5 AAD17805.1 AF092432 Lotus japonicus
DESCRIPTION: protein phosphatase type 2C. PP2C2.
- 10 CAC09575.1 AJ298987 Fagus sylvatica
DESCRIPTION: protein phosphatase 2C (PP2C). pp2Cf1.
- 15 AAC36699.1 AF075581 Mesembryanthemum crystallinum
DESCRIPTION: protein phosphatase-2C. PP2C.
- 20 AAD11430.1 AF097667 Mesembryanthemum crystallinum
DESCRIPTION: protein phosphatase 2C homolog. PP2C.
- 25 CAB90634.1 AJ277744 Fagus sylvatica
DESCRIPTION: protein phosphatase 2C (PP2C). pp2C2. ABA and calcium induced protein.
- 30 AAC26828.1 AF075603 Oryza sativa
DESCRIPTION: kinase interaction domain mediates phosphorylation-dependent binding to a subset of active receptor-like protein kinases. kinase associated protein phosphatase. kapp. type 2C protein phosphatase.
- 35 AAC35951.1 AF079355 Mesembryanthemum crystallinum
DESCRIPTION: protein phosphatase-2c. PP2C.
- 40 AAK20060.1 AC025783 Oryza sativa
DESCRIPTION: putative protein phosphatase 2C. OSJNBa0001O14.1.
- 45 AAB93832.1 U81960 Zea mays
DESCRIPTION: kinase interaction domain mediates phosphorylation-dependent binding to a subset of active receptor-like protein kinases; type 2C protein phosphatase. kinase associated protein phosphatase. KAPP.
- 50 CAC09576.1 AJ298988 Fagus sylvatica
DESCRIPTION: protein phosphatase 2C (PP2C). pp2Cf2.

134

AAD26116.1 AF106954 Brassica napus

5 DESCRIPTION: galactinol synthase. GS. UDP-D-galactose:myo-inositol-D-galactosyltransferase.

CAB51130.1 AJ243815 Pisum sativum

10 DESCRIPTION: role in alpha galactoside synthesis. putative galactinol synthase.

CAB51533.1 AJ237693 Ajuga reptans

15 DESCRIPTION: galactosyl transfer from UDP-galactose to myo-inositol to form galactinol. galactinol synthase, isoform GolS-1. GolS.

CAB51534.1 AJ237694 Ajuga reptans

20 DESCRIPTION: galactosyl transfer from UDP-galactose to myo-inositol. galactinol synthase, isoform GolS-2. GolS.

AAD55726.1 AF178569 Vitis riparia

25 DESCRIPTION: galactinol synthase. WSI76. water stress induced protein.

135

AAB57734.1 U64818 Lycopersicon esculentum

30 DESCRIPTION: fructokinase. Frk2.

AAB51108.1 U62329 Lycopersicon esculentum

35 DESCRIPTION: fructokinase. FK.

AAA80675.1 U37838 Beta vulgaris

DESCRIPTION: fructokinase.

40 CAA78283.1 Z12823 Solanum tuberosum

DESCRIPTION: fructokinase.

AAB57733.1 U64817 Lycopersicon esculentum

45 DESCRIPTION: fructokinase. Frk1.

BAA94601.1 AB033504 *Populus euramericana*

DESCRIPTION: 1-aminocyclopropane-1-carboxylate oxidase. peaco-1.

5

AAA33697.1 L21978 *Petunia x hybrida*

DESCRIPTION: 1-aminocyclopropane-1-carboxylate oxidase. ACO3.

10

AAC48977.1 U07953 *Pelargonium x hortorum*

DESCRIPTION: 1-aminocyclopropane-1-carboxylate oxidase.

15

CAA54449.1 X77232 *Prunus persica*

DESCRIPTION: 1-aminocyclopropane-1-carboxylate oxidase. PAO1.

20

AAF36483.1 AF129073 *Prunus persica*

DESCRIPTION: 1-aminocyclopropane-1-carboxylate oxidase. ACO1.

25

AAC33524.1 AF026793 *Prunus armeniaca*

DESCRIPTION: 1-aminocyclopropane-1-carboxylate oxidase. ACC oxidase.

30

AAB70884.1 U67861 *Pelargonium x hortorum*

DESCRIPTION: 1-aminocyclopropane-1-carboxylate oxidase. GACO3.

35

BAA90550.1 AB031027 *Prunus mume*

DESCRIPTION: ACC oxidase. PM-ACO1. 1-aminocyclopropane-1-carboxylic acid oxidase.

40

AAA99792.1 U54565 *Nicotiana glutinosa*

DESCRIPTION: oxidation of 1-aminocyclopropane-1-carboxylic acid.
1-aminocyclopropane-1-carboxylic acid oxidase. NGACO1. ACC oxidase.

45

AAB05171.1 U62764 *Nicotiana glutinosa*

DESCRIPTION: oxidation of 1-aminocyclopropane-1-carboxylic acid. ACC
oxidase. NGACO3.

5 AAC37381.1 L21976 Petunia x hybrida

DESCRIPTION: 1-aminocyclopropane-1-carboxylate oxidase. ACO1.

10 CAA71738.1 Y10749 Betula pendula

DESCRIPTION: 1-aminocyclopropane-1-carboxylate oxidase. ACO.

15 CAA86468.1 Z46349 Nicotiana tabacum

DESCRIPTION: 1-aminocyclopropane-1-carboxylate deaminase.

20 BAA83466.1 AB012857 Nicotiana tabacum

DESCRIPTION: ACC oxidase.

25 AAC98808.1 U68215 Carica papaya

DESCRIPTION: ACC oxidase. fruit specific; ripening related.

30 BAA06526.1 D31727 Cucumis melo

DESCRIPTION: 1-aminocyclopropane-1-carboxylate oxidase.

35 CAA64797.1 X95551 Cucumis melo

DESCRIPTION: ACC oxidase.

CAA58232.1 X83229 Nicotiana tabacum

DESCRIPTION: ethylene forming enzyme. 1-aminocyclopropane-1-carboxylate
oxidase.

40 BAA34924.1 AB013101 Lycopersicon esculentum

DESCRIPTION: 1-aminocyclopropane-1-carboxylate oxidase. LE-ACO4. ACC
oxidase.

45 AAF64528.1 AF254125 Carica papaya

DESCRIPTION: 1-aminocyclopropane-1-carboxylate oxidase. ACC oxidase.

- AAA33698.1 L21979 *Petunia x hybrida*
DESCRIPTION: 1-aminocyclopropane-1-carboxylate oxidase. ACO4.
- 5 CAA41212.1 X58273 *Lycopersicon esculentum*
DESCRIPTION: conversion of ACC to ethylene.
1-Aminocyclopropane-1-carboxylic acid oxidase. LEACO1.
- 10 BAA21541.1 AB003514 *Actinidia deliciosa*
DESCRIPTION: 1-aminocyclopropane-1-carboxylic acid oxidase.
- 15 AAB71421.1 L29405 *Helianthus annuus*
DESCRIPTION: 1-aminocyclopropane-1-carboxylic acid oxidase. ACC oxidase.
- 20 AAA99793.1 U54566 *Nicotiana glutinosa*
DESCRIPTION: oxidation of 1-aminocyclopropane-1-carboxylic acid.
1-aminocyclopropane-1-carboxylic acid oxidase. NGACO2. ACC oxidase.
- 25 AAF36484.1 AF129074 *Prunus persica*
DESCRIPTION: 1-aminocyclopropane-1-carboxylate oxidase. ACO2.
- 30 CAA64799.1 X95553 *Cucumis melo*
DESCRIPTION: ACC oxidase.
- 35 CAA90904.1 Z54199 *Lycopersicon esculentum*
DESCRIPTION: catalyses the final step in ethylene biosynthesis.
1-aminocyclopropane-1-carboxylic acid oxidase. ACO3.
- 40 CAA68538.1 Y00478 *Lycopersicon esculentum*
DESCRIPTION: conversion of ACC to ethylene.
1-aminocyclopropane-1-carboxylate oxidase. LEACO2.
- 45 CAB97173.1 AJ297435 *Mangifera indica*
DESCRIPTION: ethene biosynthesis. putative
1-aminocyclopropane-1-carboxylic acid oxidase. aco1.

- CAA82646.1 Z29529 *Nicotiana tabacum*
DESCRIPTION: oxidation of 1-aminocyclopropane-1-carboxylic acid. ethylene forming enzyme (EFE).
- 5 AAC12934.1 AF053354 *Phaseolus vulgaris*
DESCRIPTION: 1-aminocyclopropane-1-carboxylic acid oxidase. ACO1. ACC oxidase.
- 10 AAB70883.1 U19856 *Pelargonium x hortorum*
DESCRIPTION: 1-aminocyclopropane-1-carboxylate oxidase.
- 15 AAC67233.1 AF033582 *Cucumis sativus*
DESCRIPTION: ACC oxidase 2. Cs-ACO2.
- 20 AAB02051.1 L76283 *Carica papaya*
DESCRIPTION: formation of ethylene. 1-aminocyclopropane-1-carboxylate oxidase. putative.
- 25 BAA33377.1 AB006806 *Cucumis sativus*
DESCRIPTION: ACC oxidase. CS-ACO1.
- 30 BAA33378.1 AB006807 *Cucumis sativus*
DESCRIPTION: ACC oxidase. CS-ACO2.
- CAA71140.1 Y10034 *Rumex palustris*
DESCRIPTION: 1-aminocyclopropane-1-carboxylic acid oxidase.
- 35 AAA33644.1 M98357 *Pisum sativum*
DESCRIPTION: convert ACC to ethylene. 1-aminocyclopropane-1-carboxylate oxidase.
- 40 AAC48921.1 U06046 *Vigna radiata*
DESCRIPTION: 1-aminocyclopropane-1-carboxylate oxidase homolog.
- 45 AAK07883.1 AF315316 *Vigna radiata*
DESCRIPTION: ACC oxidase. ACO.

AAB65777.1 U97522 *Vitis vinifera*
DESCRIPTION: class IV endochitinase. VvChi4B.

15 AAB65776.1 U97521 Vitis vinifera
DESCRIPTION: class IV endochitinase. VvChi4A.

20 CAC17793.1 AJ301671 *Nicotiana sylvestris*
DESCRIPTION: hydrolysis of chitin. endochitinase. chnb. class I
chitinase.

25 AAA34070.1 M15173 *Nicotiana tabacum*
DESCRIPTION: endochitinase precursor (EC 3.2.1.14).

CAA30142.1 X07130 Solanum tuberosum
30 DESCRIPTION: endochitinase.

CAA53626.1 X76041 *Triticum aestivum*
DESCRIPTION: endochitinase. CHI.

140

AAB94587.1 AF022458 Glycine max
DESCRIPTION: CYP98A2p. CYP98A2. cytochrome P450 monooxygenase.

40

BAA92894.1 AB006790 Petunia x hybrida
DESCRIPTION: cytochrome P450. IMT-2.

45 AAD56282.1 AF155332 Petunia x hybrida

DESCRIPTION: flavonoid 3'-hydroxylase. Ht1. cytochrome P450; CYP75B2.

- 5 AAG44132.1 AF218296 *Pisum sativum*
DESCRIPTION: cytochrome P450. P450 isolog.
- 10 CAA65580.1 X96784 *Nicotiana tabacum*
DESCRIPTION: cytochrome P450. hsr515.
- 15 AAA32913.1 M32885 *Persea americana*
DESCRIPTION: cytochrome P-450LXXIA1 (cyp71A1).
- 20 CAA64635.1 X95342 *Nicotiana tabacum*
DESCRIPTION: cytochrome P450. hsr515. hypersensitivity-related gene.
- 25 CAA70575.1 Y09423 *Nepeta racemosa*
DESCRIPTION: cytochrome P450. CYP71A5.
- 30 BAB40323.1 AB037244 *Asparagus officinalis*
DESCRIPTION: cytochrome P450. ASPI-1.
- BAB40324.1 AB037245 *Asparagus officinalis*
DESCRIPTION: cytochrome P450. ASPI-2.
- 35 CAA50312.1 X70981 *Solanum melongena*
DESCRIPTION: P450 hydroxylase. CYPEG2.
- CAA50155.1 X70824 *Solanum melongena*
DESCRIPTION: flavonoid hydroxylase (P450). CYP75.
- 40 AAB17562.1 U72654 *Eustoma grandiflorum*
DESCRIPTION: flavonoid 3'5'-hydroxylase. F3'5'H. cytochrome P450; CYP75.
- 45 BAA84071.1 AB028151 *Antirrhinum majus*
DESCRIPTION: flavone synthase II. cytochrome P450. AFNS2.

- AAC32274.1 AF081575 *Petunia x hybrida*
DESCRIPTION: flavonoid 3',5'-hydroxylase. Hfl. P450 enzyme.
- 5
- AAG34695.1 AF313492 *Matthiola incana*
DESCRIPTION: putative cytochrome P450.
- 10
- AAB94588.1 AF022459 *Glycine max*
DESCRIPTION: CYP71D10p. CYP71D10. cytochrome P450 monooxygenase.
- 15
- AAD37433.1 AF150881 *Lycopersicon esculentum x Lycopersicon peruvianum*
DESCRIPTION: catalyzes the hydroxylation of ferulic acid to
5-hydroxyferulic acid. ferulate-5-hydroxylase. CYP84. cytochrome
P450-dependent monooxygenase; F5H; FAH1.
- 20
- CAA71517.1 Y10493 *Glycine max*
DESCRIPTION: putative cytochrome P450.
- 25
- BAA13414.1 D87520 *Glycyrrhiza echinata*
DESCRIPTION: putative trans-cinnamic acid 4-hydroxylase. cytochrome P450
(CYP73A14). CYP Ge-1.
- 30
- AAA19701.1 L24438 *Thlaspi arvense*
DESCRIPTION: cytochrome P450.
- 35
- CAA50645.1 X71654 *Solanum melongena*
DESCRIPTION: P450 hydroxylase.
- 40
- BAA03635.1 D14990 *Solanum melongena*
DESCRIPTION: Cytochrome P-450EG4.
- 45
- BAA93634.1 AB025016 *Lotus japonicus*
DESCRIPTION: cytochrome P450.
- 50
- AAC05148.1 AF049067 *Pinus radiata*
DESCRIPTION: cytochrome P450. PRE74.

CAA70576.1 Y09424 *Nepeta racemosa*
DESCRIPTION: cytochrome P450. CYP71A6.

5

AAG10196.1 AF286647 *Gossypium arboreum*
DESCRIPTION: cinnamate-4-hydroxylase. LP89. P450.

10

AAB94584.1 AF022157 *Glycine max*
DESCRIPTION: capable of catalyzing the metabolism of phenylurea
herbicides. CYP71A10. CYP71A10. cytochrome P450 monooxygenase.

15

CAA50648.1 X71657 *Solanum melongena*
DESCRIPTION: P450 hydroxylase.

20

CAB43505.1 AJ239051 *Cicer arietinum*
DESCRIPTION: cytochrome P450. cyp81E2.

141

25

AAB97167.1 AF030882 *Zea mays*
DESCRIPTION: SU1 isoamylase. sugary1. starch debranching enzyme.

30

AAA91298.1 U18908 *Zea mays*
DESCRIPTION: Su1p. Sugary1. similar to *Pseudomonas* sp. isoamylase,
Swiss-Prot Accession Number P26501.

35

AAD33889.1 AF142589 *Hordeum vulgare*
DESCRIPTION: isoamylase 1.

40

BAA29041.1 AB015615 *Oryza sativa*
DESCRIPTION: isoamylase.

45

AAD33891.1 AF142591 *Solanum tuberosum*
DESCRIPTION: isoamylase 1.

AAD33890.1 AF142590 *Triticum aestivum*

DESCRIPTION: isoamylase 1.

5 AAD53260.1 AF142588 Hordeum vulgare
DESCRIPTION: isoamylase 1.

145

10 AAG35777.1 AF273844 Brassica oleracea var. alboglabra
DESCRIPTION: thioredoxin-h-like protein 1. THL1.

15 AAB53694.1 U59379 Brassica napus
DESCRIPTION: thioredoxin-h-like-1. THL-1. thioredoxin-h homolog.

20 CAA61908.1 X89759 Brassica oleracea
DESCRIPTION: pollen coat protein. bopcl7.

BAA25681.1 AB010434 Brassica rapa
DESCRIPTION: Thioredoxin. PEC-2.

25 BAB20886.1 AB053294 Oryza sativa
DESCRIPTION: thioredoxin h. RTRXH2.

30 AAB53695.1 U59380 Brassica napus
DESCRIPTION: thioredoxin-h-like-2. THL-2. Description: thioredoxin-h
homolog.

35 AAF88067.1 AF286593 Triticum aestivum
DESCRIPTION: thioredoxin H. similar to wheat thioredoxin H.

40 CAA94534.1 Z70677 Ricinus communis
DESCRIPTION: thioredoxin.

CAA05081.1 AJ001903 Triticum turgidum subsp. durum
DESCRIPTION: thioredoxin H.

45 CAA49540.1 X69915 Triticum aestivum

DESCRIPTION: unnamed protein product.

5 BAA13524.1 D87984 Fagopyrum esculentum
DESCRIPTION: thioredoxin.

10 CAA41415.1 X58527 Nicotiana tabacum
DESCRIPTION: thioredoxin.

CAA77847.1 Z11803 Nicotiana tabacum
DESCRIPTION: THIOREDOXIN.

15 AAC32111.1 AF051206 Picea mariana
DESCRIPTION: probable thioredoxin H. Sb09. similar to Nicotiana tabacum
thioredoxin H1 encoded by GenBank Accession Number X58527.

20 BAA05546.1 D26547 Oryza sativa
DESCRIPTION: rice thioredoxin h.

25 BAA04864.1 D21836 Oryza sativa
DESCRIPTION: thioredoxin h. encoding rice phloem sap 13kD protein-1.

30 AAB51522.1 U92541 Oryza sativa
DESCRIPTION: thioredoxin h.

35 AAD49232.1 AF159387 Lolium perenne
DESCRIPTION: thioredoxin-like protein. Trx.

AAD56954.1 AF186240 Secale cereale
DESCRIPTION: thioredoxin-like protein. Trx.

40 AAD49231.1 AF159386 Secale cereale
DESCRIPTION: thioredoxin-like protein. Trx.

45 AAD49230.1 AF159385 Hordeum bulbosum
DESCRIPTION: thioredoxin-like protein. Trx.

- AAC04671.1 AF018174 *Brassica napus*
DESCRIPTION: thioredoxin-f. TRXF.
- 5 AAB47556.1 U87141 *Mesembryanthemum crystallinum*
DESCRIPTION: thioredoxin h.
- 10 CAA53900.1 X76269 *Pisum sativum*
DESCRIPTION: thioredoxin m.
- 15 AAC49358.1 U35831 *Pisum sativum*
DESCRIPTION: thioredoxin m. chloroplastic.
- 20 CAA33082.1 X14959 *Spinacia oleracea*
DESCRIPTION: pre-thioredoxin f (AA -77 to 113).
- 25 CAA06736.1 AJ005841 *Oryza sativa*
DESCRIPTION: thioredoxin M.
- 30 CAA55398.1 X78821 *Chlamydomonas reinhardtii*
DESCRIPTION: thioredoxin m. Trx.
- 35 CAA56851.1 X80888 *Chlamydomonas reinhardtii*
DESCRIPTION: thioredoxin m. Trx m.
- 40 CAA44209.1 X62335 *Chlamydomonas reinhardtii*
DESCRIPTION: thioredoxin Ch2. Trx.
- 45 AAA92464.1 L40957 *Zea mays*
DESCRIPTION: regulation of activities of photosynthetic enzymes.
thioredoxin M. putative.
- CAA06735.1 AJ005840 *Triticum aestivum*
DESCRIPTION: thioredoxin M.

- CAB91554.1 AJ277900 *Vitis vinifera*
DESCRIPTION: beta 1-3 glucanase. gl.
- 5 AAB03501.1 U41323 *Glycine max*
DESCRIPTION: beta-1,3-glucanase. SGN1.
- 10 AAA34078.1 M63634 *Nicotiana plumbaginifolia*
DESCRIPTION: regulator of beta(1,3)-glucanase. beta(1,3)-glucanase
regulator.
- 15 CAA30261.1 X07280 *Nicotiana plumbaginifolia*
DESCRIPTION: beta-glucanase.
- 20 AAA51643.1 M23120 *Nicotiana plumbaginifolia*
DESCRIPTION: beta-glucanase precursor.
- 25 AAA87456.1 U22147 *Hevea brasiliensis*
DESCRIPTION: beta-1,3-glucanase. HGN1. hydrolytic enzyme.
- CAB38443.1 AJ133470 *Hevea brasiliensis*
DESCRIPTION: beta-1,3-glucanase. hgn1.
- 30 AAA03618.1 M80608 *Lycopersicon esculentum*
DESCRIPTION: beta-1,3-glucanase.
- 35 AAA18928.1 U01901 *Solanum tuberosum*
DESCRIPTION: catalyzes the hydrolysis of 1,3-beta-D-glucoside linkages in
1,3,-beta-D-glucans (such as laminarin). 1,3-beta-D-glucan
glucanohydrolase; endo-1,3-beta-D-glucanase; 1,3-beta-glucanase (basic,
class I). glub2. plant defense gene; induced expression in response to
40 infection, elicitor, ethylene, wounding.
- AAC19114.1 AF067863 *Solanum tuberosum*
DESCRIPTION: 1,3-beta-glucan glucanohydrolase. glucanase.
- 45

CAA92278.1 Z68154 *Gossypium hirsutum*
DESCRIPTION: 1,3-beta-glucanase.

5 AAG24921.1 AF311749 *Hevea brasiliensis*
DESCRIPTION: beta-1,3-glucanase.

10 AAA63539.1 M60402 *Nicotiana tabacum*
DESCRIPTION: glucan beta-1,3-glucanase. glucanase GLA.

15 AAA63540.1 M60403 *Nicotiana tabacum*
DESCRIPTION: glucan-1,3-beta-glucosidase. glucanase GLB.

20 AAA88794.1 U01900 *Solanum tuberosum*
DESCRIPTION: catalyzes the hydrolysis of 1,3-beta-D-glucoside linkages in
1,3,-beta-D-glucans (such as laminarin). 1,3-beta-D-glucan
glucanohydrolase; endo-1,3-beta-D-glucanase; 1,3-beta-glucanase (basic,
class I). gluB1. plant defense gene; induced expression in response to
infection, elicitor, ethylene, wounding.

25 AAA63541.1 M59442 *Nicotiana tabacum*
DESCRIPTION: basic beta-1,3-glucanase. glucanase.

30 AAB82772.2 AF001523 *Musa acuminata*
DESCRIPTION: beta-1, 3-glucanase. similar to beta-1, 3-glucanase.

35 CAA37289.1 X53129 *Phaseolus vulgaris*
DESCRIPTION: 1,3,-beta-D-glucanase.

AAF08679.1 AF004838 *Musa acuminata*
DESCRIPTION: beta-1,3-glucanase.

40 AAD33881.1 AF141654 *Nicotiana tabacum*
DESCRIPTION: beta-1,3-glucanase. GGL4.

45 AAD33880.1 AF141653 *Nicotiana tabacum*
DESCRIPTION: beta-1,3-glucanase. GGL1.

AAA33648.1 L02212 *Pisum sativum*
 DESCRIPTION: beta-1,3-glucan hydrolysis. beta-1,3-glucanase. putative.

AAA34082.1 M20620 *Nicotiana tabacum*
 DESCRIPTION: prepro-beta-1,3-glucanase precursor.

AAA19111.1 U01902 *Solanum tuberosum*
 DESCRIPTION: catalyzes the hydrolysis of 1,3-beta-D-glucoside linkages in
 1,3,-beta-D-glucans (such as laminarin). 1,3-beta-D-glucan
 glucanohydrolase; endo-1,3-beta-D-glucanase; 1,3-beta-glucanase (basic,
 class I). gluB3. plant defense gene; induced expression in response to
 infection, elicitor, ethylene, wounding.

CAA57255.1 X81560 *Nicotiana tabacum*
 DESCRIPTION: (1-)-beta-glucanase. Sp41a.

AAA34053.1 M60464 *Nicotiana tabacum*
 DESCRIPTION: beta-1,3-glucanase.

AAA63542.1 M59443 *Nicotiana tabacum*
 DESCRIPTION: acidic beta-1,3-glucanase. glucanase.

AAB24398.1 S51479 *Pisum sativum*
 DESCRIPTION: beta-1,3-glucanase. beta-1,3-glucanase. This sequence comes
 from Fig. 1B.

AAB41551.1 U27179 *Medicago sativa* subsp. *sativa*
 DESCRIPTION: acidic glucanase.

AAD10384.1 U72253 *Oryza sativa*
 DESCRIPTION: beta-1,3-glucanase precursor. Gns7.

AAA03617.1 M80604 *Lycopersicon esculentum*
 DESCRIPTION: beta-1,3-glucanase.

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- 631 -

3-O-methyltransferase. CCoAOMT.

- 5 CAB05369.1 Z82982 *Nicotiana tabacum*
DESCRIPTION: methylation of caffeoyl-CoA in lignin biosynthesis.
caffeoyl-CoA O-methyltransferase 5. CCoAOMT-5.
- 10 AAA80651.1 U27116 *Populus tremuloides*
DESCRIPTION: caffeoyl-CoA 3-O-methyltransferase. S-adenyosyl-methionine
caffeoyl-CoA 3-O-methyltransferase; similar to Swiss-Prot Accession Number
P28034; similar to proteins encoded by GenBank accession Numbers U20736,
U13151, and L22203; Mr = 27.9 kDa and pI = 5.16.
- 15 AAC08395.1 AF053553 *Mesembryanthemum crystallinum*
DESCRIPTION: caffeoyl-CoA O-methyltransferase.
- 20 CAA12200.1 AJ224896 *Populus balsamifera* subsp. *trichocarpa*
DESCRIPTION: methylates lignin precursors. caffeoyl-CoA
3-O-methyltransferase.
- 25 CAA12199.1 AJ224895 *Populus balsamifera* subsp. *trichocarpa*
DESCRIPTION: methylates lignin precursors. caffeoyl-CoA
3-O-methyltransferase.
- 30 CAA11495.1 AJ223620 *Populus balsamifera* subsp. *trichocarpa*
DESCRIPTION: caffeoyl CoA 3-O-methyltransferase. CCoAOMT2.
- 35 AAD50443.1 AF168780 *Eucalyptus globulus*
DESCRIPTION: caffeoyl-CoA O-methyltransferase. CCoAOMT2.
- 40 AAF44689.1 AF240466 *Populus tomentosa*
DESCRIPTION: caffeoyl-CoA O-methyltransferase. CCoAOMT.
- 45 AAC49913.1 U38612 *Nicotiana tabacum*
DESCRIPTION: methylation of caffeoyl-CoA in feruloyl-coA in
phenylpropanoid pathway. caffeoyl-coenzymeA O-methyltransferase.
CCoAOMT-1.

CAA72911.1 Y12228 Eucalyptus gunnii
DESCRIPTION: caffeoyl-CoA O-methyltransferase. COOAMT.

5

AAC49916.1 U62736 Nicotiana tabacum
DESCRIPTION: methylation of caffeoyl-CoA in feruloyl-CoA in
phenylpropanoid pathway (lignin biosynthesis). caffeoyl-CoA
O-methyltransferase 4. CCoAOMT-4.

10

BAA78733.1 AB023482 Oryza sativa
DESCRIPTION: ESTs AU058067(E20733), AAU058070(E20873) correspond
to a
15 region of the predicted gene.; Similar to Populus tremuloides caffeoyl-CoA
3-O-methyltransferase mRNA, complete cds.(U27116).

20

CAA91228.1 Z56282 Nicotiana tabacum
DESCRIPTION: plant defense and lignification. caffeoyl-CoA
O-methyltransferase. NTCCOAOMT.

25

AAC49914.1 U62734 Nicotiana tabacum
DESCRIPTION: methylation of caffeoyl-CoA in feruloyl-CoA in
phenylpropanoid pathway (lignin biosynthesis). caffeoyl-CoA
O-methyltransferase 2. CCoAOMT-2.

30

AAC26191.1 AF046122 Eucalyptus globulus
DESCRIPTION: catalyses the methylation of caffeoyl CoA in lignin
biosynthesis. caffeoyl-CoA 3-O-methyltransferase. CCOMT.
S-adenosyl-L-methionine:caffeoyl-CoA 3-O-methyltransferase.

35

AAC49915.1 U62735 Nicotiana tabacum
DESCRIPTION: methylation of caffeoyl-CoA in feruloyl-CoA in
phenylpropanoid pathway (lignin biosynthesis). caffeoyl-CoA
O-methyltransferase 3. CCoAOMT-3.

40

AAD02050.1 AF036095 Pinus taeda
DESCRIPTION: caffeoyl-CoA O-methyltransferase. CCoAOMT. lignin
pathway
45 O-methyltransferase.

AAK16714.1 AF327458 *Populus alba* x *Populus glandulosa*
DESCRIPTION: caffeoyl-CoA 3-O-methyltransferase. CCoAOMT.

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CAB45150.1 AJ242981 *Zea mays*
DESCRIPTION: lignin synthesis. Caffeoyl CoA O-methyltransferase.
ccoAOMT.

10

CAB45149.1 AJ242980 *Zea mays*
DESCRIPTION: lignin synthesis. Caffeoyl CoA O-methyltransferase.
ccoAOMT.

15

AAB61680.1 L22203 *Stellaria longipes*
DESCRIPTION: S-adenosyl-L-methionine:trans-caffeoyl-CoA
3-O-methyltransferase. 26.7-kDa; pI=5.3.

20

BAA88234.1 AB035144 *Citrus natsudaoidai*
DESCRIPTION: Methylation of caffeoyl-coA in feruloyl-coA in
phenylpropanoid pathway. caffeoyl-CoA 3-O-methyltransferase. CCoAMT.

25

BAA81776.1 AP000364 *Oryza sativa*
DESCRIPTION: ESTs C98431(E0144),C71728(E0144) correspond to a region
of
the predicted gene.; Similar to *Medicago sativa* S-adenosyl-L-methionine.
(U20736).

30

BAA81774.1 AP000364 *Oryza sativa*
DESCRIPTION: ESTs AU030740(E60171),AU030739(E60171) correspond to
a
region of the predicted gene.; Similar to *Populus tremuloides* caffeoyl-CoA
3-O-methyltransferase. (U27116).

35

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BAA81777.1 AP000364 *Oryza sativa*
DESCRIPTION: Similar to *Petroselinum crispum* caffeoyl-CoA
3-O-methyltransferase. (S49342).

45

CAA10217.1 AJ130841 *Populus balsamifera* subsp. *trichocarpa*
DESCRIPTION: methylates lignin precursors. caffeoyl-CoA

3-O-methyltransferase.

- CAA04769.1 AJ001447 *Fragaria vesca*
5 DESCRIPTION: caffeoyl-CoA 3-O-methyltransferase. putative.
- AAD50441.1 AF168778 *Eucalyptus globulus*
10 DESCRIPTION: caffeoyl-CoA O-methyltransferase. CCoAOMT1.
- AAD50442.1 AF168779 *Eucalyptus globulus*
DESCRIPTION: caffeoyl-CoA O-methyltransferase. CCoAOMT2.
- 15 AAC15067.1 AF060180 *Nicotiana tabacum*
DESCRIPTION: plant lignification and defense. caffeoyl-coenzyme A trunc2.
truncated caffeoyl-coenzyme A.
- 20 152

- AAK11255.1 AF329729 *Nicotiana tabacum*
DESCRIPTION: regulator of gene silencing. rgs-CaM; calmodulin-related
protein.
- 25 AAD10245.1 AF030033 *Phaseolus vulgaris*
DESCRIPTION: calmodulin. CaM. EF-hand protein; calcium-dependent
protein;
30 functions in calcium signal transduction pathways.
- CAA62150.1 X90560 *Physcomitrella patens*
DESCRIPTION: Calmodulin. CaM.
- 35 BAA94696.1 AB041711 *Chara corallina*
DESCRIPTION: calmodulin. cccam1.
- 40 BAA96536.1 AB044286 *Chara corallina*
DESCRIPTION: calmodulin. ccam.
- 45 BAA94697.1 AB041712 *Chara corallina*
DESCRIPTION: calmodulin. cccam2.

- 5 BAA87825.1 AP000815 *Oryza sativa*
DESCRIPTION: ESTs AU030013(E50493),AU081341(E50493) correspond to
a region of the predicted gene. Similar to *O.sativa* gene encoding
calmodulin. (Z12828).
- 10 CAA61980.1 X89890 *Bidens pilosa*
DESCRIPTION: Calmodulin.
- 15 AAA19571.1 U10150 *Brassica napus*
DESCRIPTION: calcium binding. calmodulin. bcm1.
- 20 AAA87347.1 M88307 *Brassica juncea*
DESCRIPTION: calmodulin.
- 25 CAA74111.1 Y13784 *Mougeotia scalaris*
DESCRIPTION: Calmodulin.
- 30 AAA92677.1 U13736 *Pisum sativum*
DESCRIPTION: binds calcium. calmodulin-like protein.
- 35 AAA34015.1 L01433 *Glycine max*
DESCRIPTION: calcium-binding regulatory protein. calmodulin. SCaM-4.
putative.
- 40 AAA33083.1 M20729 *Chlamydomonas reinhardtii*
DESCRIPTION: calmodulin.
- 45 AAK25753.1 AF334833 *Castanea sativa*
DESCRIPTION: calmodulin. CAM2.
- AAF73157.1 AF150059 *Brassica napus*
DESCRIPTION: calmodulin. CaM1. involved in seed germination.

CAA74307.1 Y13974 Zea mays
DESCRIPTION: calmodulin.

5 AAA34238.1 L20507 Vigna radiata
DESCRIPTION: calmodulin.

10 AAA34237.1 L20691 Vigna radiata
DESCRIPTION: calmodulin.

15 AAC49587.1 U49105 Triticum aestivum
DESCRIPTION: calmodulin TaCaM4-1. calcium-binding protein.

20 AAC49586.1 U49104 Triticum aestivum
DESCRIPTION: calmodulin TaCaM3-3. calcium-binding protein.

AAC49585.1 U49103 Triticum aestivum
DESCRIPTION: calmodulin TaCaM3-2. calcium-binding protein.

25 AAC49584.1 U48693 Triticum aestivum
DESCRIPTION: calmodulin TaCaM3-1. calcium-binding protein.

30 AAC49580.1 U48689 Triticum aestivum
DESCRIPTION: calmodulin TaCaM1-3. calcium-binding protein.

35 AAC49579.1 U48688 Triticum aestivum
DESCRIPTION: calmodulin TaCaM1-2. calcium binding protein.

AAC49578.1 U48242 Triticum aestivum
DESCRIPTION: calmodulin TaCaM1-1. calcium-binding.

40 AAA34014.1 L01432 Glycine max
DESCRIPTION: calcium-binding regulatory protein. calmodulin. SCaM-3.
putative.

45 AAA03580.1 L01431 Glycine max

DESCRIPTION: calcium-binding regulatory protein. calmodulin. SCaM-2.
putative.

5 AAA34013.1 L01430 Glycine max

DESCRIPTION: calcium-binding regulatory protein. calmodulin. SCaM-1.
putative.

10 AAB36130.1 S81594 Vigna radiata

DESCRIPTION: auxin-regulated calmodulin. auxin-regulated calmodulin,
arCaM. This sequence comes from Fig. 1; arCaM.

15 AAA33901.1 L18913 Oryza sativa

DESCRIPTION: calcium binding protein, signal transduction. calmodulin.
putative.

20 AAA92681.1 U13882 Pisum sativum

DESCRIPTION: calcium-binding protein. calmodulin.

25 AAA33706.1 M80836 Petunia x hybrida

DESCRIPTION: calmodulin. CAM81.

30 AAA33705.1 M80831 Petunia x hybrida

DESCRIPTION: calmodulin-related protein. CAM53.

CAA78287.1 Z12827 Oryza sativa

DESCRIPTION: calcium binding protein, signal transduction. calmodulin.

35

CAA46150.1 X65016 Oryza sativa

DESCRIPTION: calmodulin. cam.

40 CAA36644.1 X52398 Medicago sativa

DESCRIPTION: calmodulin (AA 1-149).

45 CAA43143.1 X60738 Malus x domestica

DESCRIPTION: Calmodulin. CaM.

DESCRIPTION: class IV endochitinase. VvChi4A.

CAA61281.1 X88803 *Vigna unguiculata*
5 DESCRIPTION: chitinase class 4. CHI4.

AAB65777.1 U97522 *Vitis vinifera*
10 DESCRIPTION: class IV endochitinase. VvChi4B.

BAA22966.1 D45182 *Chenopodium amaranticolor*
DESCRIPTION: chitinase.

15 BAA22968.1 D45184 *Chenopodium amaranticolor*
DESCRIPTION: chitinase.

20 BAA22965.1 D45181 *Chenopodium amaranticolor*
DESCRIPTION: chitinase.

CAA43708.1 X61488 *Brassica napus*
25 DESCRIPTION: chitinase.

BAA22967.1 D45183 *Chenopodium amaranticolor*
30 DESCRIPTION: chitinase.

CAA53544.1 X75945 *Beta vulgaris*
DESCRIPTION: chitinase. Ch4.

35 AAC49435.1 U52845 *Daucus carota*
DESCRIPTION: class IV chitinase EP3-1/H5. EP3.

40 AAB08468.1 U52846 *Daucus carota*
DESCRIPTION: class IV chitinase EP3-2/H1. EP3.

AAB08470.1 U52848 *Daucus carota*
45 DESCRIPTION: class IV chitinase EP3B/E6. EP3.

AAB08469.1 U52847 Daucus carota
DESCRIPTION: class IV chitinase EP3-3/E7. EP3.

5

AAA33445.1 M84165 Zea mays
DESCRIPTION: chitinase B. seed chitinase.

10

AAA33444.1 M84164 Zea mays
DESCRIPTION: chitinase A. seed chitinase.

15

AAA32916.1 L25826 Beta vulgaris
DESCRIPTION: chitinase. SP2.

20

AAD28733.1 AF112966 Triticum aestivum
DESCRIPTION: chitinase IV precursor. Cht4.

25

BAB21377.1 AB054811 Oryza sativa
DESCRIPTION: PR-3 class IV chitinase. Cht4. Catalytic domain.

BAB21374.1 AB054687 Oryza sativa
DESCRIPTION: PR-3 class IV chitinase. Cht4. catalytic domain.

30

BAA19793.1 AB003194 Oryza sativa
DESCRIPTION: chitinase IIb.

35

AAA85364.1 L42467 Picea glauca
DESCRIPTION: chitinase. chi.

40

AAB01665.1 U21848 Brassica napus
DESCRIPTION: chitinase class IV. LSC222.

AAC35981.1 AF090336 Citrus sinensis
DESCRIPTION: chitin hydrolase. chitinase CHI1. chi1.

45

AAD28730.1 AF112963 Triticum aestivum

DESCRIPTION: chitinase II precursor. Cht2.

5 AAF04454.1 AF000966 *Poa pratensis*
DESCRIPTION: chitinase. Chi2.

10 CAC17793.1 AJ301671 *Nicotiana sylvestris*
DESCRIPTION: hydrolysis of chitin. endochitinase. chnb. class I
chitinase.

15 AAF04453.1 AF000964 *Poa pratensis*
DESCRIPTION: chitinase. Chi1.

20 CAA34812.1 X16938 *Nicotiana tabacum*
DESCRIPTION: chitinase precursor.

CAA34813.1 X16939 *Nicotiana tabacum*
DESCRIPTION: chitinase precursor (AA -23 to 306).

25 CAA45822.1 X64519 *Nicotiana tabacum*
DESCRIPTION: chitinase B class I. CHN200.

30 CAA35945.1 X51599 *Nicotiana tabacum*
DESCRIPTION: chitinase. CHN50.

35 AAB23374.1 S44869 *Nicotiana tabacum*
DESCRIPTION: basic chitinase. basic chitinase. This sequence comes from
Fig. 1.

40 AAA34070.1 M15173 *Nicotiana tabacum*
DESCRIPTION: endochitinase precursor (EC 3.2.1.14).

CAA30142.1 X07130 *Solanum tuberosum*
DESCRIPTION: endochitinase.

45 CAA33517.1 X15494 *Solanum tuberosum*

DESCRIPTION: pre-chitinase (AA -26 to 302).

- 5 AAG53609.1 AF280437 *Secale cereale*
DESCRIPTION: 31.7 kDa class I endochitinase-antifreeze protein precursor.
cht9.
- 10 CAB01591.1 Z78202 *Persea americana*
DESCRIPTION: hydrolysis of the 1,4-beta-linkages of chitin.
endochitinase. chl1.
- 15 CAA53626.1 X76041 *Triticum aestivum*
DESCRIPTION: endochitinase. CHI.
- 20 CAA78845.1 Z15140 *Lycopersicon esculentum*
DESCRIPTION: chitinase. Encodes 30 kD basic intracellular chitinase.
- 25 AAC16010.1 AF061805 *Elaeagnus umbellata*
DESCRIPTION: acidic chitinase.
- 30 AAA32640.1 M94106 *Allium sativum*
DESCRIPTION: chitinase. chitinase.
- 35 AAA32641.1 M94105 *Allium sativum*
DESCRIPTION: chitinase. chitinase.
- 40 AAA56787.1 L34211 *Hordeum vulgare*
DESCRIPTION: hydrolysis of chitin. chitinase. CHI33.
- 45 AAA17409.1 U02607 *Solanum tuberosum*
DESCRIPTION: catalyzes the random hydrolysis of
1,4-beta-(2-acetamido-2-deoxy-D-glucoside) linkages in chitin; plant
defense gene. chitinase. chtB3. induced expression in response to
infection, elicitor, ethylene, wounding; preproprotein; gene product
subunit is monomer.
- AAA18332.1 U02605 *Solanum tuberosum*

DESCRIPTION: chalcone synthase. CHS.

5 AAF23578.1 AF112103 *Arabidopsis lyrata* subsp. *petraea*
DESCRIPTION: chalcone synthase. CHS.

10 AAF23576.1 AF112101 *Arabis parishii*
DESCRIPTION: chalcone synthase. CHS.

AAF23574.1 AF112099 *Arabis lyallii*
DESCRIPTION: chalcone synthase. CHS.

15 AAF23566.1 AF112091 *Arabis glabra*
DESCRIPTION: chalcone synthase. CHS.

20 AAF23565.1 AF112090 *Arabis fendleri*
DESCRIPTION: chalcone synthase. CHS.

25 AAF23563.1 AF112088 *Arabis drummondii*
DESCRIPTION: chalcone synthase. CHS.

30 AAF23564.1 AF112089 *Arabis drummondii*
DESCRIPTION: chalcone synthase. CHS.

AAF23579.1 AF112104 *Arabidopsis lyrata* subsp. *petraea*
DESCRIPTION: chalcone synthase. CHS.

35 AAF23573.1 AF112098 *Arabis lignifera*
DESCRIPTION: chalcone synthase. CHS.

40 AAF23560.1 AF112085 *Cardamine amara*
DESCRIPTION: chalcone synthase. CHS.

45 AAG43348.1 AF144530 *Rorippa amphibia*
DESCRIPTION: chalcone synthase. chs.

AAG43356.1 AF144538 *Cardamine penzesii*
DESCRIPTION: chalcone synthase. chs.

5

AAG43359.1 AF144541 *Sisymbrium irio*
DESCRIPTION: chalcone synthase. chs.

10 AAG43352.1 AF144534 *Lepidium campestre*
DESCRIPTION: chalcone synthase. chs.

15 CAA32495.1 X14314 *Sinapis alba*
DESCRIPTION: chalcone synthase (AA 1-395).

20 AAG43357.1 AF144539 *Cardamine rivularis*
DESCRIPTION: chalcone synthase. chs.

AAF23583.1 AF112108 *Barbarea vulgaris*
DESCRIPTION: chalcone synthase. CHS.

25 AAC31914.1 AF076336 *Brassica napus*
DESCRIPTION: chalcone synthase B2. CHSB2.

30 AAC31912.1 AF076334 *Brassica napus*
DESCRIPTION: chalcone synthase A2. CHSA2.

35 AAF23577.1 AF112102 *Arabis pauciflora*
DESCRIPTION: chalcone synthase. CHS.

40 AAG43350.1 AF144532 *Cochlearia danica*
DESCRIPTION: chalcone synthase. chs.

CAA34460.1 X16437 *Sinapis alba*
DESCRIPTION: chalcone synthase.

45 CAA35600.1 X17577 *Matthiola incana*

DESCRIPTION: chalcone synthase (AA 1-394).

5 AAG43358.1 AF144540 Cardamine pratensis
DESCRIPTION: chalcone synthase. chs.

10 AAG43353.1 AF144535 Thlaspi arvense
DESCRIPTION: chalcone synthase. chs.

AAC31913.1 AF076335 Brassica napus
DESCRIPTION: chalcone synthase B1. CHSB1.

15 AAF23571.1 AF112096 Arabis hirsuta
DESCRIPTION: chalcone synthase. CHS.

20 AAF23582.1 AF112107 Arabis turrita
DESCRIPTION: chalcone synthase. CHS.

25 AAG43406.1 AF174529 Aubrieta deltoidea
DESCRIPTION: chalcone synthase. chs.

30 AAG43355.1 AF144537 Alliaria petiolata
DESCRIPTION: chalcone synthase. chs.

AAF23580.1 AF112105 Arabis procurrens
DESCRIPTION: chalcone synthase. CHS.

35 AAF23572.1 AF112097 Arabis jacquinii
DESCRIPTION: chalcone synthase. CHS.

40 AAF23562.1 AF112087 Arabis blepharophylla
DESCRIPTION: chalcone synthase. CHS.

45 AAF23584.1 AF112109 Aubrieta deltoidea
DESCRIPTION: chalcone synthase. CHS.

- AAG43354.1 AF144536 *Microthlaspi perfoliatum*
DESCRIPTION: chalcone synthase. chs.
- 5 AAF23557.1 AF112082 *Aethionema grandiflora*
DESCRIPTION: chalcone synthase. CHS.
- 10 AAF23558.1 AF112083 *Arabis alpina*
DESCRIPTION: chalcone synthase. CHS.
- 15 AAF23559.1 AF112084 *Arabis alpina*
DESCRIPTION: chalcone synthase. CHS.
- 20 AAB87072.1 AF031922 *Raphanus sativus*
DESCRIPTION: chalcone synthase. CHS.
- AAG43360.1 AF144542 *Ionopsidium abulense*
DESCRIPTION: chalcone synthase. chs.
- 25 AAC31911.1 AF076333 *Brassica napus*
DESCRIPTION: chalcone synthase A1. CHSA1.
- 156
- 30 -----
AAD10327.1 U63534 *Fragaria x ananassa*
DESCRIPTION: catalyzes the reduction of cinnamylaldehydes leading to
monolignols. cinnamyl alcohol dehydrogenase. CAD. involved with lignin
biosynthesis.
- 35
- AAK28509.1 AF320110 *Fragaria x ananassa*
DESCRIPTION: cinnamyl alcohol dehydrogenase.
- 40 AAB38503.1 U79770 *Mesembryanthemum crystallinum*
DESCRIPTION: cinnamyl-alcohol dehydrogenase Eli3.
- 45 CAA48028.1 X67817 *Petroselinum crispum*
DESCRIPTION: Eli3.

- AAC15467.1 U24561 *Apium graveolens*
 DESCRIPTION: converts mannitol to mannose. mannitol dehydrogenase. Mtd.
 5 1-oxidoreductase; induced with sodium salicylate; similar to the plant
 defense gene ELI3 in *Arabidopsis thaliana*, PIR Accession Number S28044; EC
 number unassigned; MTD.
- 10 AAC35846.1 AF083333 *Medicago sativa*
 DESCRIPTION: cinnamyl-alcohol dehydrogenase. MsaCad1.
- 15 AAC61854.1 AF067082 *Apium graveolens*
 DESCRIPTION: oxidizes mannitol to mannose. mannitol dehydrogenase. Mtd.
 mannitol 1-oxidoreductase.
- 20 AAA74882.1 L36823 *Stylosanthes humilis*
 DESCRIPTION: cinnamyl-alcohol dehydrogenase. CAD1.
- 25 AAA74883.1 L36456 *Stylosanthes humilis*
 DESCRIPTION: cinnamyl-alcohol dehydrogenase. CAD3.
- 30 AAF72100.1 AF146691 *Lycopersicon esculentum*
 DESCRIPTION: ELI3. Eli3. similar] to cinnamyl alcohol dehydrogenase.
- CAA86072.1 Z37991 *Pinus taeda*
 DESCRIPTION: cinnamyl alcohol dehydrogenase.
- 35 CAA05095.1 AJ001924 *Picea abies*
 DESCRIPTION: cinnamyl alcohol dehydrogenase. cad2.
- 40 AAB38774.1 U62394 *Pinus radiata*
 DESCRIPTION: cinnamyl alcohol dehydrogenase. CAD.
- 45 CAA51226.1 X72675 *Picea abies*
 DESCRIPTION: cinnamyl-alcohol dehydrogenase.

- CAA05097.1 AJ001926 *Picea abies*
DESCRIPTION: cinnamyl alcohol dehydrogenase. cad8.
- 5 CAA05096.1 AJ001925 *Picea abies*
DESCRIPTION: cinnamyl alcohol dehydrogenase. cad7.
- 10 AAC31166.1 AF060491 *Pinus radiata*
DESCRIPTION: cinnamyl alcohol dehydrogenase. CAD.
- 15 CAA86073.1 Z37992 *Pinus taeda*
DESCRIPTION: cinnamyl alcohol dehydrogenase.
- 20 CAA44216.1 X62343 *Nicotiana tabacum*
DESCRIPTION: cinnamyl-alcohol dehydrogenase. CAD14.
- CAA44217.1 X62344 *Nicotiana tabacum*
DESCRIPTION: cinnamyl-alcohol dehydrogenase. CAD19.
- 25 BAA03099.1 D13991 *Aralia cordata*
DESCRIPTION: cinnamyl alcohol dehydrogenase. cadac1.
- 30 CAA79625.1 Z19573 *Medicago sativa*
DESCRIPTION: lignin biosynthesis. cinnamyl alcohol dehydrogenase.
- 35 AAF43140.1 AF217957 *Populus tremuloides*
DESCRIPTION: cinnamyl alcohol dehydrogenase. CAD.
- 40 AAC35845.1 AF083332 *Medicago sativa*
DESCRIPTION: cinnamyl-alcohol dehydrogenase. MsaCad2.
- CAC07423.1 AJ295837 *Populus balsamifera* subsp. *trichocarpa*
DESCRIPTION: lignin monomer biosynthesis. cinnamyl alcohol dehydrogenase.
cad.
- 45 CAA79622.1 Z19568 *Populus deltoides*

DESCRIPTION: lignin biosynthesis. cinnamyl alcohol dehydrogenase.

- 5 AAC07987.1 AF038561 Eucalyptus globulus
DESCRIPTION: catalyses the reduction of cinnamaldehydes to the corresponding cinnamyl alcohols as the last step in the production of lignin monomers. cinnamyl alcohol dehydrogenase. CAD.
- 10 AAG15553.1 AF294793 Eucalyptus saligna
DESCRIPTION: cinnamyl alcohol dehydrogenase. cad. CAD.
- 15 AAK00679.1 AF229407 Brassica napus
DESCRIPTION: Eli3 product. ELI3-BN-2. protein identity based on similarity to Arabidopsis sequence; intron/exon junctions deduced from alignments to DNA or mRNA sequences already present in the GenBank database.
- 20 CAA46585.1 X65631 Eucalyptus gunnii
DESCRIPTION: cinnamyl-alcohol dehydrogenase. cad.
- 25 CAA53211.1 X75480 Eucalyptus gunnii
DESCRIPTION: cinnamyl-alcohol dehydrogenase. CAD.
- 30 AAK00681.1 AF229409 Brassica napus
DESCRIPTION: Eli3 product. ELI3-BN-4. protein identity based on similarity to Arabidopsis sequence; intron/exon junctions deduced from alignments to DNA or mRNA sequences already present in the GenBank database.
- 35 AAB70908.1 AF010290 Lolium perenne
DESCRIPTION: cinnamyl alcohol dehydrogenase. CAD.
- 40 AAK00682.1 AF229410 Brassica oleracea
DESCRIPTION: Eli3 product. ELI3-BO-1. protein identity based on similarity to Arabidopsis sequence; intron/exon junctions deduced from alignments to DNA or mRNA sequences already present in the GenBank database.
- 45

CAA74070.1 Y13733 Zea mays
DESCRIPTION: cinnamyl alcohol dehydrogenase. cad.

5 CAA06687.1 AJ005702 Zea mays
DESCRIPTION: cinnamyl alcohol dehydrogenase. cad.

10 AAK00678.1 AF229406 Brassica napus
DESCRIPTION: Eli3 product. ELI3-BN-1. protein identity based on
similarity to Arabidopsis sequence; intron/exon junctions deduced from
alignments to DNA or mRNA sequences already present in the GenBank
database.

15 CAA13177.1 AJ231135 Saccharum officinarum
DESCRIPTION: lignin biosynthesis. cinnamyl alcohol dehydrogenase. cad.

20 AAK00684.1 AF229412 Brassica rapa
DESCRIPTION: Eli3 product. ELI3-BR-2. protein identity based on
similarity to Arabidopsis sequence; intron/exon junctions deduced from
alignments to DNA or mRNA sequences already present in the GenBank
database.

25 AAK00680.1 AF229408 Brassica napus
DESCRIPTION: Eli3 product. ELI3-BN-3. protein identity based on
similarity to Arabidopsis sequence; intron/exon junctions deduced from
30 alignments to DNA or mRNA sequences already present in the GenBank
database.

35 AAK00683.1 AF229411 Brassica rapa
DESCRIPTION: Eli3 product. ELI3-BR-1. protein identity based on
similarity to Arabidopsis sequence; intron/exon junctions deduced from
alignments to DNA or mRNA sequences already present in the GenBank
database.

40 BAA19487.1 D86590 Zinnia elegans
DESCRIPTION: cinnamyl alcohol dehydrogenase. ZCAD1.

45 BAA04046.1 D16624 Eucalyptus botryoides
DESCRIPTION: cinnamyl alcohol dehydrogenase. Cad1:Eb:1.

- 5 AAD18000.1 AF109157 *Eucalyptus globulus*
DESCRIPTION: cinnamyl alcohol dehydrogenase. CAD.
- 10 AAF23409.1 AF207552 *Brassica napus*
DESCRIPTION: cinnamyl alcohol dehydrogenase. CADa-1.
- 15 AAF23412.1 AF207555 *Brassica rapa*
DESCRIPTION: cinnamyl alcohol dehydrogenase. CADa.
- 20 AAF23411.1 AF207554 *Brassica oleracea*
DESCRIPTION: cinnamyl alcohol dehydrogenase. CADa.
- 25 AAF23410.1 AF207553 *Brassica napus*
DESCRIPTION: cinnamyl alcohol dehydrogenase. CADa-2.
- 30 AAF23416.1 AF207559 *Brassica rapa*
DESCRIPTION: cinnamyl alcohol dehydrogenase. CADb.
- 35 AAF23415.1 AF207558 *Brassica oleracea*
DESCRIPTION: cinnamyl alcohol dehydrogenase. CADb.
- 158

BAA87853.1 AP000816 *Oryza sativa*
DESCRIPTION: EST AU030604(E51294) corresponds to a region of the
predicted gene. Similar to putative NAK-like Ser/Thr protein kinase.
(AF001308).
- 40 BAA78764.1 AB023482 *Oryza sativa*
DESCRIPTION: ESTs C98382(C2985),D22444(C11129) correspond to a region
of
the predicted gene.; Similar to *Arabidopsis thaliana* APK1 gene for protein
tyrosine-serine-threonine kinase.(D12522).
- 45 AAF43496.1 AF131222 *Lophopyrum elongatum*
DESCRIPTION: protein serine/threonine kinase. ESI47. induced in roots by

salt stress, osmotic stress, and ABA treatment.

- 5 AAK11674.1 AF339747 *Lophopyrum elongatum*
DESCRIPTION: protein kinase. ESI47.
- 10 BAB16871.1 AP002537 *Oryza sativa*
DESCRIPTION: putative protein kinase APK1A*Arabidopsis thaliana*.
P0001B06.24. contains ESTs C22608(R3192),D25110(R3192).
- 15 AAG16628.1 AY007545 *Brassica napus*
DESCRIPTION: protein serine/threonine kinase BNK1.
- 20 AAC27894.1 AF023164 *Zea mays*
DESCRIPTION: leucine-rich repeat transmembrane protein kinase 1. ltk1.
- 25 BAA94509.1 AB041503 *Populus nigra*
DESCRIPTION: protein kinase 1. PnPK1.
- 30 BAA94510.1 AB041504 *Populus nigra*
DESCRIPTION: protein kinase 2. PnPK2.
- 35 BAB03429.1 AP002817 *Oryza sativa*
DESCRIPTION: EST C22619(S11214) corresponds to a region of the predicted
gene. Similar to *Arabidopsis thaliana* chromosome 2, BAC clone T17D12;
putative protein kinase (AC006587).
- 40 BAB07999.1 AP002525 *Oryza sativa*
DESCRIPTION: putative protein kinase. P0462H08.22. contains EST
C22619(S11214).
- 45 BAB39409.1 AP002901 *Oryza sativa*
DESCRIPTION: putative protein kinase. P0456F08.9. contains EST
C23560(R0290).
- 45 AAC27895.1 AF023165 *Zea mays*
DESCRIPTION: leucine-rich repeat transmembrane protein kinase 2. ltk2.

- BAB21241.1 AP002953 *Oryza sativa*
 DESCRIPTION: Putative Pto kinase interactor 1. P0426D06.21. contains ESTs
 5 AU108280(E0721),D48017(S13927).
- AAG59657.1 AC084319 *Oryza sativa*
 DESCRIPTION: putative protein kinase. OSJNBa0004B24.20.
 10
- AAF91337.1 AF249318 *Glycine max*
 DESCRIPTION: Pti1 kinase-like protein. Pti1b. protein kinase.
 15
- AAF91336.1 AF249317 *Glycine max*
 DESCRIPTION: Pti1 kinase-like protein. Pti1a. protein kinase.
 20
- CAB51834.1 00069 *Oryza sativa*
 DESCRIPTION: I1332.5. contains eukaryotic protein kinase domain PF.
 25
- BAA87852.1 AP000816 *Oryza sativa*
 DESCRIPTION: Similar to putative Ser/Thr protein kinase. (AC004218).
 30
- BAA92221.1 AP001278 *Oryza sativa*
 DESCRIPTION: Similar to *Arabidopsis thaliana* chromosome II BAC F12L6
 35 genomic sequence, putative protein kinase. (AC004218).
- AAK00425.1 AC069324 *Oryza sativa*
 DESCRIPTION: Putative protein kinase. OSJNBa0071K19.11.
 40
- AAB09771.1 U67422 *Zea mays*
 DESCRIPTION: CRINKLY4 precursor. cr4. receptor kinase homolog.
 45
- BAB18321.1 AP002865 *Oryza sativa*
 DESCRIPTION: putative receptor protein kinase. P0034C11.11.
- BAB40081.1 AP003074 *Oryza sativa*
 DESCRIPTION: putative receptor protein kinase. OSJNBa0004G10.30.

- 5 AAC61805.1 U28007 *Lycopersicon esculentum*
DESCRIPTION: serine/threonine protein kinase. Pto kinase interactor 1.
Pti1. Pti1 kinase.
- 10 BAB39873.1 AP002882 *Oryza sativa*
DESCRIPTION: putative protein kinase. P0439B06.8. contains ESTs
AU056701(S20808),AU056702(S20808).
- 15 AAD38286.1 AC007789 *Oryza sativa*
DESCRIPTION: putative protein kinase. OSJNBa0049B20.13.
- 20 BAB21240.1 AP002953 *Oryza sativa*
DESCRIPTION: Putative protein kinase. P0426D06.20. contains ESTs
C22359(C11461),C22360(C11461).
- 25 AAK21965.1 AY028699 *Brassica napus*
DESCRIPTION: receptor protein kinase PERK1.
- 30 AAG03090.1 AC073405 *Oryza sativa*
DESCRIPTION: Similar to an Arabidopsis somatic embryogenesis
receptor-like kinase (AC007504).
- 35 BAB18292.1 AP002860 *Oryza sativa*
DESCRIPTION: putative receptor-like protein kinase. P0409B08.19.
- 40 AAF34428.1 AF172282 *Oryza sativa*
DESCRIPTION: receptor-like protein kinase. DUPR11.18.
- 45 AAG25966.1 AF302082 *Nicotiana tabacum*
DESCRIPTION: cytokinin-regulated kinase 1. CRK1. protein kinase;
transcript abundance decreases rapidly after cytokinin treatment.
- AAF66615.1 AF142596 *Nicotiana tabacum*
DESCRIPTION: LRR receptor-like protein kinase.

DESCRIPTION: Similar to Arabidopsis thaliana wak4 gene; wall-associated kinase 4. (AJ009695).

- 5 AAC36318.1 AF053127 Malus x domestica
DESCRIPTION: leucine-rich receptor-like protein kinase. LRPKm1.

159

- 10 AAA86687.1 U15777 Lupinus albus
DESCRIPTION: farnesyl pyrophosphate synthase. fps1.

- 15 AAA87729.1 U20771 Lupinus albus
DESCRIPTION: farnesyl pyrophosphate synthase. fps1.

- 20 CAA72793.1 Y12072 Gossypium arboreum
DESCRIPTION: farnesyl pyrophosphate synthase. fps1.

- 25 BAB40665.1 AB053486 Humulus lupulus
DESCRIPTION: farnesyl pyrophosphate synthase. fpps.

- 30 BAB40666.1 AB053487 Humulus lupulus
DESCRIPTION: farnesyl pyrophosphate synthase. fpps.

- 35 CAA57893.1 X82543 Parthenium argentatum
DESCRIPTION: farnesyl diphosphate synthase. fps2.

- 40 AAC78557.1 AF019892 Helianthus annuus
DESCRIPTION: farnesyl pyrophosphate synthase. FPS.

- 45 CAA57892.1 X82542 Parthenium argentatum
DESCRIPTION: farnesyl diphosphate synthase. fps1.

- 50 AAC49452.1 U36376 Artemisia annua
DESCRIPTION: farnesyl diphosphate synthase. fps1.

- 55 CAA59170.1 X84695 Capsicum annuum

DESCRIPTION: dimethylallyltransferase. Fps, farnesyl pyrophosphate synthase gene.

- 5 AAC73051.1 AF048747 *Lycopersicon esculentum*
DESCRIPTION: synthesis of farnesyl pyrophosphate. farnesyl pyrophosphate synthase. FPS1. prenyl transferase; farnesyl diphosphate synthetase.
- 10 AAD17204.1 AF112881 *Artemisia annua*
DESCRIPTION: farnesyl diphosphate synthase.
- 15 BAA19856.1 D85317 *Oryza sativa*
DESCRIPTION: farnesyl pyrophosphate synthase. dimethylallyltransferase; geranyltranstransferase.
- 20 BAA36276.1 AB021747 *Oryza sativa*
DESCRIPTION: farnesyl diphosphate synthase. FPPS1.
- 25 AAD32648.1 AF136602 *Artemisia annua*
DESCRIPTION: farnesyl diphosphate synthase. fps2.
- 30 AAB39276.1 L39789 *Zea mays*
DESCRIPTION: farnesyl pyrophosphate synthetase. fps. putative.
- 35 AAD27558.1 AF111710 *Oryza sativa* subsp. indica
DESCRIPTION: putative farnesyl pyrophosphate synthase. similar to *Oryza sativa* EST clones E10230_1A, C52647_1A, 232.
- 40 BAA36347.1 AB021979 *Oryza sativa*
DESCRIPTION: farnesyl diphosphate synthase. FPPS2.
- 45 AAD37789.1 AF149257 *Artemisia annua*
DESCRIPTION: farnesyl diphosphate synthase. FPP synthase.
- BAB20822.1 AB045713 *Taraxacum japonicum*
DESCRIPTION: putative FPP synthase. TJFPPS.

- BAB16688.1 AB041627 *Eucommia ulmoides*
DESCRIPTION: FPP synthase 2. EUFPPS2. putative.
- 5 BAB21061.1 AB046212 *Sonchus oleraceus*
DESCRIPTION: putative FPP synthase. SoFPPS.
- 10 AAD45122.1 AF164026 *Xanthoceras sorbifolium*
DESCRIPTION: synthesis of farnesyl pyrophosphate. farnesyl pyrophosphate
synthase. FPS. prenyl transferase; farnesyl diphosphate synthetase.
- 15 AAB93951.1 U97330 *Nicotiana tabacum*
DESCRIPTION: farnesylpyrophosphate synthase. FPPS.
- 20 BAB16687.1 AB041626 *Eucommia ulmoides*
DESCRIPTION: FPP synthase 1. EUFPPS1. putative.
- 25 BAB39479.1 AB049086 *Youngia japonica*
DESCRIPTION: putative FPP synthase 1. YjFPPS1.
- AAB93984.1 AF005201 *Parthenium argentatum*
DESCRIPTION: farnesyl pyrophosphate synthase. FPS3.
- 30 160

BAB03615.1 AP002522 *Oryza sativa*
DESCRIPTION: putative gamma-glutamyltransferase. P0009G03.15. contains
ESTs AU056150(S20332),AU056151(S20332).
- 35 BAB03616.1 AP002522 *Oryza sativa*
DESCRIPTION: putative gamma-glutamyltransferase. P0009G03.16. contains
EST AU056150(S20332).
- 40 162

CAB96145.1 AJ250951 *Mesembryanthemum crystallinum*
DESCRIPTION: phospholipid hydroperoxide glutathione peroxidase-like
protein. gpxmc1.
- 45

CAA42780.1 X60219 *Nicotiana sylvestris*
DESCRIPTION: homologous to animal glutathione peroxidases.

5

BAB16430.1 AB041518 *Nicotiana tabacum*
DESCRIPTION: glutathione peroxidase Nt-SubC08. Nt-SubC08.

10

CAA75054.1 Y14762 *Lycopersicon esculentum*
DESCRIPTION: glutathione peroxidase. GPXle-1.

15

AAB94892.1 AF037051 *Gossypium hirsutum*
DESCRIPTION: glutathione peroxidase.

20

CAB59893.1 AJ238697 *Hordeum vulgare*
DESCRIPTION: GPX12Hv, glutathione peroxidase-like protein.

25

BAA22194.1 D63425 *Spinacia oleracea*
DESCRIPTION: phospholipid hydroperoxide glutathione peroxidase-like protein. similar to mammalian phospholipid hydroperoxide glutathione peroxidases.

30

CAB59895.1 AJ238745 *Hordeum vulgare*
DESCRIPTION: glutathione peroxidase-like protein GPX54Hv.

35

AAC78466.1 AF053311 *Zantedeschia aethiopica*
DESCRIPTION: glutathione peroxidase. gpx.

40

CAA04142.1 AJ000508 *Pisum sativum*
DESCRIPTION: phospholipid glutathione peroxidase. plastid-localised.

45

CAB59894.1 AJ238744 *Hordeum vulgare*
DESCRIPTION: glutathione peroxidase-like protein GPX15Hv.

- CAA74775.1 Y14429 *Helianthus annuus*
DESCRIPTION: glutathione peroxidase. GPxha-1.
- 5 CAC17628.1 AJ270955 *Oryza sativa*
DESCRIPTION: putative role in antioxidative systems. putative
phospholipid hydroperoxide glutathione peroxidase. riPHGPX.
- 10 BAA83594.1 AB009083 *Chlamydomonas* sp. W80
DESCRIPTION: glutathione peroxidase.
- 15 AAB66330.1 AF014927 *Chlamydomonas reinhardtii*
DESCRIPTION: glutathione peroxidase homolog. gpxh.
- 20 CAA75055.1 Y14763 *Lycopersicon esculentum*
DESCRIPTION: glutathione peroxidase. GPXle-2.
- 25 CAA09194.1 AJ010455 *Triticum aestivum*
DESCRIPTION: glutathione peroxidase. PHGPX6.
- CAB66331.1 AJ279689 *Betula pendula*
DESCRIPTION: glutathione peroxidase. gpx.
- 30 163

AAF67753.1 AF255651 *Brassica rapa* subsp. *pekinensis*
DESCRIPTION: conversion of oxidized glutathione to reduced glutathione.
cytosolic glutathione reductase. GR1.
- 35 AAC49980.2 AF008441 *Brassica rapa*
DESCRIPTION: glutathione reductase. BcGR1. cytosolic.
- 40 BAA11214.1 D78136 *Oryza sativa*
DESCRIPTION: Glutathione Reductase. putative.
- 45 CAA66924.1 X98274 *Pisum sativum*
DESCRIPTION: glutathione reductase. cytosolic.

- 5 BAA36283.1 D85751 *Oryza sativa*
DESCRIPTION: glutathione reductase.
- 10 BAA37092.1 AB009592 *Oryza sativa*
DESCRIPTION: conversion of oxidized glutathione to reduced glutathione.
cytosolic glutathione reductase. RGRC2. Amino Acids 1-496.
- 15 BAA07108.1 D37870 *Spinacia oleracea*
DESCRIPTION: Glutathione Reductase precursor. Chloroplastic glutathione
reductase.
- 20 CAC13956.1 AJ400816 *Mesembryanthemum crystallinum*
DESCRIPTION: reduction of glutathione. glutathione reductase. gr1.
- 25 CAB66332.1 AJ279690 *Betula pendula*
DESCRIPTION: glutathione reductase. gr.
- 30 CAA53925.1 X76293 *Nicotiana tabacum*
DESCRIPTION: glutathione reductase (NADPH). gor.
- CAA42921.1 X60373 *Pisum sativum*
DESCRIPTION: glutathione reductase (NADPH). Protein sequence is in
conflict with the conceptual translation.
- 35 AAK27157.1 AF349449 *Brassica juncea*
DESCRIPTION: glutathione reductase. GR2.
- 40 AAD28177.1 AF109694 *Brassica juncea*
DESCRIPTION: glutathione reductase. GR1.
- 45 CAA62482.1 X90996 *Pisum sativum*
DESCRIPTION: glutathione reductase (NADPH). gr. alpha II subunit.
- AAF26175.1 AF105199 *Glycine max*

DESCRIPTION: glutathione reductase. GR-5.

- 5 AAB70837.1 AF019907 *Vitis vinifera*
DESCRIPTION: glutathione reductase (NADPH). GOR. VvGR1.
- 10 AAA33962.1 L11632 *Glycine max*
DESCRIPTION: glutathione reductase. GR.
- 15 CAA54043.1 X76533 *Nicotiana tabacum*
DESCRIPTION: glutathione reductase (NADPH). gor.
- 20 CAA06835.1 AJ006055 *Zea mays*
DESCRIPTION: NADPH-dependent reduction of glutathione disulphide.
glutathione reductase. gor1.
- 25 CAA53993.1 X76455 *Nicotiana tabacum*
DESCRIPTION: glutathione reductase. gor.
- 30 AAB30526.1 S70187 *Glycine max*
DESCRIPTION: ferric leghemoglobin reductase. ferric leghemoglobin
reductase, FLbR. Method: conceptual translation with partial peptide
sequencing; This sequence comes from Fig. 3; FLbR.
- 35 AAC26053.1 AF074940 *Glycine max*
DESCRIPTION: ferric leghemoglobin reductase-2 precursor. FLbR
homolog;FLbR-2.
- 40 AAD53185.1 AF181096 *Vigna unguiculata*
DESCRIPTION: ferric leghemoglobin reductase. flbr.
- 45 AAA60979.1 U06461 *Pisum sativum*
DESCRIPTION: catalyzes the conversion of monodehydroascorbate to
ascorbate, oxidizing NADH in the process, binds to flavin as a single
subunit. monodehydroascorbate reductase.
- BAA05408.1 D26392 *Cucumis sativus*

DESCRIPTION: monodehydroascorbate reductase.

5 AAC41654.1 L41345 Lycopersicon esculentum
DESCRIPTION: ascorbate free radical reductase. AFRR.

10 AAD53522.1 AF158602 Zantedeschia aethiopica
DESCRIPTION: monodehydroascorbate reductase. MDAR. putative.

AAD28178.1 AF109695 Brassica juncea
DESCRIPTION: monodehydroascorbate reductase. MDAR1.

15 BAA77214.1 D85764 Oryza sativa
DESCRIPTION: cytosolic monodehydroascorbate reductase.

164
20 -----
CAA04391.1 AJ000923 Carica papaya
DESCRIPTION: glutathione transferase. PGST1.

25 AAC18566.1 AF048978 Glycine max
DESCRIPTION: 2,4-D inducible glutathione S-transferase. GSTa.

30 AAG34800.1 AF243365 Glycine max
DESCRIPTION: glutathione S-transferase GST 10.

35 AAF22647.1 AF193439 Lycopersicon esculentum
DESCRIPTION: glutathione S-transferase/peroxidase. BI-GST/GPX.

CAA71784.1 Y10820 Glycine max
DESCRIPTION: glutathione transferase.

40 AAG34799.1 AF243364 Glycine max
DESCRIPTION: glutathione S-transferase GST 9.

45 AAG16760.1 AY007562 Lycopersicon esculentum
DESCRIPTION: putative glutathione S-transferase T5.

- 5 CAA48717.1 X68819 Glycine max
DESCRIPTION: lactoylglutathione lyase. glyoxalase I.
- 10 CAC24549.1 AJ296343 Cichorium intybus x Cichorium endivia
DESCRIPTION: glutathione S-transferase. chi-GST1. auxin-induced GST.
- 15 AAC28101.1 AF079511 Mesembryanthemum crystallinum
DESCRIPTION: glutathione S-transferase.
- 20 AAG34806.1 AF243371 Glycine max
DESCRIPTION: glutathione S-transferase GST 16.
- 25 AAF23357.1 AF109194 Hordeum vulgare
DESCRIPTION: glutathione-S-transferase.
- 30 CAA73369.1 Y12862 Zea mays
DESCRIPTION: glutathione transferase. GST5.
- 35 AAG32470.1 AF309377 Oryza sativa subsp. japonica
DESCRIPTION: putative glutathione S-transferase OsGSTU5.
- 40 CAA74197.1 Y13898 Brassica juncea
DESCRIPTION: glutathione-S-transferase. gst.
- 45 AAG34827.1 AF244684 Zea mays
DESCRIPTION: glutathione S-transferase GST 19.
- 40 AAC05216.1 AF050102 Oryza sativa
DESCRIPTION: glutathione s-transferase. GST1.
- 45 AAC32118.1 AF051214 Picea mariana
DESCRIPTION: probable glutathione S-transferase. Sb18. similar to
Nicotiana tabacum probable glutathione S-transferase encoded by GenBank
Accession Number X56266.

5 AAG16758.1 AY007560 *Lycopersicon esculentum*
DESCRIPTION: putative glutathione S-transferase T3.

10 AAG34798.1 AF243363 *Glycine max*
DESCRIPTION: glutathione S-transferase GST 8.

15 AAG34842.1 AF244699 *Zea mays*
DESCRIPTION: glutathione S-transferase GST 34.

20 AAG34807.1 AF243372 *Glycine max*
DESCRIPTION: glutathione S-transferase GST 17.

25 AAG34809.1 AF243374 *Glycine max*
DESCRIPTION: glutathione S-transferase GST 19.

30 AAG34839.1 AF244696 *Zea mays*
DESCRIPTION: glutathione S-transferase GST 31.

35 AAG34804.1 AF243369 *Glycine max*
DESCRIPTION: glutathione S-transferase GST 14.

40 AAG34844.1 AF244701 *Zea mays*
DESCRIPTION: glutathione S-transferase GST 36.

45 AAG34831.1 AF244688 *Zea mays*
DESCRIPTION: glutathione S-transferase GST 23.

AAG34797.1 AF243362 *Glycine max*
DESCRIPTION: glutathione S-transferase GST 7.

AAG34832.1 AF244689 *Zea mays*
DESCRIPTION: glutathione S-transferase GST 24.

AAG32471.1 AF309378 *Oryza sativa* subsp. *japonica*
 DESCRIPTION: putative glutathione S-transferase OsGSTU4.

5 AAG34796.1 AF243361 *Glycine max*
 DESCRIPTION: glutathione S-transferase GST 6.

10 AAG34810.1 AF243375 *Glycine max*
 DESCRIPTION: glutathione S-transferase GST 20.

15 AAG34835.1 AF244692 *Zea mays*
 DESCRIPTION: glutathione S-transferase GST 27.

20 AAC32139.1 AF051238 *Picea mariana*
 DESCRIPTION: probable glutathione S-transferase. Sb52. similar to
Nicotiana tabacum probable glutathione S-transferase encoded by GenBank
 Accession Number X56266.

165 -----

25 CAA71878.1 Y10984 *Brassica juncea*
 DESCRIPTION: ATP-dependent addition of glycine to gamma-
 glutamylcysteine.
 glutathione synthetase. gshII.

30 AAB71231.1 AF017984 *Lycopersicon esculentum*
 DESCRIPTION: glutathione synthetase. GSH2.

35 AAF98157.1 AF258320 *Phaseolus vulgaris*
 DESCRIPTION: homoglutathione synthetase. hgshs.

40 AAF98156.1 AF258319 *Pisum sativum*
 DESCRIPTION: putative homoglutathione synthetase. hgshs.

45 CAB91078.1 AJ272035 *Glycine max*
 DESCRIPTION: homoglutathione synthetase. hGS. putatively predicted to be
 targetted to the chloroplast.

- AAF98121.1 AF231137 *Pisum sativum*
DESCRIPTION: glutathione synthetase precursor. gshs. putative
mitochondrial protein.
- 5 AAD29848.1 AF075699 *Medicago truncatula*
DESCRIPTION: putative glutathione synthetase. GSHS1.
- 10 AAD29849.1 AF075700 *Medicago truncatula*
DESCRIPTION: putative glutathione synthetase. GSHS2.
- 166

- 15 BAA83711.1 AB014484 *Nicotiana tabacum*
DESCRIPTION: heat shock factor. NtHSF2.
- 20 AAF37579.1 AF235958 *Medicago sativa*
DESCRIPTION: heat shock transcription factor. HSFA4-6. MsHSFA4-6.
- 25 CAA58117.1 X82943 *Zea mays*
DESCRIPTION: heat shock factor. hsfb.
- 30 CAA47868.1 X67599 *Lycopersicon esculentum*
DESCRIPTION: heat stress transcription factor 8. hsf8.
- CAA47869.1 X67600 *Lycopersicon peruvianum*
DESCRIPTION: heat shock transcription factor 8. hsf8.
- 35 CAA47870.1 X67601 *Lycopersicon peruvianum*
DESCRIPTION: heat stress transcription factor HSF30. hsf30.
- 40 AAF74563.1 AF208544 *Lycopersicon peruvianum*
DESCRIPTION: heat stress transcription factor A3. HSFA3.
- 45 CAA87080.1 Z46956 *Glycine max*
DESCRIPTION: heat shock transcription factor 5. HSF.

- CAA87079.1 Z46955 Glycine max
DESCRIPTION: heat shock transcription factor 31. HSF.
- 5 BAB19067.1 AP002744 Oryza sativa
DESCRIPTION: putative heat shock factor protein 1 (HSF 1). P0006C01.9.
- 10 CAA09301.1 AJ010644 Pisum sativum
DESCRIPTION: heat shock transcription factor (HSFA). hsfA.
- 15 CAA09300.1 AJ010643 Pisum sativum
DESCRIPTION: heat shock transcription factor (HSFA). hsfA.
- 169

- 20 AAB72109.1 AF022217 Brassica rapa
DESCRIPTION: low molecular weight heat-shock protein. BcHSP17.6. 17.6 kDa; cytosolic class I.
- 25 CAB93512.1 AJ243565 Brassica oleracea
DESCRIPTION: putative class I small heat shock protein. HSP17.7-a protein. hsp17.7-a.
- 30 CAA37847.1 X53851 Daucus carota
DESCRIPTION: heat shock protein.
- 35 AAD49336.1 AF166277 Nicotiana tabacum
DESCRIPTION: low molecular weight heat-shock protein. LHS-1. TLHS-1.
- 40 BAA33062.1 AB017273 Cuscuta japonica
DESCRIPTION: low-molecular-weight heat shock protein. CJHSP17.
- 45 CAB36910.1 AJ000691 Quercus suber
DESCRIPTION: stress protein chaperone. heat shock protein 17.4. hsp17.
- CAA08908.1 AJ009880 Castanea sativa
DESCRIPTION: molecular chaperone. cytosolic class I small heat-shock

protein HSF17.5. hsp17.5.

5 AAA33975.1 M11395 Glycine max
DESCRIPTION: small heat shock protein.

10 CAA25578.1 X01104 Glycine max
DESCRIPTION: heat shock protein 6871 (aa 1-153).

AAB03893.1 M11318 Glycine max
DESCRIPTION: 17.5 kd heat shock protein Gmhsp17.6L.

15 CAA41547.1 X58711 Medicago sativa
DESCRIPTION: heat shock protein.

20 AAB63310.1 U46544 Helianthus annuus
DESCRIPTION: 18.6 kDa heat-shock protein. Class I low-molecular-weight
heat-shock protein.

25 CAB08441.1 Z95153 Helianthus annuus
DESCRIPTION: 17.6 kD class I small heat-shock protein HSP17.6. Ha
hsp17.6.

30 CAA42222.1 X59701 Helianthus annuus
DESCRIPTION: 17.6 kDa heat shock protein.

35 CAA37848.1 X53852 Daucus carota
DESCRIPTION: heat shock protein.

40 AAC39360.1 U63631 Fragaria x ananassa
DESCRIPTION: LMW heat shock protein.

AAA33672.1 M33899 Pisum sativum
DESCRIPTION: 18.1 kDa heat shock protein (hsp18.1).

45 AAB63311.1 U46545 Helianthus annuus

DESCRIPTION: 17.1 kDa heat shock protein. Class I low-molecular-weight heat-shock protein.

5 AAA33974.1 M11317 Glycine max
DESCRIPTION: 17.6 kd heat shock protein Gmhsp17.6L.

10 CAA63903.1 X94193 Pennisetum glaucum
DESCRIPTION: heat shock protein 17.9. hsp17.9.

15 AAA61632.1 U08601 Papaver somniferum
DESCRIPTION: low molecular weight heat-shock protein.

CAB55634.2 AJ237596 Helianthus annuus
DESCRIPTION: 17.9 kDa heat-shock protein. hsp17.9.

20 AAC78392.1 U83669 Oryza sativa
DESCRIPTION: low molecular mass heat shock protein Oshsp17.3.
OSHSP17.3.
class I LMMHSP.

25 AAA33910.1 M80939 Oryza sativa
DESCRIPTION: 16.9 kDa heat shock protein.

30 BAA02160.1 D12635 Oryza sativa
DESCRIPTION: 'low molecular weight heat shock protein'.

35 CAA43210.1 X60820 Oryza sativa
DESCRIPTION: 16.9 KD low molecular weight heat shock protein.

40 CAA37864.1 X53870 Chenopodium rubrum
DESCRIPTION: heat-shock protein.

45 AAA33909.1 M80938 Oryza sativa
DESCRIPTION: 16.9 kDa heat shock protein.

5 AAC78393.1 U83670 *Oryza sativa*
DESCRIPTION: low molecular mass heat shock protein Oshsp18.0.
OSHSP18.0.
class I LMMHSP.

10 AAB39856.1 U81385 *Oryza sativa*
DESCRIPTION: heat shock protein. Oshsp16.9C. class I, low molecular mass.

15 AAD30454.1 AF123257 *Lycopersicon esculentum*
DESCRIPTION: 17.6 kD class I small heat shock protein. HSP17.6.

20 AAA33671.1 M33900 *Pisum sativum*
DESCRIPTION: 17.9 kDa heat shock protein (hsp17.9).

25 AAC78394.1 U83671 *Oryza sativa*
DESCRIPTION: low molecular mass heat shock protein Oshsp17.7.
OSHSP17.7.
class I LMMHSP.

30 CAB93514.1 AJ243567 *Brassica oleracea*
DESCRIPTION: Putative class I small heat shock protein. HSP17.x protein.
hsp17.x.

35 CAA63901.1 X94191 *Pennisetum glaucum*
DESCRIPTION: heat shock protein 17.0. hsp17.0.

40 CAA63902.1 X94192 *Pennisetum glaucum*
DESCRIPTION: heat shock protein 16.9. hsp16.9.

45 AAD30452.1 AF123255 *Lycopersicon esculentum*
DESCRIPTION: 17.7 kD class I small heat shock protein. HSP17.7.

CAA46641.1 X65725 *Zea mays*
DESCRIPTION: heat shock protein 17.2. Zmhs17.2. Class I low molecular weight heat shock protein.

- CAA39603.1 X56138 *Lycopersicon esculentum*
DESCRIPTION: small heat shock protein (class I).
- 5 CAA63570.1 X92983 *Pseudotsuga menziesii*
DESCRIPTION: low molecular weight heat-shock protein.
- 10 AAD30453.1 AF123256 *Lycopersicon esculentum*
DESCRIPTION: 17.8 kD class I small heat shock protein. HSP17.8.
- 15 CAA63571.1 X92984 *Pseudotsuga menziesii*
DESCRIPTION: low molecular weight heat-shock protein.
- CAA31785.1 X13431 *Triticum aestivum*
DESCRIPTION: put. heat shock protein (AA 1 -151).
- 20 CAA53286.1 X75616 *Oryza sativa*
DESCRIPTION: heat shock protein 17.8.
- 170
- 25 -----
AAC14577.1 U72396 *Lycopersicon esculentum*
DESCRIPTION: class II small heat shock protein Le-HSP17.6. heat
treatment/chilling tolerance related protein from tomato fruit.
- 30 AAA33670.1 M33901 *Pisum sativum*
DESCRIPTION: 17.7 kDa heat shock protein (hsp17.7).
- 35 CAA82653.1 Z29554 *Helianthus annuus*
DESCRIPTION: 17.9 kDa heat-shock protein.
- 40 AAD41409.1 AF159562 *Prunus dulcis*
DESCRIPTION: cytosolic class II low molecular weight heat shock protein.
hsp17.5.
- 45 CAA65020.1 X95716 *Petroselinum crispum*
DESCRIPTION: small heat shock protein. cytoplasmic class II HSP.

AAC36312.1 AF090115 *Lycopersicon esculentum*
DESCRIPTION: cytosolic class II small heat shock protein HCT2. HSP17.4.

5

AAB01561.1 L47717 *Picea glauca*
DESCRIPTION: heat shock protein 17.0. EMB27.

10

AAB39336.1 M99430 *Ipomoea nil*
DESCRIPTION: small heat shock protein.

15

AAB01562.1 L47740 *Picea glauca*
DESCRIPTION: class II cytoplasmic small molecular weight heat shock protein 17.1. EMB29, SMW HSP17.1.

20

CAA67206.1 X98617 *Medicago sativa*
DESCRIPTION: 17kD heat shock protein.

25

BAA99529.1 AP002484 *Oryza sativa*
DESCRIPTION: putative heat shock protein, 18K - maize. P0489A01.20.
contains ESTs C99035(E4351),AU093460(E3974).

30

CAA41218.1 X58279 *Triticum aestivum*
DESCRIPTION: heat shock protein 17.3. Tahsp17.3.

35

CAA67726.1 X99346 *Picea abies*
DESCRIPTION: small heat shock protein.

40

CAA38012.1 X54075 *Zea mays*
DESCRIPTION: 18kDa heat shock protein.

45

CAA38013.1 X54076 *Zea mays*
DESCRIPTION: 18kDa heat shock protein.

AAB26481.1 S59777 *Zea mays*
DESCRIPTION: HSP18. HSP18. 18 kda heat shock protein; This sequence comes

from Fig. 2B.

- 5 AAB39335.1 M99429 *Ipomoea nil*
DESCRIPTION: small heat shock protein.
- 10 AAD09184.1 AF089845 *Funaria hygrometrica*
DESCRIPTION: cytosolic II small heat shock protein HSP16.4II. HSP16.4II.
- 15 BAA04841.1 D21817 *Lilium longiflorum*
DESCRIPTION: small heat shock protein. LIM11.
- AAD09185.1 AF089846 *Funaria hygrometrica*
DESCRIPTION: cytosolic II small heat shock protein HSP18.3II. HSP18.3II.
- 20 BAA04842.1 D21818 *Lilium longiflorum*
DESCRIPTION: small heat shock protein. LIM12.
- 25 CAA63570.1 X92983 *Pseudotsuga menziesii*
DESCRIPTION: low molecular weight heat-shock protein.
- 30 CAA63571.1 X92984 *Pseudotsuga menziesii*
DESCRIPTION: low molecular weight heat-shock protein.
- AAC39360.1 U63631 *Fragaria x ananassa*
DESCRIPTION: LMW heat shock protein.
- 35 AAD09178.1 AF087640 *Funaria hygrometrica*
DESCRIPTION: cytosolic I small heat shock protein HSP17.2IA. HSP17.2IA.
- 40 AAD09182.1 AF089843 *Funaria hygrometrica*
DESCRIPTION: cytosolic I small heat shock protein HSP17.2IC. HSP17.2IC.
- 45 BAA04840.1 D21816 *Lilium longiflorum*
DESCRIPTION: small heat shock protein. LIM10.

- 5 CAB93514.1 AJ243567 *Brassica oleracea*
DESCRIPTION: Putative class I small heat shock protein. HSP17.x protein.
hsp17.x.
- 10 AAD30452.1 AF123255 *Lycopersicon esculentum*
DESCRIPTION: 17.7 kD class I small heat shock protein. HSP17.7.
- 15 AAB63311.1 U46545 *Helianthus annuus*
DESCRIPTION: 17.7 kDa heat shock protein. Class I low-molecular-weight
heat-shock protein.
- 20 CAA31785.1 X13431 *Triticum aestivum*
DESCRIPTION: put. heat shock protein (AA 1 -151).
- 25 CAA63901.1 X94191 *Pennisetum glaucum*
DESCRIPTION: heat shock protein 17.0. hsp17.0.
- 30 AAA33672.1 M33899 *Pisum sativum*
DESCRIPTION: 18.1 kDa heat shock protein (hsp18.1).
- 35 CAA41547.1 X58711 *Medicago sativa*
DESCRIPTION: heat shock protein.
- 40 CAA46641.1 X65725 *Zea mays*
DESCRIPTION: heat shock protein 17.2. Zmhsp 17.2. Class I low molecular
weight heat shock protein.
- 45 AAB39856.1 U81385 *Oryza sativa*
DESCRIPTION: heat shock protein. Oshsp16.9C. class I, low molecular mass.
- AAC78394.1 U83671 *Oryza sativa*
DESCRIPTION: low molecular mass heat shock protein Oshsp17.7.
OSHSP17.7.
class I LMMHSP.

- 5 AAC78392.1 U83669 *Oryza sativa*
 DESCRIPTION: low molecular mass heat shock protein Oshsp17.3.
 OSHSP17.3.
 class I LMMHSP.
- 10 CAA39603.1 X56138 *Lycopersicon esculentum*
 DESCRIPTION: small heat shock protein (class I).
- 15 AAA33910.1 M80939 *Oryza sativa*
 DESCRIPTION: 16.9 kDa heat shock protein.
- 20 AAA33909.1 M80938 *Oryza sativa*
 DESCRIPTION: 16.9 kDa heat shock protein.
- 25 CAA43210.1 X60820 *Oryza sativa*
 DESCRIPTION: 16.9 KD low molecular weight heat shock protein.
- 30 AAD30453.1 AF123256 *Lycopersicon esculentum*
 DESCRIPTION: 17.8 kD class I small heat shock protein. HSP17.8.
- 35 AAA34294.1 L14444 *Triticum aestivum*
 DESCRIPTION: heat shock protein 16.9C. hsp16.9C.
- 40 CAA69172.1 Y07844 *Hordeum vulgare*
 DESCRIPTION: 17 kDa class I small heat shock protein. hsp17. putative.
- 45 AAD30454.1 AF123257 *Lycopersicon esculentum*
 DESCRIPTION: 17.6 kD class I small heat shock protein. HSP17.6.
- 171

 40 CAA82653.1 Z29554 *Helianthus annuus*
 DESCRIPTION: 17.9 kDa heat-shock protein.
- 45 AAC14577.1 U72396 *Lycopersicon esculentum*
 DESCRIPTION: class II small heat shock protein Le-HSP17.6. heat
 treatment/chilling tolerance related protein from tomato fruit.

DESCRIPTION: HSP18. HSP18. 18 kda heat shock protein; This sequence comes from Fig. 2B.

5

AAB01561.1 L47717 *Picea glauca*
DESCRIPTION: heat shock protein 17.0. EMB27.

10

AAB39335.1 M99429 *Ipomoea nil*
DESCRIPTION: small heat shock protein.

15

AAB01562.1 L47740 *Picea glauca*
DESCRIPTION: class II cytoplasmic small molecular weight heat shock protein 17.1. EMB29, SMW HSP17.1.

20

CAA67726.1 X99346 *Picea abies*
DESCRIPTION: small heat shock protein.

25

AAD09184.1 AF089845 *Funaria hygrometrica*
DESCRIPTION: cytosolic II small heat shock protein HSP16.4II. HSP16.4II.

30

BAA04841.1 D21817 *Lilium longiflorum*
DESCRIPTION: small heat shock protein. LIM11.

35

BAA04842.1 D21818 *Lilium longiflorum*
DESCRIPTION: small heat shock protein. LIM12.

AAD09185.1 AF089846 *Funaria hygrometrica*
DESCRIPTION: cytosolic II small heat shock protein HSP18.3II. HSP18.3II.

40

BAA04840.1 D21816 *Lilium longiflorum*
DESCRIPTION: small heat shock protein. LIM10.

45

CAA63570.1 X92983 *Pseudotsuga menziesii*
DESCRIPTION: low molecular weight heat-shock protein.

- CAA63571.1 X92984 *Pseudotsuga menziesii*
DESCRIPTION: low molecular weight heat-shock protein.
- 5 AAD30452.1 AF123255 *Lycopersicon esculentum*
DESCRIPTION: 17.7 kD class I small heat shock protein. HSP17.7.
- 10 AAD09178.1 AF087640 *Funaria hygrometrica*
DESCRIPTION: cytosolic I small heat shock protein HSP17.2IA. HSP17.2IA.
- 15 AAB63311.1 U46545 *Helianthus annuus*
DESCRIPTION: 17.7 kDa heat shock protein. Class I low-molecular-weight heat-shock protein.
- 20 CAA39603.1 X56138 *Lycopersicon esculentum*
DESCRIPTION: small heat shock protein (class I).
- 25 AAC39360.1 U63631 *Fragaria x ananassa*
DESCRIPTION: LMW heat shock protein.
- 30 AAA33672.1 M33899 *Pisum sativum*
DESCRIPTION: 18.1 kDa heat shock protein (hsp18.1).
- 35 AAD30453.1 AF123256 *Lycopersicon esculentum*
DESCRIPTION: 17.8 kD class I small heat shock protein. HSP17.8.
- AAD30454.1 AF123257 *Lycopersicon esculentum*
DESCRIPTION: 17.6 kD class I small heat shock protein. HSP17.6.
- 40 CAA41547.1 X58711 *Medicago sativa*
DESCRIPTION: heat shock protein.
- 45 CAA31785.1 X13431 *Triticum aestivum*
DESCRIPTION: put. heat shock protein (AA 1 -151).
- AAB39856.1 U81385 *Oryza sativa*

DESCRIPTION: heat shock protein. Oshsp16.9C. class I, low molecular mass.

CAA41546.1 X58710 Medicago sativa
5 DESCRIPTION: heat shock protein.

CAB93514.1 AJ243567 Brassica oleracea
10 DESCRIPTION: Putative class I small heat shock protein. HSP17.x protein.
hsp17.x.

CAA63901.1 X94191 Pennisetum glaucum
15 DESCRIPTION: heat shock protein 17.0. hsp17.0.

AAA33910.1 M80939 Oryza sativa
20 DESCRIPTION: 16.9 kDa heat shock protein.

AAA33909.1 M80938 Oryza sativa
DESCRIPTION: 16.9 kDa heat shock protein.

CAA43210.1 X60820 Oryza sativa
25 DESCRIPTION: 16.9 KD low molecular weight heat shock protein.

AAB03097.1 U21723 Glycine max
30 DESCRIPTION: Hsp22.3. Gmhsp22.3. low molecular weight heat shock
protein.

AAC78394.1 U83671 Oryza sativa
35 DESCRIPTION: low molecular mass heat shock protein Oshsp17.7.
OSHSP17.7.
class I LMMHSP.

AAC78392.1 U83669 Oryza sativa
40 DESCRIPTION: low molecular mass heat shock protein Oshsp17.3.
OSHSP17.3.
class I LMMHSP.

AAD09182.1 AF089843 Funaria hygrometrica
45

DESCRIPTION: cytosolic I small heat shock protein HSP17.2IC. HSP17.2IC.

173

5 AAD30456.1 AF123259 *Lycopersicon esculentum*
DESCRIPTION: heat shock protein 90. HSP90.

10 AAF31705.1 AF221856 *Euphorbia esula*
DESCRIPTION: heat-shock protein 80.

15 AAC32131.1 AF051230 *Picea mariana*
DESCRIPTION: heat shock protein. Sb40. similar to *Oryza sativa* heat shock
protein 82 encoded by GenBank Accession Number Z11920.

20 AAF64453.1 AF239931 *Euphorbia esula*
DESCRIPTION: putative heat-shock protein 90. GRP94; similar to
endoplasmic reticulum precursor; contains the endoplasmic reticulum
targeting sequence KDEL at the 3'-tail.

25 CAA78738.1 Z15018 *Oryza sativa*
DESCRIPTION: heat shock protein. heat shock protein hsp82. hsp82.

174

30 AAG43546.1 AF211528 *Nicotiana tabacum*
DESCRIPTION: Avr9/Cf-9 rapidly elicited protein 4. ACRE4. similar to
Nicotiana glutinosa Ntr truncated N resistance protein encoded by GenBank
Accession Number U15605.

35 AAA50763.1 U15605 *Nicotiana glutinosa*
DESCRIPTION: virus resistance. N.

40 CAA08797.1 AJ009719 *Solanum tuberosum*
DESCRIPTION: disease resistance. NL25. nl25.

45 CAA08798.1 AJ009720 *Solanum tuberosum*
DESCRIPTION: disease resistance. NL27. nl27.

- AAG09951.1 AF175388 Glycine max
DESCRIPTION: resistance protein LM6.
- 5 AAG09954.1 AF175399 Glycine max
DESCRIPTION: resistance protein MG13.
- 10 AAD25974.1 AF093647 Linum usitatissimum
DESCRIPTION: flax rust resistance protein. L.
- 15 AAD25966.1 AF093639 Linum usitatissimum
DESCRIPTION: flax rust resistance protein. L.
- 20 AAD25969.1 AF093642 Linum usitatissimum
DESCRIPTION: flax rust resistance protein. L.
- 25 AAD25965.1 AF093638 Linum usitatissimum
DESCRIPTION: flax rust resistance protein. L.
- 30 AAD25968.1 AF093641 Linum usitatissimum
DESCRIPTION: flax rust resistance protein. L.
- 35 AAA91021.1 U27081 Linum usitatissimum
DESCRIPTION: rust resistance. L6tr. L6. The shorter of two alternate protein products of The L6 gene that results from retention of intron 3 in the mRNA; truncated L6 gene product.
- 40 AAA91022.1 U27081 Linum usitatissimum
DESCRIPTION: rust resistance. L6. L6. The longer of two alternate proteins encoded by the L6 gene.
- 45 AAD25967.1 AF093640 Linum usitatissimum
DESCRIPTION: flax rust resistance protein. L.
- AAK28803.1 AF310958 Linum usitatissimum
DESCRIPTION: resistance-like protein P1-A. p1-A.

AAK28808.1 AF310961 *Linum usitatissimum*
DESCRIPTION: resistance-like protein P3-A. p3-A.

5

AAK28805.1 AF310960 *Linum usitatissimum*
DESCRIPTION: resistance-like protein P2-A. p2-A.

10 AAD25976.1 AF093649 *Linum usitatissimum*
DESCRIPTION: flax rust resistance protein. L.

15 AAD25973.1 AF093646 *Linum usitatissimum*
DESCRIPTION: flax rust resistance protein. L.

20 AAD25972.1 AF093645 *Linum usitatissimum*
DESCRIPTION: flax rust resistance protein. L.

AAD25971.1 AF093644 *Linum usitatissimum*
DESCRIPTION: flax rust resistance protein. L.

25

AAD25970.1 AF093643 *Linum usitatissimum*
DESCRIPTION: flax rust resistance protein. L.

30 AAD25975.1 AF093648 *Linum usitatissimum*
DESCRIPTION: flax rust resistance protein. L.

35 AAG48132.1 AF322632 *Glycine max*
DESCRIPTION: putative resistance protein. L20a.

AAG01052.1 AF175395 *Glycine max*
DESCRIPTION: resistance protein MG23.

40

CAC35330.1 AJ310155 *Linum usitatissimum*
DESCRIPTION: N1-D protein. N1-D. N locus resistance gene homolog:
TIR-NBS-LRR protein.

45

CAC35333.1 AJ310158 *Linum usitatissimum*
DESCRIPTION: N2-C protein. N2-C. N locus rust resistance gene homolog:
TIR-NBS-LRR protein.

5

AAG48133.1 AF322633 *Glycine max*
DESCRIPTION: putative resistance protein. L33.

10

AAF61452.1 AF139523 *Tagetes erecta*
DESCRIPTION: disease-resistance protein NRSA1.

15

CAC35334.1 AJ310159 *Linum usitatissimum*
DESCRIPTION: N2-D protein. N2-D. N locus rust resistance gene homolog:
TIR-NBS-LRR protein.

20

CAC35337.1 AJ310162 *Linum usitatissimum*
DESCRIPTION: Nbi-C protein. Nbi-C. N locus rust resistance gene homolog:
TIR-NBS-LRR protein.

25

CAC35339.1 AJ310164 *Linum usitatissimum*
DESCRIPTION: Nho-C protein. Nho-C. N locus rust resistance gene homolog:
TIR-NBS-LRR protein.

30

CAC35326.1 AJ310151 *Linum usitatissimum*
DESCRIPTION: Ngc-C protein. Ngc-C. N rust resistance gene homolog:
TIR-NBS-LRR protein.

35

AAG01051.1 AF175394 *Glycine max*
DESCRIPTION: resistance protein LM12.

40

CAC35338.1 AJ310163 *Linum usitatissimum*
DESCRIPTION: Nbi-D protein. Nbi-D. N locus rust resistance gene homolog:
TIR-NBS-LRR protein.

45

CAC35329.1 AJ310154 *Linum usitatissimum*
DESCRIPTION: N1-C protein. N1-C. N locus resistance gene homolog:
TIR-NBS-LRR protein.

AAK28804.1 AF310959 *Linum usitatissimum*
DESCRIPTION: resistance-like protein P1-B. p1-B.

5

AAK28809.1 AF310962 *Linum usitatissimum*
DESCRIPTION: resistance-like protein P3-B. p3-B.

10 CAC35332.1 AJ310157 *Linum usitatissimum*
DESCRIPTION: N2-B protein. N2-B. N locus rust resistance gene homolog:
TIR-NBS-LRR protein.

15 CAC35328.1 AJ310153 *Linum usitatissimum*
DESCRIPTION: N1-B protein. N1-B. N locus resistance gene homolog:
TIR-NBS-LRR protein.

20 CAC35325.1 AJ310150 *Linum usitatissimum*
DESCRIPTION: Ngc-B protein. Ngc-B. N rust resistance gene homolog:
TIR-NBS-LRR protein.

25 CAC35336.1 AJ310161 *Linum usitatissimum*
DESCRIPTION: Nbi-B protein. Nbi-B. N locus rust resistance gene homolog:
TIR-NBS-LRR protein.

30 CAC35321.1 AJ310150 *Linum usitatissimum*
DESCRIPTION: Ngc-D protein. Ngc-D. N rust resistance gene: TIR-NBS-LRR
protein.

35 CAC35331.1 AJ310156 *Linum usitatissimum*
DESCRIPTION: N2-A protein. N2-A. N locus rust resistance gene homolog:
TIR-NBS-LRR protein.

40 CAC35323.1 AJ310150 *Linum usitatissimum*
DESCRIPTION: Ngc-A protein. Ngc-A. N rust resistance gene homolog:
TIR-NBS-LRR protein.

45 AAB47618.1 U73916 *Linum usitatissimum*
DESCRIPTION: rust resistance protein M. nucleotide-binding site,

leucine-rich repeat class of plant disease resistance protein.

5 AAG01053.1 AF175396 Glycine max
DESCRIPTION: resistance protein MG55.

10 CAC35327.1 AJ310152 Linum usitatissimum
DESCRIPTION: N1-A protein. N1-A. N locus resistance gene homolog:
TIR-NBS-LRR protein.

15 AAK28811.1 AF310966 Linum usitatissimum
DESCRIPTION: resistance-like protein P-B. p-B.
175

20 CAB52796.1 AJ245861 Solanum tuberosum
DESCRIPTION: respiratory chain. putative internal rotenone-insensitive
NADH dehydrogenase. nda1.

25 CAB52797.1 AJ245862 Solanum tuberosum
DESCRIPTION: respiratory chain. putative external rotenone-insensitive
NADH dehydrogenase. ndb1.

176

30 BAA05648.1 D26601 Nicotiana tabacum
DESCRIPTION: protein kinase.

35 CAA08997.1 AJ010093 Brassica napus
DESCRIPTION: MAP3K beta 1 protein kinase. MAP3K beta 1.

40 CAA08995.1 AJ010091 Brassica napus
DESCRIPTION: MAP3K alpha 1 protein kinase. MAP3K alpha 1.

AAF34436.1 AF172282 Oryza sativa
DESCRIPTION: similar to mitogen-activated protein kinases. DUPR11.32.

45 CAB54520.1 AJ238845 Brassica napus
DESCRIPTION: putative role in cell cycle control. MAP3K epsilon 1 protein

kinase. MAP3Ke1.

5 CAA08758.1 AJ009609 Brassica napus
DESCRIPTION: BnMAP4K alpha2.

10 CAA08757.1 AJ009608 Brassica napus
DESCRIPTION: BnMAP4K alpha1.

15 AAC83393.1 U83625 Zea mays
DESCRIPTION: protein kinase ZmMEK1. mitogen-activated; ERK-activating
protein kinase (MEK) homolog.

20 AAG53979.1 AF325168 Nicotiana tabacum
DESCRIPTION: mitogen-activated protein kinase 2. MEK2. upstream kinase
for SIPK and WIPK, two tobacco MAP kinases.

25 AAG40578.1 AF216314 Oryza sativa
DESCRIPTION: MAP kinase kinase 1. protein kinase; MEK1.

CAA04261.2 AJ000728 Lycopersicon esculentum
DESCRIPTION: MAP kinase kinase. mek1.

30 AAF67262.1 AF165186 Nicotiana tabacum
DESCRIPTION: MAP kinase kinase.

35 AAG45491.1 AY013245 Oryza sativa
DESCRIPTION: 36I5.3. putative serine/threonine kinase.

40 BAB32405.1 AB055514 Nicotiana tabacum
DESCRIPTION: NQK1 MAPKK. nqk1.

45 AAG49001.1 AY013246 Hordeum vulgare
DESCRIPTION: putative serine/threonine kinase. 635P2.3.

AAF19403.1 AF203481 Lycopersicon esculentum

DESCRIPTION: phosphoenolpyruvate carboxylase kinase. protein kinase;
member of Ca²⁺/CaM kinase family; lacks the autoinhibitory region and EF
hands.

5

AAF19402.1 AF203480 *Lycopersicon esculentum*

DESCRIPTION: phosphoenolpyruvate carboxylase kinase. protein kinase;
member of Ca²⁺/CaM kinase family; lacks the autoinhibitory region and EF
hands.

10

CAC24705.1 AJ302651 *Nicotiana tabacum*

DESCRIPTION: protein kinase. MAP kinase. mek1.

15

BAA06731.1 D31964 *Nicotiana tabacum*

DESCRIPTION: NPK2. protein kinase.

20

AAG31141.1 AF305911 *Oryza sativa*

DESCRIPTION: EDR1. EDR1. MAP kinase kinase kinase; similar to
Arabidopsis thaliana EDR1.

25

AAF19401.1 AF203479 *Glycine max*

DESCRIPTION: phosphoenolpyruvate carboxylase kinase. protein kinase;
member of Ca²⁺/CaM kinase family; lacks the autoinhibitory region and EF
hands.

30

AAD46406.1 AF096250 *Lycopersicon esculentum*

DESCRIPTION: ethylene-responsive protein kinase TCTR1. ER50.

serine/threonine kinase; similar to *Arabidopsis thaliana* negative

35

regulator of the ethylene response pathway encoded by GenBank Accession
Number L08789.

40

CAA73722.1 Y13273 *Lycopersicon esculentum*

DESCRIPTION: putative protein kinase.

45

BAA05649.1 D26602 *Nicotiana tabacum*

DESCRIPTION: protein kinase.

- 5 AAD23582.1 AF128443 *Glycine max*
DESCRIPTION: probably involved in plant stress responses possibly
regulates gene expression. SNF-1-like serine/threonine protein kinase.
expressed in nodules, roots and leaves.
- 10 CAA06334.1 AJ005077 *Lycopersicon esculentum*
DESCRIPTION: protein kinase. TCTR2 protein. TCTR2.
- 15 AAD10057.1 AF110519 *Lycopersicon esculentum*
DESCRIPTION: ethylene-inducible CTR1-like protein kinase. protein kinase
homolog; ethylene and fruit ripening inducible CTR1-like protein kinase;
TCTR1v.
- 20 CAB89082.1 AJ277534 *Asparagus officinalis*
DESCRIPTION: S6 ribosomal protein kinase. pk1. putative.
- 25 AAC78558.1 AF030879 *Solanum tuberosum*
DESCRIPTION: protein kinase CPK1.
- 30 AAD10056.1 AF110518 *Lycopersicon esculentum*
DESCRIPTION: ethylene-inducible CTR1-like protein kinase. protein kinase
homolog; ethylene and fruit ripening inducible CTR1-like protein kinase;
TCTR1.
- 35 AAK18832.1 AC082645 *Oryza sativa*
DESCRIPTION: putative protein kinase. OSJNBb0033N16.9.
- 40 AAG31142.1 AF305912 *Hordeum vulgare*
DESCRIPTION: EDR1. EDR1. MAP kinase kinase kinase; similar to
Arabidopsis thaliana EDR1.
- 45 AAC24961.1 AF009337 *Tradescantia virginiana*
DESCRIPTION: CDPK-related protein kinase. CRK1.
- 50 BAB21278.1 AP002844 *Oryza sativa*
DESCRIPTION: putative MAP kinase. P0410E03.9.

- AAD17800.1 AF090835 *Mesembryanthemum crystallinum*
 DESCRIPTION: Ca²⁺-dependent protein kinase. CPK1. serine/threonine
 protein kinase.
- 5 CAA07813.1 AJ007990 *Hordeum vulgare*
 DESCRIPTION: SnRK1-type protein kinase. kin12a.
- 177

- 10 BAB16335.1 AP002818 *Oryza sativa*
 DESCRIPTION: putative NAM protein. P0436E04.18. contains ESTs
 E10793(C19698),E10793(C99379).
- 15 BAA84803.1 AP000559 *Oryza sativa*
 DESCRIPTION: Similar to NAM like protein (AC005310).
- 20 BAB19365.1 AP002542 *Oryza sativa*
 DESCRIPTION: putative NAM (no apical meristem) protein. P0679C08.4.
- 25 BAB16328.1 AP002818 *Oryza sativa*
 DESCRIPTION: putative NAM protein. P0436E04.11. contains ESTs
 R4069(AU032425),R4069(AU082730).
- 30 CAA63102.2 X92205 *Petunia x hybrida*
 DESCRIPTION: apical meristem formation. NAM.
- 35 CAA63101.1 X92204 *Petunia x hybrida*
 DESCRIPTION: apical meristem formation. NAM.
- 40 AAK13151.1 AC078829 *Oryza sativa*
 DESCRIPTION: putative NAM (no apical meristem) protein.
 OSJNBa0026012.6.
- 45 BAB03447.1 AP002817 *Oryza sativa*
 DESCRIPTION: ESTs C96615(C10106),C26336(C12127),D21959(C10106)
 correspond
 to a region of the predicted gene. Similar to *Arabidopsis thaliana* DNA
 chromosome 4, BAC clone T6K21; NAM (no apical meristem) - like protein

(AL021889).

- 5 BAA92400.1 AP001366 *Oryza sativa*
DESCRIPTION: ESTs C96615(C10106),C26336(C12127),D21959(C10106)
correspond
to a region of the predicted gene. Similar to NAM (AL021889).

- 10 178

BAA25434.1 AB000708 *Raphanus sativus*
DESCRIPTION: SAUR.

- 15 AAG14454.1 AF283706 *Tulipa gesneriana*
DESCRIPTION: auxin-induced protein TGSAUR12. SAUR12. small auxin
upregulated RNA.

- 20 AAG14455.1 AF283707 *Tulipa gesneriana*
DESCRIPTION: auxin-induced protein TGSAUR21. SAUR21. small auxin
upregulated RNA.

- 25 AAG14456.1 AF283708 *Tulipa gesneriana*
DESCRIPTION: auxin-induced protein TGSAUR22. SAUR22. small auxin
upregulated RNA.

- 30 179

BAA78738.1 AB023482 *Oryza sativa*
DESCRIPTION: EST AU055776(S20048) corresponds to a region of the
predicted gene.; Similar to *Arabidopsis thaliana* AP2 domain containing
protein RAP2.10 mRNA, partial cds.(AF003103).

- 35 CAB96899.1 AJ251249 *Catharanthus roseus*
DESCRIPTION: transcription factor. AP2-domain DNA-binding protein. orca3.

- 40 CAB96900.1 AJ251250 *Catharanthus roseus*
DESCRIPTION: transcription factor. AP2-domain DNA-binding protein. orca3.

- 45 AAF76898.1 AF274033 *Atriplex hortensis*
DESCRIPTION: apetala2 domain-containing protein.

5 CAC12822.1 AJ299252 *Nicotiana tabacum*
 DESCRIPTION: AP2 domain-containing transcription factor. ap2.

10 AAC14323.1 AF058827 *Nicotiana tabacum*
 DESCRIPTION: TSI1. Tsi1. contains putative AP2 DNA-binding domain;
 similar to Pti6.

15 BAA97123.1 AB016265 *Nicotiana sylvestris*
 DESCRIPTION: ERF (EREBP); ethylene-responsive element binding factor for
 basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive
 element binding factor. nserf3.

20 CAB93940.1 AJ238740 *Catharanthus roseus*
 DESCRIPTION: putative transcription factor. AP2-domain DNA-binding
 protein. orca2.

25 AAC24587.1 AF071893 *Prunus armeniaca*
 DESCRIPTION: AP2 domain containing protein. AP2DCP.

30 BAB03248.1 AB037183 *Oryza sativa*
 DESCRIPTION: ERF protein transcriptional repressor. ethylene responsive
 element binding factor3. osERF3.

35 BAB16083.1 AB036883 *Oryza sativa*
 DESCRIPTION: transcriptional repressor. osERF3. osERF3. ERF protein
 family ERF3 associated repression domain.

40 BAA76734.1 AB024575 *Nicotiana tabacum*
 DESCRIPTION: ethylene responsive element binding factor.

45 CAB93939.1 AJ238739 *Catharanthus roseus*
 DESCRIPTION: putative transcription factor. AP2-domain DNA-binding
 protein. orca1.

AAG43545.1 AF211527 *Nicotiana tabacum*

DESCRIPTION: Avr9/Cf-9 rapidly elicited protein 1. ACRE1. similar to EREBP transcription factors.

- 5 AAG43548.1 AF211530 *Nicotiana tabacum*
DESCRIPTION: Avr9/Cf-9 rapidly elicited protein 111A. ACRE111A. similar to EREBP transcription factors.
- 10 AAG43549.1 AF211531 *Nicotiana tabacum*
DESCRIPTION: Avr9/Cf-9 rapidly elicited protein 111B. ACRE111B. similar to EREBP transcription factors.
- 15 AAF23899.1 AF193803 *Oryza sativa*
DESCRIPTION: transcription factor EREBP1. EREBP/AP2-like transcription factor.
- 20 AAK31271.1 AC079890 *Oryza sativa*
DESCRIPTION: putative transcriptional factor. OSJNBb0089A17.22.
- 25 AAF63205.1 AF245119 *Mesembryanthemum crystallinum*
DESCRIPTION: AP2-related transcription factor. CDBP. stress induced transcription factor.
- 30 BAA07321.1 D38123 *Nicotiana tabacum*
DESCRIPTION: ERF1. ethylene-responsive transcription factor.
- 35 BAA97122.1 AB016264 *Nicotiana sylvestris*
DESCRIPTION: ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf2.
- 40 BAA97124.1 AB016266 *Nicotiana sylvestris*
DESCRIPTION: ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf4.
- 45 BAA94514.2 AP001800 *Oryza sativa*
DESCRIPTION: Similar to *Arabidopsis thaliana* chromosome 4, BAC clone

F9D16; putative Ap2 domain protein (AL035394).

- 5 AAC62619.1 AF057373 *Nicotiana tabacum*
DESCRIPTION: transcription factor. ethylene response element binding protein 1. EREBP1.
- 10 AAK01088.1 AF298230 *Hordeum vulgare*
DESCRIPTION: CBF1-like protein BCBF1. BCBF1. AP2 domain protein; putative DRE binding factor.
- 15 BAA99376.1 AP002526 *Oryza sativa*
DESCRIPTION: ESTs AU093391(E60370),AU091593(C60458), AU093392(E60370) correspond to a region of the predicted gene. Similar to Arabidopsis thaliana BAC F21J9; AP2 domain protein. (AC000103).
20
- AAK01089.1 AF298231 *Hordeum vulgare*
DESCRIPTION: CBF3-like protein BCBF3. BCBF3. AP2 domain protein; DRE binding factor.
25
- AAG59618.1 AF239616 *Hordeum vulgare*
DESCRIPTION: CRT/DRE-binding factor. CBF.
30 181
- CAB71134.1 AJ271667 *Cicer arietinum*
DESCRIPTION: putative proteasome regulatory subunit.
- 35 185
- BAA85440.1 AP000616 *Oryza sativa*
DESCRIPTION: ESTs AU055729(S20023),AU055730(S20023) correspond to a region of the predicted gene.; similar to Medicago nodulin N21-like protein (AC004218).
40
- CAB53493.1 AJ245900 *Oryza sativa*
DESCRIPTION: CAA303720.1 protein. q3037.20. Similar to Medicago nodulin N21 (MtN21).
45

BAB17350.1 AP002747 Oryza sativa
 DESCRIPTION: putative nodulin. P0698G03.34. contains ESTs
 D39891(S1543),D41717(S4395),AU033037(S1543).
 5
 186

 BAA02724.1 D13506 Glycine max
 DESCRIPTION: early nodulin.
 10
 BAA33816.1 AB018378 Glycine max
 DESCRIPTION: early nodulin. GmENOD93.
 15
 BAA83560.1 AP000399 Oryza sativa
 DESCRIPTION: EST AU077941(C12908) corresponds to a region of the
 predicted gene. Similar to OsENOD93a gene for early nodulin (AB018375).
 20
 BAA33815.1 AB018377 Oryza sativa
 DESCRIPTION: early nodulin. OsENOD93b.
 25
 BAA83566.1 AP000399 Oryza sativa
 DESCRIPTION: ESTs C98280(C1391),D15843(C1391) correspond to a region
 of
 the predicted gene. Similar to OsENOD93a gene for early nodulin
 (AB018375).
 30
 BAA83568.1 AP000399 Oryza sativa
 DESCRIPTION: EST AU077972(C53511) corresponds to a region of the
 predicted gene. Similar to OsENOD93a gene for early nodulin (AB018375).
 35
 BAA83565.1 AP000399 Oryza sativa
 DESCRIPTION: ESTs C98096(C0688),C98097(C0688) correspond to a region
 of
 the predicted gene. Similar to OsENOD93a gene for early nodulin
 (AB018375).
 40
 AAD30134.1 AF140229 Oryza sativa
 DESCRIPTION: early nodulin.
 45

- BAA33814.1 AB018376 *Oryza sativa*
DESCRIPTION: early nodulin. OsENOD93a.
- 5
- BAA33813.1 AB018375 *Oryza sativa*
DESCRIPTION: early nodulin. OsENOD93a.
- 10 BAA83567.1 AP000399 *Oryza sativa*
DESCRIPTION: EST C97982(C0324) corresponds to a region of the predicted gene. Similar to OsENOD93a gene for early nodulin (AB018375).
- 15 BAA83559.1 AP000399 *Oryza sativa*
DESCRIPTION: EST C97982(C0324) corresponds to a region of the predicted gene. Similar to OsENOD93a gene for early nodulin (AB018375).
- 20 BAA83557.1 AP000399 *Oryza sativa*
DESCRIPTION: Similar to OsENOD93a gene for early nodulin (AB018375).
- 188
-
- 25 AAA33811.1 L02830 *Solanum tuberosum*
DESCRIPTION: calcium-binding protein.
- AAG43547.1 AF211529 *Nicotiana tabacum*
- 30 DESCRIPTION: Avr9/Cf-9 rapidly elicited protein 31. ACRE31. similar to *Solanum tuberosum* CAST calcium binding protein encoded by GenBank Accession Number L02830.
- 35 CAB63264.1 AJ251808 *Lotus japonicus*
DESCRIPTION: calcium-binding protein. cbp1.
- AAA34015.1 L01433 *Glycine max*
- 40 DESCRIPTION: calcium-binding regulatory protein. calmodulin. SCaM-4. putative.
- AAA92677.1 U13736 *Pisum sativum*
- 45 DESCRIPTION: binds calcium. calmodulin-like protein.

- AAF31152.1 AF078680 *Olea europaea*
DESCRIPTION: calcium-binding protein. PCA23. Pca23.
- 5 AAA33948.1 L19359 *Glycine max*
DESCRIPTION: calcium-binding regulatory protein. calmodulin. SCaM-5.
putative.
- 10 AAD10245.1 AF030033 *Phaseolus vulgaris*
DESCRIPTION: calmodulin. CaM. EF-hand protein; calcium-dependent
protein;
functions in calcium signal transduction pathways.
- 15 AAF31151.1 AF078679 *Olea europaea*
DESCRIPTION: calcium-binding protein. PCA18. Pca18.
- 20 AAA19571.1 U10150 *Brassica napus*
DESCRIPTION: calcium binding. calmodulin. bcm1.
- 25 AAC49587.1 U49105 *Triticum aestivum*
DESCRIPTION: calmodulin TaCaM4-1. calcium-binding protein.
- 30 AAC49586.1 U49104 *Triticum aestivum*
DESCRIPTION: calmodulin TaCaM3-3. calcium-binding protein.
- 35 AAC49585.1 U49103 *Triticum aestivum*
DESCRIPTION: calmodulin TaCaM3-2. calcium-binding protein.
- 40 AAC49584.1 U48693 *Triticum aestivum*
DESCRIPTION: calmodulin TaCaM3-1. calcium-binding protein.
- 45 AAC49580.1 U48689 *Triticum aestivum*
DESCRIPTION: calmodulin TaCaM1-3. calcium-binding protein.
- 45 AAC49579.1 U48688 *Triticum aestivum*
DESCRIPTION: calmodulin TaCaM1-2. calcium binding protein.

AAA92681.1 U13882 Pisum sativum
DESCRIPTION: calcium-binding protein. calmodulin.

5 CAA78288.1 Z12828 Oryza sativa
DESCRIPTION: calcium binding protein, signal transduction. calmodulin.

190

10 AAF72197.1 AF263737 Euphorbia esula
DESCRIPTION: glutathione S-transferase. theta class GST.

AAG34815.1 AF243380 Glycine max
15 DESCRIPTION: glutathione S-transferase GST 25.

AAG34825.1 AF244682 Zea mays
20 DESCRIPTION: glutathione S-transferase GST 17.

AAG32474.1 AF309381 Oryza sativa subsp. japonica
DESCRIPTION: putative glutathione S-transferase OsGSTZ1.

25 AAG34826.1 AF244683 Zea mays
DESCRIPTION: glutathione S-transferase GST 18.

30 AAA33277.1 M64268 Dianthus caryophyllus
DESCRIPTION: glutathione transferase. CARSR8.

CAA41279.1 X58390 Dianthus caryophyllus
35 DESCRIPTION: glutathione s-transferase. CARSR8.

AAD09190.1 AF109714 Triticum aestivum
DESCRIPTION: glutathione S-transferase. GST.
40

AAB60886.1 AF002211 Triticum aestivum
DESCRIPTION: glutathione-S-transferase.

45 AAA51450.1 L05916 Dianthus caryophyllus

DESCRIPTION: glutathione s-transferase. GST2.

5 AAC50036.1 U42463 Coccomyxa sp. PA
DESCRIPTION: glutathione S-transferase. GST.

10 AAG34801.1 AF243366 Glycine max
DESCRIPTION: glutathione S-transferase GST 11.

AAG32469.1 AF309376 Oryza sativa subsp. japonica
DESCRIPTION: putative glutathione S-transferase OsGSTU6.

15 AAG34850.1 AF244707 Zea mays
DESCRIPTION: glutathione S-transferase GST 42.

20 AAG34807.1 AF243372 Glycine max
DESCRIPTION: glutathione S-transferase GST 17.

25 CAB38119.1 AJ010296 Zea mays
DESCRIPTION: Glutathione transferase III(b). gst3b.

30 AAF23357.1 AF109194 Hordeum vulgare
DESCRIPTION: glutathione-S-transferase.

AAG34849.1 AF244706 Zea mays
DESCRIPTION: glutathione S-transferase GST 41.

35 CAB38118.1 AJ010295 Zea mays
DESCRIPTION: Glutathione transferase III(a). gst3a.

40 AAG32475.1 AF309382 Oryza sativa subsp. japonica
DESCRIPTION: putative glutathione S-transferase OsGSTF5.

45 AAB65163.1 AF002692 Solanum commersonii
DESCRIPTION: glutathione S-transferase, class-phi. GST1. low temperature induced.

- 5 AAF29773.1 AF159229 *Gossypium hirsutum*
DESCRIPTION: glutathione S-transferase. GST.
- 10 BAB39927.1 AP002914 *Oryza sativa*
DESCRIPTION: putative glutathione S-transferase. P0493G01.1. contains
ESTs AU031696(R0596),C97559(C60386),C28218(C60386), D28287(R0596).
- 15 AAG32473.1 AF309380 *Oryza sativa* subsp. *japonica*
DESCRIPTION: putative glutathione S-transferase OsGSTU2.
- 20 CAA09188.1 AJ010449 *Alopecurus myosuroides*
DESCRIPTION: glutathione transferase. GST1b.
- 25 AAG34846.1 AF244703 *Zea mays*
DESCRIPTION: glutathione S-transferase GST 38.
- 30 AAG34812.1 AF243377 *Glycine max*
DESCRIPTION: glutathione S-transferase GST 22.
- CAA55039.1 X78203 *Hyoscyamus muticus*
DESCRIPTION: glutathione transferase.
- 35 AAG34803.1 AF243368 *Glycine max*
DESCRIPTION: glutathione S-transferase GST 13.
- CAA09189.1 AJ010450 *Alopecurus myosuroides*
DESCRIPTION: glutathione transferase. GST1c.
- 40 AAG34808.1 AF243373 *Glycine max*
DESCRIPTION: glutathione S-transferase GST 18.
- 45 AAG34813.1 AF243378 *Glycine max*
DESCRIPTION: glutathione S-transferase GST 23.

- 5 AAD10129.1 AF004358 *Aegilops tauschii*
DESCRIPTION: chloroacetamide herbicide metabolism. glutathione S-transferase TSI-1. GST isozyme.
- 10 AAG41204.1 AF321437 *Suaeda maritima*
DESCRIPTION: glutathione transferase.
- 15 AAG34810.1 AF243375 *Glycine max*
DESCRIPTION: glutathione S-transferase GST 20.
- 20 AAG34804.1 AF243369 *Glycine max*
DESCRIPTION: glutathione S-transferase GST 14.
- 25 AAG34814.1 AF243379 *Glycine max*
DESCRIPTION: glutathione S-transferase GST 24.
- 30 AAG32472.1 AF309379 *Oryza sativa* subsp. *japonica*
DESCRIPTION: putative glutathione S-transferase OsGSTU3.
- 35 AAG32471.1 AF309378 *Oryza sativa* subsp. *japonica*
DESCRIPTION: putative glutathione S-transferase OsGSTU4.
- 40 CAA09187.1 AJ010448 *Alopecurus myosuroides*
DESCRIPTION: glutathione transferase. GST1a.
- 45 AAG34835.1 AF244692 *Zea mays*
DESCRIPTION: glutathione S-transferase GST 27.
- AAF64449.1 AF239927 *Euphorbia esula*
DESCRIPTION: glutathione S-transferase. theta class GST.
- AAG16758.1 AY007560 *Lycopersicon esculentum*
DESCRIPTION: putative glutathione S-transferase T3.

AAG34848.1 AF244705 Zea mays
DESCRIPTION: glutathione S-transferase GST 40.

191

5

AAD32141.1 AF123503 Nicotiana tabacum
DESCRIPTION: Nt-gh3 deduced protein.

10 CAA42636.1 X60033 Glycine max
DESCRIPTION: auxin-responsive GH3 product. GH3.

BAA96221.1 AP002094 Oryza sativa
15 DESCRIPTION: ESTs C19814(E10971),AU090481(E10971) correspond to a
region
of the predicted gene. Similar to Arabidopsis thaliana chromosome 2,
sequence from clones T3F17, F11C10, F13A10; auxin-responsive GH3-like
protein (AC006526).

20

192

AAG13589.1 AC051633 Oryza sativa
DESCRIPTION: putative ubiquitin protein. OSJNBb001511.23.

25

193

CAC09348.1 AL442007 Oryza sativa
DESCRIPTION: putative phosphoglycerate dehydrogenase. H0212B02.4.

30

CAA79702.2 Z21493 Solanum tuberosum
DESCRIPTION: mitochondrial formate dehydrogenase precursor.

35

BAA77337.1 AB019533 Oryza sativa
DESCRIPTION: Nad-dependent formate dehydrogenase.

40 BAA36181.1 D88272 Hordeum vulgare
DESCRIPTION: formate dehydrogenase.

194

45 AAD46412.1 AF096262 Lycopersicon esculentum
DESCRIPTION: ER6 protein. ethylene-inducible; similar to sequence F21M12

from *Arabidopsis thaliana* encoded by GenBank Accession Number AC000132.

195

-
- 5 AAK13154.1 AC078829 *Oryza sativa*
 DESCRIPTION: putative casein kinase. OSJNBa0026O12.5.
- 10 BAA92986.1 AP001550 *Oryza sativa*
 DESCRIPTION: ESTs D41826(S4655),C22685(S4655) correspond to a region
 of
 the predicted gene.; Similar to *Arabidopsis thaliana* chromosome 4, BAC
 clone F16A16; protein kinase-like protein (AL035353).
- 15 AAF19807.1 AF180356 *Brassica oleracea*
 DESCRIPTION: casein kinase I-like protein. CK1b. strong similarity to
 Arabidopsis thaliana casein kinase 1.
- 20 AAD20819.1 AF107592 *Dendrobium grex Madame Thong-In*
 DESCRIPTION: putative casein kinase I. otg16.
- 25 AAF19403.1 AF203481 *Lycopersicon esculentum*
 DESCRIPTION: phosphoenolpyruvate carboxylase kinase. protein kinase;
 member of Ca²⁺/CaM kinase family; lacks the autoinhibitory region and EF
 hands.
- 30 AAF19402.1 AF203480 *Lycopersicon esculentum*
 DESCRIPTION: phosphoenolpyruvate carboxylase kinase. protein kinase;
 member of Ca²⁺/CaM kinase family; lacks the autoinhibitory region and EF
 hands.
- 35 BAA05648.1 D26601 *Nicotiana tabacum*
 DESCRIPTION: protein kinase.
- 40 AAF23901.2 AF194414 *Oryza sativa*
 DESCRIPTION: calcium-dependent protein kinase. CDPK5. OsCDPK5.
- 45 AAC04324.1 U73937 *Nicotiana tabacum*
 DESCRIPTION: ethylene signal transduction. PK12 protein kinase. PK12.

component of the LAMMER family of protein kinases; dual-specificity protein kinase.

- 5 AAF23900.1 AF194413 *Oryza sativa*
 DESCRIPTION: calcium-dependent protein kinase. CDPK1. OsCDPK1.
- 10 BAA34675.1 AB011670 *Triticum aestivum*
 DESCRIPTION: wpk4 protein kinase. wpk4.
- 15 BAA13440.1 D87707 *Ipomoea batatas*
 DESCRIPTION: calcium dependent protein kinase. CDPK.
- 20 AAD17800.1 AF090835 *Mesembryanthemum crystallinum*
 DESCRIPTION: Ca²⁺-dependent protein kinase. CPK1. serine/threonine protein kinase.
- 25 CAA57157.1 X81394 *Oryza sativa*
 DESCRIPTION: calcium-dependent protein kinase. OSCPK2.
- 30 AAD23582.1 AF128443 *Glycine max*
 DESCRIPTION: probably involved in plant stress responses possibly regulates gene expression. SNF-1-like serine/threonine protein kinase. expressed in nodules, roots and leaves.
- 35 CAA39936.1 X56599 *Daucus carota*
 DESCRIPTION: calcium- dependent protein kinase. DcPK431.
- 40 BAA12715.1 D85039 *Zea mays*
 DESCRIPTION: calcium-dependent protein kinase.
- 45 CAA58750.1 X83869 *Daucus carota*
 DESCRIPTION: CDPK-related protein kinase. CRK (or PK421).
- AAB80693.1 U69174 *Glycine max*
 DESCRIPTION: calmodulin-like domain protein kinase isoenzyme gamma. CDPK

gamma.

- 5 AAF21062.1 AF216527 *Dunaliella tertiolecta*
DESCRIPTION: calcium-dependent protein kinase. CPK1; CDPK.
- 10 CAA74646.1 Y14274 *Sorghum bicolor*
DESCRIPTION: putative serine/threonine protein kinase. SNFL3.
- 15 AAD28192.2 AF115406 *Solanum tuberosum*
DESCRIPTION: calcium-dependent protein kinase. CDPK; catalytic domain.
- 20 BAA05649.1 D26602 *Nicotiana tabacum*
DESCRIPTION: protein kinase.
- 25 AAA69507.1 U28376 *Zea mays*
DESCRIPTION: calcium-dependent protein kinase. MZECDPK2.
- 30 AAB05457.1 U55768 *Oryza sativa*
DESCRIPTION: SNF1-related protein kinase. RSk1. Ser/Thr protein kinase homolog.
- 35 AAG36872.1 AF239819 *Zea mays*
DESCRIPTION: protein kinase CK2 catalytic subunit CK2 alpha-3.
- 40 CAA89202.1 Z49233 *Chlamydomonas eugametos*
DESCRIPTION: calcium-stimulated protein kinase.
- 45 CAA72362.1 Y11649 *Zea mays*
DESCRIPTION: protein kinase CK2, alpha subunit.
- CAA72290.1 Y11526 *Zea mays*
DESCRIPTION: casein kinase II alpha subunit. CK2.
- CAA43659.1 X61387 *Zea mays*
DESCRIPTION: casein kinase II alpha subunit. ZMACK2.

- CAA65244.1 X95997 *Solanum tuberosum*
 DESCRIPTION: SNF1-related protein kinase. PKIN1.
 5
- AAF76187.1 AF271237 *Zea mays*
 DESCRIPTION: casein kinase II alpha subunit.
 10
- BAB21591.1 AB036788 *Oryza sativa*
 DESCRIPTION: casein kinase II alpha subunit. OSCKA2.
 15
- BAB21589.1 AB036786 *Oryza sativa*
 DESCRIPTION: casein kinase II alpha subunit. OSCKA2.
 20
- CAB89082.1 AJ277534 *Asparagus officinalis*
 DESCRIPTION: S6 ribosomal protein kinase. pk1. putative.
 25
- AAF06970.1 AF162662 *Kalanchoe fedtschenkoi*
 DESCRIPTION: phosphoenolpyruvate carboxylase kinase. calcium-independent
 protein kinase.
 30
- AAF06969.1 AF162661 *Kalanchoe fedtschenkoi*
 DESCRIPTION: phosphoenolpyruvate carboxylase kinase. calcium-independent
 protein kinase.
 35
- CAA41172.1 X58194 *Oryza sativa*
 DESCRIPTION: cdc2+/CDC28-related protein kinase.
 40
- CAA65500.1 X96723 *Medicago sativa*
 DESCRIPTION: protein kinase. CDPK.
 45
- BAA12691.1 D84507 *Zea mays*
 DESCRIPTION: CDPK-related protein kinase. Does not require calcium for
 its activity (by similarity).
- AAB47181.1 S82324 *Zea mays*

DESCRIPTION: /gene="calcium/calmodulin-dependent
protein kinase. This sequence comes from Fig. 1.

5 CAA07481.1 AJ007366 Zea mays
DESCRIPTION: calcium-dependent protein kinase.

10 BAA99439.1 AP002743 Oryza sativa
DESCRIPTION: putative protein kinase. P0710E05.26. contains ESTs
C22394(C30013),C22393(C30013).

15 BAB12687.1 AP002746 Oryza sativa
DESCRIPTION: putative protein kinase. P0671B11.2. contains ESTs
C22394(C30013),C22393(C30013).

20 AAF40430.1 AF234652 Mesembryanthemum crystallinum
DESCRIPTION: protein kinase MK5.

25 BAB21081.1 AP002819 Oryza sativa
DESCRIPTION: putative calcium-dependent protein kinase. P0501G01.10.
196

30 AAF37267.1 AF220406 Vitis riparia
DESCRIPTION: 26S proteasome regulatory ATPase subunit S10b. Rev136-3.
197

35 BAA08104.1 D45074 Panicum miliaceum
DESCRIPTION: 2-oxoglutarate/malate translocator. mitochondrial
2-oxoglutarate/malate translocator.

40 BAA08103.1 D45073 Panicum miliaceum
DESCRIPTION: 2-oxoglutarate/malate translocator. mitochondrial
2-oxoglutarate/malate translocator.

45 BAA08105.1 D45075 Panicum miliaceum
DESCRIPTION: 2-oxoglutarate/malate translocator. mitochondrial
2-oxoglutarate/malate translocator.

- CAA72107.1 Y11220 *Solanum tuberosum*
DESCRIPTION: mitochondrial uncoupling protein.
- 5 CAC12820.1 AJ299250 *Nicotiana tabacum*
DESCRIPTION: mitochondrial 2-oxoglutarate/malate carrier protein. momc1.
- 10 AAB71744.1 U75346 *Chlamydomonas reinhardtii*
DESCRIPTION: envelope protein. LIP-36G2. low CO2 inducible carrier protein LIP-36 with a molecular weight of 36 kDa.
- 15 AAB71743.1 U75345 *Chlamydomonas reinhardtii*
DESCRIPTION: envelope protein. LIP-36G1. low CO2 inducible carrier protein LIP-36 with a molecular weight of 36 kDa.
- 20 CAA07568.1 AJ007580 *Ribes nigrum*
DESCRIPTION: Mitochondrial carrier protein. prib7.
- BAB40117.1 AP003311 *Oryza sativa*
25 DESCRIPTION: putative peroxisomal Ca-dependent solute carrier protein. P0024G09.9.
- BAB16462.1 AP002483 *Oryza sativa*
30 DESCRIPTION: putative peroxisomal Ca-dependent solute carrier protein. P0019D06.21.
- CAA56325.1 X80023 *Triticum turgidum*
35 DESCRIPTION: ATP/ADP carrier protein.
- CAA46311.1 X65194 *Chlamydomonas reinhardtii*
DESCRIPTION: mitochondrial ADP/ATP translocator protein. CRANT.
40
- CAA67107.1 X98474 *Solanum tuberosum*
DESCRIPTION: mitochondrial energy transfer protein. brittle1.
- 45 CAC27140.1 AJ132535 *Picea abies*

DESCRIPTION: ADP, ATP carrier protein precursor.

- CAA69726.1 Y08499 Betula pendula
5 DESCRIPTION: mitochondrial phosphate translocator.
- BAA31583.1 AB016064 Zea mays
10 DESCRIPTION: mitochondrial phosphate transporter.
- CAB61741.1 AJ275306 Cicer arietinum
DESCRIPTION: mitochondrial phosphate transporter.
- 15 AAG45489.1 AY013245 Oryza sativa
DESCRIPTION: 3615.1. putative mitochondrial carrier protein.
- 20 BAA31584.1 AB016065 Oryza sativa
DESCRIPTION: mitochondrial phosphate transporter.
- 25 BAA92520.1 AP001383 Oryza sativa
DESCRIPTION: ESTs AU068633(C30614),AU068634(C30614) correspond to
a region of the predicted gene. Similar to Bos taurus mitochondrial solute
carrier protein. (AF049236).
- 30 199

BAA03455.1 D14605 Daucus carota
DESCRIPTION: AX110P. AX110.
- 35 204

AAD21872.1 AF078082 Phaseolus vulgaris
DESCRIPTION: receptor-like protein kinase homolog RK20-1.
- 40 AAC23542.1 U20948 Ipomoea trifida
DESCRIPTION: receptor protein kinase. IRK1.
- 45 CAA73133.1 Y12530 Brassica oleracea
DESCRIPTION: serine /threonine kinase. ARLK.

- CAA67145.1 X98520 Brassica oleracea
DESCRIPTION: receptor-like kinase. SFR2.
- 5
- CAB41879.1 Y18260 Brassica oleracea
DESCRIPTION: SRK15 protein. SRK15. receptor-like kinase.
- 10
- BAA92836.1 AB032473 Brassica oleracea
DESCRIPTION: S18 S-locus receptor kinase. SRK18.
- 15
- CAA74662.1 Y14286 Brassica oleracea
DESCRIPTION: SFR3. extracellular S domain: 123-1346; transmembrane domain: 1347-1412; intracellular kinase domain: from 1413.
- 20
- AAB93834.1 U82481 Zea mays
DESCRIPTION: KI domain interacting kinase 1. KIK1. receptor-like protein kinase; serine/threonine protein kinase.
- 25
- CAB41878.1 Y18259 Brassica oleracea
DESCRIPTION: SRK5 protein. SRK5. receptor-like kinase.
- 30
- CAA73134.1 Y12531 Brassica oleracea
DESCRIPTION: serine/threonine kinase. BRLK.
- 35
- CAA74661.1 Y14285 Brassica oleracea
DESCRIPTION: SFR1. extracellular S domain: 8-1342; transmembrane domain: 1343-1411; intracellular kinase domain: 1412-2554.
- 40
- BAA23676.1 AB000970 Brassica rapa
DESCRIPTION: receptor kinase 1. BcRK1.
- 45
- AAA33000.1 M76647 Brassica oleracea
DESCRIPTION: receptor protein kinase. SKR6.
- AAA62232.1 U00443 Brassica napus

DESCRIPTION: S-receptor kinase. protein contains an immunoglobulin-like domain.

5 CAB89179.1 AJ245479 Brassica napus subsp. napus
DESCRIPTION: ser /thr kinase. S-locus receptor kinase. srk.

10 AAA33008.1 M97667 Brassica napus
DESCRIPTION: serine/threonine kinase receptor.

15 BAA21132.1 D88193 Brassica rapa
DESCRIPTION: S-receptor kinase. SRK9 (B.c).

BAA06285.1 D30049 Brassica rapa
DESCRIPTION: S-receptor kinase SRK9.

20 AAK02023.1 AC074283 Oryza sativa
DESCRIPTION: Putative protein kinase-like. OSJNBa0087H07.5.

25 CAA79355.1 Z18921 Brassica oleracea
DESCRIPTION: S-receptor kinase-like protein.

30 BAA92837.1 AB032474 Brassica oleracea
DESCRIPTION: S60 S-locus receptor kinase. SRK60.

35 BAB21001.1 AB054061 Brassica rapa
DESCRIPTION: S locus receptor kinase. SRK22.

BAA07577.2 D38564 Brassica rapa
DESCRIPTION: receptor protein kinase SRK12.

40 BAA07576.1 D38563 Brassica rapa
DESCRIPTION: receptor protein kinase SRK8.

45 AAD52097.1 AF088885 Nicotiana tabacum
DESCRIPTION: receptor-like kinase CHRK1. Chrkl.

- 5 BAB18292.1 AP002860 *Oryza sativa*
DESCRIPTION: putative receptor-like protein kinase. P0409B08.19.
- 10 BAB21240.1 AP002953 *Oryza sativa*
DESCRIPTION: Putative protein kinase. P0426D06.20. contains ESTs
C22359(C11461),C22360(C11461).
- 15 BAA87853.1 AP000816 *Oryza sativa*
DESCRIPTION: EST AU030604(E51294) corresponds to a region of the
predicted gene. Similar to putative NAK-like Ser/Thr protein kinase.
(AF001308).
- 20 BAB16871.1 AP002537 *Oryza sativa*
DESCRIPTION: putative protein kinase APK1A*Arabidopsis thaliana*.
P0001B06.24. contains ESTs C22608(R3192),D25110(R3192).
- 25 BAB39873.1 AP002882 *Oryza sativa*
DESCRIPTION: putative protein kinase. P0439B06.8. contains ESTs
AU056701(S20808),AU056702(S20808).
- 30 AAA33915.1 L27821 *Oryza sativa*
DESCRIPTION: receptor type serine/threonine kinase. protein kinase.
- 35 CAB51836.1 AJ243961 *Oryza sativa*
DESCRIPTION: Putitive Ser/Thr protein kinase. I1332.7.
- 40 CAA97692.1 Z73295 *Catharanthus roseus*
DESCRIPTION: receptor-like protein kinase. CRPK1. Autophosphorylation
predominantly on Thr, less on Ser. Mechanism: autophosphorylation in cis.
- 45 AAK21965.1 AY028699 *Brassica napus*
DESCRIPTION: receptor protein kinase PERK1.
- 45 BAA94529.2 AP001800 *Oryza sativa*
DESCRIPTION: Similar to *Zea mays* S-domain receptor-like protein kinase

(AJ010166).

5 BAA94510.1 AB041504 Populus nigra
DESCRIPTION: protein kinase 2. PnPK2.

10 BAA92954.1 AP001551 Oryza sativa
DESCRIPTION: Similar to Oryza sativa protein kinase (OSPK10) mRNA.
(L27821).

15 BAA94509.1 AB041503 Populus nigra
DESCRIPTION: protein kinase 1. PnPK1.

211

20 AAG13478.1 AC026758 Oryza sativa
DESCRIPTION: putative trehalose-6-phosphate phosphatase.
OSJNBa0015J15.3.

212

25 AAC27894.1 AF023164 Zea mays
DESCRIPTION: leucine-rich repeat transmembrane protein kinase 1. ltk1.

30 AAC27895.1 AF023165 Zea mays
DESCRIPTION: leucine-rich repeat transmembrane protein kinase 2. ltk2.

35 AAK21965.1 AY028699 Brassica napus
DESCRIPTION: receptor protein kinase PERK1.

AAC61805.1 U28007 Lycopersicon esculentum
DESCRIPTION: serine/threonine protein kinase. Pto kinase interactor 1.
Pti1. Pti1 kinase.

40 BAB21241.1 AP002953 Oryza sativa
DESCRIPTION: Putative Pto kinase interactor 1. P0426D06.21. contains ESTs
AU108280(E0721),D48017(S13927).

45 AAF91336.1 AF249317 Glycine max

DESCRIPTION: Pti1 kinase-like protein. Pti1a. protein kinase.

AAF91337.1 AF249318 Glycine max

5 DESCRIPTION: Pti1 kinase-like protein. Pti1b. protein kinase.

BAA82394.1 AP000367 Oryza sativa

10 DESCRIPTION: ESTs D23521(C2939),C22481(C2939) correspond to a region of
of
the predicted gene.; Similar to serine/threonine protein kinase like
protein. (AL022140).

15 BAA87853.1 AP000816 Oryza sativa

DESCRIPTION: EST AU030604(E51294) corresponds to a region of the
predicted gene. Similar to putative NAK-like Ser/Thr protein kinase.
(AF001308).

20

AAG16628.1 AY007545 Brassica napus

DESCRIPTION: protein serine/threonine kinase BNK1.

25 BAB07999.1 AP002525 Oryza sativa

DESCRIPTION: putative protein kinase. P0462H08.22. contains EST
C22619(S11214).

30 BAB03429.1 AP002817 Oryza sativa

DESCRIPTION: EST C22619(S11214) corresponds to a region of the predicted
gene. Similar to Arabidopsis thaliana chromosome 2, BAC clone T17D12;
putative protein kinase (AC006587).

35

BAB16871.1 AP002537 Oryza sativa

DESCRIPTION: putative protein kinase APK1AArabidopsis thaliana.
P0001B06.24. contains ESTs C22608(R3192),D25110(R3192).

40

BAA94510.1 AB041504 Populus nigra

DESCRIPTION: protein kinase 2. PnPK2.

45 BAB39409.1 AP002901 Oryza sativa

DESCRIPTION: putative protein kinase. P0456F08.9. contains EST

C23560(R0290).

- 5 BAA94509.1 AB041503 *Populus nigra*
DESCRIPTION: protein kinase 1. PnPK1.
- 10 BAB39873.1 AP002882 *Oryza sativa*
DESCRIPTION: putative protein kinase. P0439B06.8. contains ESTs
AU056701(S20808),AU056702(S20808).
- 15 AAK11674.1 AF339747 *Lophopyrum elongatum*
DESCRIPTION: protein kinase. ESI47.
- 20 AAF43496.1 AF131222 *Lophopyrum elongatum*
DESCRIPTION: protein serine/threonine kinase. ESI47. induced in roots by
salt stress, osmotic stress, and ABA treatment.
- 25 BAB21240.1 AP002953 *Oryza sativa*
DESCRIPTION: Putative protein kinase. P0426D06.20. contains ESTs
C22359(C11461),C22360(C11461).
- 30 BAA78764.1 AB023482 *Oryza sativa*
DESCRIPTION: ESTs C98382(C2985),D22444(C11129) correspond to a region
of
the predicted gene.; Similar to *Arabidopsis thaliana* APK1 gene for protein
tyrosine-serine-threonine kinase.(D12522).
- 35 AAB09771.1 U67422 *Zea mays*
DESCRIPTION: CRINKLY4 precursor. cr4. receptor kinase homolog.
- 40 AAK00425.1 AC069324 *Oryza sativa*
DESCRIPTION: Putative protein kinase. OSJNBa0071K19.11.
- 45 AAG59657.1 AC084319 *Oryza sativa*
DESCRIPTION: putative protein kinase. OSJNBa0004B24.20.
- AAF66615.1 AF142596 *Nicotiana tabacum*

DESCRIPTION: LRR receptor-like protein kinase.

- 5 AAG03090.1 AC073405 *Oryza sativa*
DESCRIPTION: Similar to an Arabidopsis somatic embryogenesis
receptor-like kinase (AC007504).
- 10 CAB51834.1 00069 *Oryza sativa*
DESCRIPTION: 11332.5. contains eukaryotic protein kinase domain PF.
- 15 AAG25966.1 AF302082 *Nicotiana tabacum*
DESCRIPTION: cytokinin-regulated kinase 1. CRK1. protein kinase;
transcript abundance decreases rapidly after cytokinin treatment.
- 20 CAA97692.1 Z73295 *Catharanthus roseus*
DESCRIPTION: receptor-like protein kinase. CRPK1. Autophosphorylation
predominantly on Thr, less on Ser. Mechanism: autophosphorylation in cis.
- 25 BAA90808.1 AP001168 *Oryza sativa*
DESCRIPTION: Similar to putative receptor-like protein kinase (AL035679).
- 30 BAB40081.1 AP003074 *Oryza sativa*
DESCRIPTION: putative receptor protein kinase. OSJNBa0004G10.30.
- 35 BAB18321.1 AP002865 *Oryza sativa*
DESCRIPTION: putative receptor protein kinase. P0034C11.11.
- 40 AAD38286.1 AC007789 *Oryza sativa*
DESCRIPTION: putative protein kinase. OSJNBa0049B20.13.
- 45 CAB51480.1 Y14600 *Sorghum bicolor*
DESCRIPTION: putative protein serine /threonine kinase. RLK1. accumulates
in mesophyll cells.
- BAB19337.1 AP003044 *Oryza sativa*
DESCRIPTION: putative protein kinase. P0038C05.10. contains ESTs
AU056335(S20481),AU056336(S20481).

5 AAF91324.1 AF244890 Glycine max
 DESCRIPTION: receptor-like protein kinase 3. RLK3. GmRLK3.

10 AAF91323.1 AF244889 Glycine max
 DESCRIPTION: receptor-like protein kinase 2. RLK2. GmRLK2.

15 BAB16326.1 AP002818 Oryza sativa
 DESCRIPTION: putative receptor ser/thr protein kinase. P0436E04.9.
 contains ESTs S10111(AU070304),S10111(AU083519).

20 BAA82556.1 AB030083 Populus nigra
 DESCRIPTION: lectin-like protein kinase. PnLPK.

25 BAA94516.1 AP001800 Oryza sativa
 DESCRIPTION: Similar to Zea mays S-domain receptor-like protein kinase
 (AJ010166).

30 BAB07906.1 AP002835 Oryza sativa
 DESCRIPTION: putative S-receptor kinase. P0417G05.14.

35 AAF59906.1 AF197947 Glycine max
 DESCRIPTION: receptor protein kinase-like protein. CLV1B.

 AAF59905.1 AF197946 Glycine max
 DESCRIPTION: receptor protein kinase-like protein. CLV1A.

40 BAB07904.1 AP002835 Oryza sativa
 DESCRIPTION: putative S-receptor kinase. P0417G05.12.

45 214

 AAB51442.1 U63012 Sophora japonica
 DESCRIPTION: lectin precursor.

 CAA93829.1 Z69999 Phaseolus lunatus

DESCRIPTION: lectin 3.

5 BAA36415.1 AB012634 Robinia pseudoacacia
DESCRIPTION: lectin.

10 CAA93828.1 Z69998 Phaseolus lunatus
DESCRIPTION: lectin 2.

AAC49137.1 U21959 Cladrastis kentukea
DESCRIPTION: lectin precursor.

15 AAC49150.1 U21940 Cladrastis kentukea
DESCRIPTION: storage protein precursor. lectin.

20 CAB96391.1 AJ271873 Phaseolus lunatus
DESCRIPTION: carbohydrate-binding. lectin. lbl5.

25 CAB96392.1 AJ271874 Phaseolus lunatus
DESCRIPTION: carbohydrate-binding. lectin. lbl6.

30 CAA76366.1 Y16754 Medicago sativa
DESCRIPTION: lectin. lec2.

BAA82556.1 AB030083 Populus nigra
DESCRIPTION: lectin-like protein kinase. PnLPK.

35 CAA93830.1 Z70000 Phaseolus lunatus
DESCRIPTION: lectin 4.

40 AAG16779.1 AF190633 Ulex europaeus
DESCRIPTION: lectin II.

45 AAC49136.1 U21958 Cladrastis kentukea
DESCRIPTION: lectin precursor.

AAB39933.1 U65009 Maackia amurensis
DESCRIPTION: lectin precursor.

5

AAB39934.1 U65010 Maackia amurensis
DESCRIPTION: lectin precursor.

10 AAA33766.1 L26237 Phaseolus lunatus
DESCRIPTION: lectin II.

15 AAA33143.1 M34270 Dolichos biflorus
DESCRIPTION: seed lectin.

20 CAA57697.1 X82216 Medicago truncatula
DESCRIPTION: lectin. lec3.

BAA36413.1 AB012632 Robinia pseudoacacia
DESCRIPTION: lectin.

25 AAA80182.1 U12783 Robinia pseudoacacia
DESCRIPTION: lectin.

30 BAA04604.1 D17757 Robinia pseudoacacia
DESCRIPTION: lectin precursor.

35 CAA68497.1 Y00440 Pisum sativum
DESCRIPTION: lectin-precursor (AA -30 to 245).

40 AAC49271.1 U24249 Robinia pseudoacacia
DESCRIPTION: lectin precursor.

AAA80181.1 U12782 Robinia pseudoacacia
DESCRIPTION: lectin.

45 BAA36416.1 AB012635 Robinia pseudoacacia

DESCRIPTION: lectin-related polypeptide.

- 5 AAA33676.1 M18160 Pisum sativum
DESCRIPTION: lectin.
- 10 CAA47011.1 X66368 Pisum sativum
DESCRIPTION: Psl lectin. psl.
- 15 AAA33141.1 J02721 Dolichos biflorus
DESCRIPTION: lectin subunit I precursor.
- 20 BAA36414.1 AB012633 Robinia pseudoacacia
DESCRIPTION: lectin.
- 25 BAA02049.1 D12481 Bauhinia purpurea
DESCRIPTION: lectin.
- 30 AAA80183.1 U12784 Robinia pseudoacacia
DESCRIPTION: lectin.
- AAC49272.1 U24250 Robinia pseudoacacia
DESCRIPTION: lectin precursor.
- 35 AAA82737.1 U18296 Medicago sativa
DESCRIPTION: lectin. Mslecl.
- 40 AAA74571.1 U22468 Arachis hypogaea
DESCRIPTION: agglutinin. galactose-binding lectin precursor. lec. lectin.
- 45 AAB51441.1 U63011 Sophora japonica
DESCRIPTION: lectin precursor.
- AAA74574.1 U22471 Arachis hypogaea
DESCRIPTION: agglutinin. galactose-binding lectin precursor. lec. lectin.

- AAG00508.1 AF285121 *Sophora flavescens*
DESCRIPTION: lectin.
- 5 AAB39932.1 U65008 *Maackia amurensis*
DESCRIPTION: lectin precursor.
- 215
- 10 -----
CAA64327.1 X94624 *Brassica napus*
DESCRIPTION: acyl-CoA synthetase.
- 15 CAA96523.1 Z72153 *Brassica napus*
DESCRIPTION: acyl CoA synthetase.
- 20 CAC19877.1 AJ401089 *Brassica napus*
DESCRIPTION: activation of free fatty acids. long chain acyl-CoA
synthetase. acs6. activity confirmed by expression in *E. coli*.
- 25 CAA06820.1 AJ006025 *Cicer arietinum*
DESCRIPTION: acyl-coA synthetase.
- 30 AAC39365.1 AF008183 *Populus x generosa*
DESCRIPTION: 4-coumarate:CoA ligase 2. 4CL2.
- 35 CAA31697.1 X13325 *Petroselinum crispum*
DESCRIPTION: 4-coumarate:CoA ligase Pc4Cl-2 (AA 1-544).
- 40 CAA31696.1 X13324 *Petroselinum crispum*
DESCRIPTION: 4-coumarate:CoA ligase Pc4Cl-1 (AA 1-544).
- 45 AAC39366.1 AF008184 *Populus x generosa*
DESCRIPTION: 4-coumarate:CoA ligase 1. 4CL1.
- AAF37734.1 AF052223 *Lolium perenne*
DESCRIPTION: 4-coumarate--CoA ligase 4CL3.

AAF91309.1 AF239686 *Rubus idaeus*
DESCRIPTION: 4-coumarate:coA ligase 2. adenylate-forming enzyme; 4CL2.

5

AAF37733.1 AF052222 *Lolium perenne*
DESCRIPTION: 4-coumarate--CoA ligase 4CL2.

10 CAA36850.1 X52623 *Oryza sativa*
DESCRIPTION: 4-coumarate-CoA ligase.

15 BAA07828.1 D43773 *Nicotiana tabacum*
DESCRIPTION: 4-coumarate:coenzyme A ligase.

20 BAA08365.1 D49366 *Lithospermum erythrorhizon*
DESCRIPTION: 4-coumarate:CoA ligase.

AAB18637.1 U50845 *Nicotiana tabacum*
DESCRIPTION: 4-coumarate:coenzyme A ligase. 4CL1. Nt4CL-1.

25

AAD40664.1 AF150686 *Solanum tuberosum*
DESCRIPTION: 4-coumarate:coenzyme A ligase. 4CL-2a.

30 AAA33842.1 M62755 *Solanum tuberosum*
DESCRIPTION: 4-coumarate--CoA ligase. St4C1-1.

35 AAB18638.1 U50846 *Nicotiana tabacum*
DESCRIPTION: 4-coumarate:coenzyme A ligase. 4CL2. Nt4CL-19.

40 AAF91310.1 AF239687 *Rubus idaeus*
DESCRIPTION: 4-coumarate:coA ligase 1. adenylate-forming enzyme; 4CL1.

AAC24503.1 AF041049 *Populus tremuloides*
DESCRIPTION: 4-coumarate:CoA ligase.

45

AAF37732.1 AF052221 *Lolium perenne*

DESCRIPTION: 4-coumarate--CoA ligase 4CL1.

5 AAA92669.1 U12013 Pinus taeda
DESCRIPTION: 4-coumarate-CoA ligase enzyme.

10 AAB42382.1 U39404 Pinus taeda
DESCRIPTION: 4-coumarate:CoA ligase. lp4CL-2.

AAB42383.1 U39405 Pinus taeda
DESCRIPTION: 4-coumarate:CoA ligase. lp4CL-1.

15 AAF91308.1 AF239685 Rubus idaeus
DESCRIPTION: 4-coumarate:coA ligase 3. adenylate-forming enzyme; 4CL3.

20 AAC24504.1 AF041050 Populus tremuloides
DESCRIPTION: 4-coumarate:CoA ligase.

25 AAA92668.1 U12012 Pinus taeda
DESCRIPTION: 4-coumarate-CoA ligase enzyme.

30 CAC36095.1 X69955 Glycine max
DESCRIPTION: 4-coumarate:Coenzyme A ligase isoenzyme 4. 4CL4.

AAG43823.1 AF212317 Capsicum annuum
DESCRIPTION: 4-coumarate:coenzyme A ligase. 4CL.

35 AAA69580.1 L43362 Oryza sativa
DESCRIPTION: 4-coumarate:CoA ligase isoform 2. 4cl.2. putative.

40 BAA08366.2 D49367 Lithospermum erythrorhizon
DESCRIPTION: 4-coumarate:CoA ligase.

45 CAA49575.1 X69954 Glycine max
DESCRIPTION: 4-coumarate--CoA ligase.

CAB97359.1 AJ278455 *Juglans nigra*
DESCRIPTION: 4-coumarate-CoA ligase. 4CL.

5
AAF73995.2 AF144502 *Pinus armandii*
DESCRIPTION: 4-coumarate:CoA ligase. 4CL.

10 AAF73994.2 AF144501 *Pinus armandii*
DESCRIPTION: 4-coumarate:CoA ligase. 4CL.

15 AAF74018.2 AF144525 *Tsuga canadensis*
DESCRIPTION: 4-coumarate:CoA ligase. 4CL.

20 AAF74010.2 AF144517 *Abies holophylla*
DESCRIPTION: 4-coumarate:CoA ligase. 4CL.

AAF74020.2 AF144527 *Pseudolarix amabilis*
DESCRIPTION: 4-coumarate:CoA ligase. 4CL.

25 AAF74016.2 AF144523 *Nothotsuga longibracteata*
DESCRIPTION: 4-coumarate:CoA ligase. 4CL.

30 AAF73997.2 AF144504 *Picea smithiana*
DESCRIPTION: 4-coumarate:CoA ligase. 4CL.

35 AAF74013.2 AF144520 *Abies beshanzuensis*
DESCRIPTION: 4-coumarate:CoA ligase. 4CL.

40 AAF74008.2 AF144515 *Abies firma*
DESCRIPTION: 4-coumarate:CoA ligase. 4CL.

AAF74022.2 AF144529 *Cedrus atlantica*
DESCRIPTION: 4-coumarate:CoA ligase. 4CL.

45 AAF74005.2 AF144512 *Larix gmelini*

DESCRIPTION: 4-coumarate:CoA ligase. 4CL.

5 AAF74021.2 AF144528 *Pseudolarix amabilis*
 DESCRIPTION: 4-coumarate:CoA ligase. 4CL.

10 AAF74003.2 AF144510 *Pseudotsuga sinensis*
 DESCRIPTION: 4-coumarate:CoA ligase. 4CL.

15 AAF74019.2 AF144526 *Tsuga canadensis*
 DESCRIPTION: 4-coumarate:CoA ligase. 4CL.

20 221

 AAB37246.1 U58971 *Nicotiana tabacum*
 DESCRIPTION: calmodulin-binding protein. TCB60.

25 224

 BAB19413.1 AP002870 *Oryza sativa*
 DESCRIPTION: putative acetone-cyanohydrin lyase. P0458A05.22.

30 AAC49184.1 U40402 *Hevea brasiliensis*
 DESCRIPTION: hydroxynitrile lyase. hnl.

35 CAA11219.1 AJ223281 *Manihot esculenta*
 DESCRIPTION: alpha-hydroxynitrile lyase. HNL4.

40 CAA82334.1 Z29091 *Manihot esculenta*
 DESCRIPTION: alpha-hydroxynitrile lyase.

45 225

 BAB16335.1 AP002818 *Oryza sativa*
 DESCRIPTION: putative NAM protein. P0436E04.18. contains ESTs
 E10793(C19698),E10793(C99379).

50 AAK13151.1 AC078829 *Oryza sativa*
 DESCRIPTION: putative NAM (no apical meristem) protein.
 OSJNBa0026012.6.

CAA63102.2 X92205 Petunia x hybrida
DESCRIPTION: apical meristem formation. NAM.

5

CAA63101.1 X92204 Petunia x hybrida
DESCRIPTION: apical meristem formation. NAM.

10

BAB16328.1 AP002818 Oryza sativa
DESCRIPTION: putative NAM protein. P0436E04.11. contains ESTs
R4069(AU032425),R4069(AU082730).

15

BAB19365.1 AP002542 Oryza sativa
DESCRIPTION: putative NAM (no apical meristem) protein. P0679C08.4.

20

BAA84803.1 AP000559 Oryza sativa
DESCRIPTION: Similar to NAM like protein (AC005310).

25

BAB03447.1 AP002817 Oryza sativa
DESCRIPTION: ESTs C96615(C10106),C26336(C12127),D21959(C10106)
correspond
to a region of the predicted gene. Similar to Arabidopsis thaliana DNA
chromosome 4, BAC clone T6K21; NAM (no apical meristem) - like protein
(AL021889).

30

BAA92400.1 AP001366 Oryza sativa
DESCRIPTION: ESTs C96615(C10106),C26336(C12127),D21959(C10106)
correspond
to a region of the predicted gene. Similar to NAM (AL021889).

35

226

BAA96221.1 AP002094 Oryza sativa
DESCRIPTION: ESTs C19814(E10971),AU090481(E10971) correspond to a
region
of the predicted gene. Similar to Arabidopsis thaliana chromosome 2,
sequence from clones T3F17, F11C10, F13A10; auxin-responsive GH3-like
protein (AC006526).

45

AAD32141.1 AF123503 *Nicotiana tabacum*
DESCRIPTION: Nt-gh3 deduced protein.

- 5 CAA42636.1 X60033 *Glycine max*
DESCRIPTION: auxin-responsive GH3 product. GH3.

227

- 10 CAA70403.1 Y09204 *Nicotiana tabacum*
DESCRIPTION: histidinol-phosphate aminotransferase. hpa.

- 15 CAC20728.1 AJ278767 *Nicotiana plumbaginifolia*
DESCRIPTION: essential for histidine biosynthesis. histidinol phosphate
aminotransferase. hpa.

229

- 20 AAF33670.1 AF079872 *Nicotiana tabacum*
DESCRIPTION: cyclic nucleotide-gated calmodulin-binding ion channel.
CBP4.

- 25 AAF33669.1 AF079871 *Nicotiana tabacum*
DESCRIPTION: cyclic nucleotide-gated calmodulin-binding ion channel.
CBP7.

- 30 AAK16188.1 AC079887 *Oryza sativa*
DESCRIPTION: putative cyclic nucleotide and calmodulin-regulated ion
channel protein. OSJNBa0040E01.13.

- 35 AAB53255.1 U65390 *Nicotiana tabacum*
DESCRIPTION: cyclic nucleotide gated channel protein. CaMB-channel
protein. channel protein homolog.

- 40 CAB54856.1 AJ132686 *Zea mays*
DESCRIPTION: potassium channel protein ZMK2. ZMK2.

- 45 AAD16278.1 AF099095 *Samanea saman*
DESCRIPTION: pulvinus inward-rectifying channel for potassium SPICK1.
similar to Arabidopsis potassium channel AKT3.

- CAA71598.1 Y10579 *Vicia faba*
DESCRIPTION: potassium channel.
- 5
- CAA56175.1 X79779 *Solanum tuberosum*
DESCRIPTION: K⁺ channel inward rectifying. KST1.
- 10
- CAC05489.1 AJ271447 *Populus tremula* x *Populus tremuloides*
DESCRIPTION: potassium channel. potassium channel 2. ptk2.
- 15
- AAD39492.1 AF145272 *Samanea saman*
DESCRIPTION: pulvinus inward-rectifying channel SPICK2. potassium channel; similar to AKT2/3.
- 20
- CAA70870.1 Y09699 *Solanum tuberosum*
DESCRIPTION: putative inward rectifying potassium channel. SKT2.
- 25
- CAB62555.1 AJ249962 *Daucus carota*
DESCRIPTION: potassium channel. kdc1.
- 30
- BAA96192.1 AP002093 *Oryza sativa*
DESCRIPTION: Similar to *Arabidopsis thaliana* potassium channel protein (M86990).
- 35
- BAA96150.1 AP002092 *Oryza sativa*
DESCRIPTION: Similar to *Arabidopsis thaliana* potassium channel protein (M86990).
- 40
- BAA84085.1 AB032074 *Nicotiana paniculata*
DESCRIPTION: potassium channel. NpKT1.
- 45
- AAF81251.1 AF267755 *Mesembryanthemum crystallinum*
DESCRIPTION: potassium channel protein Mkt2p.
- CAA68912.1 Y07632 *Zea mays*

DESCRIPTION: potassium channel. ZMK1.

CAA60016.1 X86021 Solanum tuberosum

5 DESCRIPTION: potassium channel. SKT1 gene. putative start codon.

CAA65254.1 X96390 Lycopersicon esculentum

10 DESCRIPTION: potassium channel. LKT1.

CAA12645.1 AJ225805 Egeria densa

15 DESCRIPTION: inward potassium channel alpha subunit. homologous to the sequences of the family of inwardly rectifying potassium channels in plants which is structurally related to the shaker family of outwardly rectifying channels in Drosophila.

AAF36832.1 AF207745 Triticum aestivum

20 DESCRIPTION: AKT1-like potassium channel. TaAKT1.

CAC10514.1 AJ299019 Samanea saman

25 DESCRIPTION: potassium release. outwardly rectifying potassium channel. spork1.

AAF81249.1 AF267753 Mesembryanthemum crystallinum

30 DESCRIPTION: putative potassium channel protein Mkt1p.

CAC05488.1 AJ271446 Populus tremula x Populus tremuloides

35 DESCRIPTION: potassium channel. outward rectifying potassium channel. ptork.

232

AAA80575.1 U13148 Pennisetum ciliare

40 DESCRIPTION: possible apospory-associated protein.

AAF34174.1 AF195243 Chlamydomonas reinhardtii

45 DESCRIPTION: apospory-associated protein C. APOC.

233

- AAC39358.1 AF005655 *Eschscholzia californica*
 DESCRIPTION: oxidizes the N-methyl group of (S)-reticuline to the
 berberine bridge carbon C-8 of (S)-scoulerine in berberine and
 benzophenanthridine alkaloid biosynthesis. berberine bridge enzyme. bbe1.
 5 covalently-bound FAD-dependent oxidase; elicitor-inducible.
- AAC61839.1 AF025430 *Papaver somniferum*
 DESCRIPTION: berberine bridge enzyme. bbe1. (S)-reticuline:oxygen
 10 oxidoreductase (methylene bridge forming).
- 247

- AAF37267.1 AF220406 *Vitis riparia*
 15 DESCRIPTION: 26S proteasome regulatory ATPase subunit S10b. Rev136-3.
- 248

- BAA78764.1 AB023482 *Oryza sativa*
 20 DESCRIPTION: ESTs C98382(C2985),D22444(C11129) correspond to a region
 of
 the predicted gene.; Similar to *Arabidopsis thaliana* APK1 gene for protein
 tyrosine-serine-threonine kinase.(D12522).
- 25
 BAA94509.1 AB041503 *Populus nigra*
 DESCRIPTION: protein kinase 1. PnPK1.
- 30 AAG16628.1 AY007545 *Brassica napus*
 DESCRIPTION: protein serine/threonine kinase BNK1.
- BAB03429.1 AP002817 *Oryza sativa*
 35 DESCRIPTION: EST C22619(S11214) corresponds to a region of the predicted
 gene. Similar to *Arabidopsis thaliana* chromosome 2, BAC clone T17D12;
 putative protein kinase (AC006587).
- 40 BAB07999.1 AP002525 *Oryza sativa*
 DESCRIPTION: putative protein kinase. P0462H08.22. contains EST
 C22619(S11214).
- 45 BAA94510.1 AB041504 *Populus nigra*
 DESCRIPTION: protein kinase 2. PnPK2.

- 5 AAK11674.1 AF339747 *Lophopyrum elongatum*
DESCRIPTION: protein kinase. ESI47.
- 10 AAF43496.1 AF131222 *Lophopyrum elongatum*
DESCRIPTION: protein serine/threonine kinase. ESI47. induced in roots by salt stress, osmotic stress, and ABA treatment.
- 15 BAB16871.1 AP002537 *Oryza sativa*
DESCRIPTION: putative protein kinase APK1A *Arabidopsis thaliana*. P0001B06.24. contains ESTs C22608(R3192), D25110(R3192).
- 20 BAA87853.1 AP000816 *Oryza sativa*
DESCRIPTION: EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative NAK-like Ser/Thr protein kinase. (AF001308).
- 25 BAB39409.1 AP002901 *Oryza sativa*
DESCRIPTION: putative protein kinase. P0456F08.9. contains EST C23560(R0290).
- 30 BAB39873.1 AP002882 *Oryza sativa*
DESCRIPTION: putative protein kinase. P0439B06.8. contains ESTs AU056701(S20808), AU056702(S20808).
- 35 BAB21240.1 AP002953 *Oryza sativa*
DESCRIPTION: Putative protein kinase. P0426D06.20. contains ESTs C22359(C11461), C22360(C11461).
- 40 AAK21965.1 AY028699 *Brassica napus*
DESCRIPTION: receptor protein kinase PERK1.
- 45 AAK00425.1 AC069324 *Oryza sativa*
DESCRIPTION: Putative protein kinase. OSJNBa0071K19.11.
- AAG03090.1 AC073405 *Oryza sativa*

DESCRIPTION: Similar to an Arabidopsis somatic embryogenesis receptor-like kinase (AC007504).

- 5 AAG59657.1 AC084319 *Oryza sativa*
DESCRIPTION: putative protein kinase. OSJNBa0004B24.20.
- 10 AAF91336.1 AF249317 *Glycine max*
DESCRIPTION: Pti1 kinase-like protein. Pti1a. protein kinase.
- 15 AAF91337.1 AF249318 *Glycine max*
DESCRIPTION: Pti1 kinase-like protein. Pti1b. protein kinase.
- 20 BAB21241.1 AP002953 *Oryza sativa*
DESCRIPTION: Putative Pto kinase interactor 1. P0426D06.21. contains ESTs AU108280(E0721),D48017(S13927).
- 25 CAB51834.1 00069 *Oryza sativa*
DESCRIPTION: 11332.5. contains eukaryotic protein kinase domain PF.
- 30 AAC61805.1 U28007 *Lycopersicon esculentum*
DESCRIPTION: serine/threonine protein kinase. Pto kinase interactor 1. Pti1. Pti1 kinase.
- 35 AAG33377.1 AF290411 *Oryza meyeriana*
DESCRIPTION: serine/threonine protein kinase. R1.
- 40 AAC27894.1 AF023164 *Zea mays*
DESCRIPTION: leucine-rich repeat transmembrane protein kinase 1. ltk1.
- 45 BAA90808.1 AP001168 *Oryza sativa*
DESCRIPTION: Similar to putative receptor-like protein kinase (AL035679).
- AAC27895.1 AF023165 *Zea mays*
DESCRIPTION: leucine-rich repeat transmembrane protein kinase 2. ltk2.

AAB61708.1 U93048 *Daucus carota*

DESCRIPTION: somatic embryogenesis receptor-like kinase. SERK.

5 CAA97692.1 Z73295 *Catharanthus roseus*

DESCRIPTION: receptor-like protein kinase. CRPK1. Autophosphorylation predominantly on Thr, less on Ser. Mechanism: autophosphorylation in cis.

10 AAK11566.1 AF318490 *Lycopersicon hirsutum*

DESCRIPTION: Pto-like protein kinase E. LhirPtoE. confers resistance to bacterial speck disease.

15 BAB18292.1 AP002860 *Oryza sativa*

DESCRIPTION: putative receptor-like protein kinase. P0409B08.19.

CAB51480.1 Y14600 *Sorghum bicolor*

20 DESCRIPTION: putative protein serine /threonine kinase. RLK1. accumulates in mesophyll cells.

AAG25966.1 AF302082 *Nicotiana tabacum*

25 DESCRIPTION: cytokinin-regulated kinase 1. CRK1. protein kinase; transcript abundance decreases rapidly after cytokinin treatment.

AAG00510.1 AF285172 *Phaseolus vulgaris*

30 DESCRIPTION: leaf senescence-associated receptor-like protein kinase. SARK.

AAC48932.1 U13923 *Lycopersicon pimpinellifolium*

35 DESCRIPTION: Fen. putative serine/threonine protein kinase; similar to product encoded by *Lycopersicon pimpinellifolium* Pto gene, GenBank Accession Number U02271; Fen is a member of the Pto gene family.

40 AAB47424.1 U59317 *Lycopersicon pimpinellifolium*

DESCRIPTION: serine/threonine protein kinase Fen. Fen. fenthion sensitivity gene from tomato.

45 AAF76307.1 AF220602 *Lycopersicon pimpinellifolium*

DESCRIPTION: Fen kinase.

0907270601

- 5 AAF66615.1 AF142596 *Nicotiana tabacum*
DESCRIPTION: LRR receptor-like protein kinase.
- 10 BAA92221.1 AP001278 *Oryza sativa*
DESCRIPTION: Similar to *Arabidopsis thaliana* chromosome II BAC F12L6
genomic sequence, putative protein kinase. (AC004218).
- 15 BAA87852.1 AP000816 *Oryza sativa*
DESCRIPTION: Similar to putative Ser/Thr protein kinase. (AC004218).
- 20 AAK11567.1 AF318491 *Lycopersicon hirsutum*
DESCRIPTION: Pto-like protein kinase F. LhirPtoF.
- 25 CAA73134.1 Y12531 *Brassica oleracea*
DESCRIPTION: serine/threonine kinase. BRLK.
- BAB19337.1 AP003044 *Oryza sativa*
DESCRIPTION: putative protein kinase. P0038C05.10. contains ESTs
AU056335(S20481),AU056336(S20481).
- 249

- 30 BAA22422.1 AB001379 *Glycyrrhiza echinata*
DESCRIPTION: cytochrome P450. CYP81E1.
- 35 BAA74465.1 AB022732 *Glycyrrhiza echinata*
DESCRIPTION: cytochrome P450. CYP Ge-31.
- 40 BAA93634.1 AB025016 *Lotus japonicus*
DESCRIPTION: cytochrome P450.
- 45 CAB43505.1 AJ239051 *Cicer arietinum*
DESCRIPTION: cytochrome P450. cyp81E2.
- CAB41490.1 AJ238439 *Cicer arietinum*

DESCRIPTION: cytochrome P450 monooxygenase. cyp81E3v2.

CAA10067.1 AJ012581 Cicer arietinum
5 DESCRIPTION: cytochrome P450. cyp81E3.

CAA04117.1 AJ000478 Helianthus tuberosus
10 DESCRIPTION: fatty acid in-chain hydroxylase. cytochrome P450. CYP81B1l.
chimeric sequence (from 5'-race).

CAA04116.1 AJ000477 Helianthus tuberosus
15 DESCRIPTION: fatty acid in-chain hydroxylase. cytochrome P450. CYP81B1c.

AAK38079.1 AF321855 Lolium rigidum
20 DESCRIPTION: putative cytochrome P450.

AAK38080.1 AF321856 Lolium rigidum
DESCRIPTION: putative cytochrome P450.

25 AAK38081.1 AF321857 Lolium rigidum
DESCRIPTION: putative cytochrome P450.

AAC34853.1 AF082028 Hemerocallis hybrid cultivar
30 DESCRIPTION: putative cyt P450-containing fatty acid hydroxylase.
senescence-associated protein 3. SA3. mRNA accumulates in senescing
petals.

35 AAB94590.1 AF022461 Glycine max
DESCRIPTION: CYP82C1p. CYP82C1. cytochrome P450 monooxygenase.

CAB56742.1 AJ249800 Cicer arietinum
40 DESCRIPTION: cytochrome P450 monooxygenase. cyp81E5.

AAD56282.1 AF155332 Petunia x hybrida
45 DESCRIPTION: flavonoid 3'-hydroxylase. Ht1. cytochrome P450; CYP75B2.

AAG09208.1 AF175278 *Pisum sativum*
DESCRIPTION: wound-inducible P450 hydroxylase. CYP82A1.

5 CAA71515.1 Y10491 *Glycine max*
DESCRIPTION: putative cytochrome P450.

10 CAA71516.1 Y10492 *Glycine max*
DESCRIPTION: putative cytochrome P450.

15 AAC49188.2 U29333 *Pisum sativum*
DESCRIPTION: cytochrome P450 monooxygenase. CYP82. new cytochrome
P450
family.

20 CAA71876.1 Y10982 *Glycine max*
DESCRIPTION: putative cytochrome P450.

25 BAA12159.1 D83968 *Glycine max*
DESCRIPTION: Cytochrome P-450 (CYP93A1).

30 AAC39454.1 AF014802 *Eschscholzia californica*
DESCRIPTION: (S)-N-methylcoclaurine 3'-hydroxylase. CYP82B1. cytochrome
P-450-dependent monooxygenase; methyl jasmonate-inducible cytochrome
P-450-dependent, homologous to wound-inducible CYP82A1 of *Pisum sativum*
GenBank Accession Number U29333.

35 CAA65580.1 X96784 *Nicotiana tabacum*
DESCRIPTION: cytochrome P450. hsr515.

40 BAA13076.1 D86351 *Glycine max*
DESCRIPTION: cytochrome P-450 (CYP93A2).

AAA32913.1 M32885 *Persea americana*
DESCRIPTION: cytochrome P-450LXXIA1 (cyp71A1).

45 CAA71877.1 Y10983 *Glycine max*

DESCRIPTION: putative cytochrome P450.

5 AAG44132.1 AF218296 Pisum sativum
DESCRIPTION: cytochrome P450. P450 isolog.

10 CAA64635.1 X95342 Nicotiana tabacum
DESCRIPTION: cytochrome P450. hsr515. hypersensitivity-related gene.

15 AAB94587.1 AF022458 Glycine max
DESCRIPTION: CYP98A2p. CYP98A2. cytochrome P450 monooxygenase.

AAD38930.1 AF135485 Glycine max
DESCRIPTION: cytochrome P450 monooxygenase CYP93D1. CYP93E1.

20 BAA84072.1 AB028152 Torenia hybrida
DESCRIPTION: flavone synthase II. cytochrome P450. TFNS5.

25 BAA74466.1 AB022733 Glycyrrhiza echinata
DESCRIPTION: cytochrome P450. CYP Ge-51.

30 BAA22423.1 AB001380 Glycyrrhiza echinata
DESCRIPTION: cytochrome P450. CYP93B1.

BAA35080.1 AB015762 Nicotiana tabacum
DESCRIPTION: putative cytochrome P450. CYP82E1.

35 BAA92894.1 AB006790 Petunia x hybrida
DESCRIPTION: cytochrome P450. IMT-2.

40 AAC32274.1 AF081575 Petunia x hybrida
DESCRIPTION: flavonoid 3',5'-hydroxylase. Hf1. P450 enzyme.

45 CAB56743.1 AJ249801 Cicer arietinum
DESCRIPTION: cytochrome P450 monooxygenase. cyp81E4.

BAA84071.1 AB028151 Antirrhinum majus
DESCRIPTION: flavone synthase II. cytochrome P450. AFNS2.

5 250

AAD55566.1 AF110784 Volvox carteri f. nagariensis
DESCRIPTION: protein disulfide isomerase precursor. pdi.

10

AAD02069.1 AF036939 Chlamydomonas reinhardtii
DESCRIPTION: redox-regulator of 5'UTR psbA mRNA binding complex and translation. protein disulfide isomerase. localized to ER and chloroplast.

15

AAC49896.1 AF027727 Chlamydomonas reinhardtii
DESCRIPTION: involved in the redox-regulated binding of chloroplast poly(A)-binding protein to the 5'-UTR of psbA mRNA; regulates chloroplast translational activation. protein disulfide isomerase RB60. PDI.

20

AAD28260.1 AF131223 Datisca glomerata
DESCRIPTION: protein disulfide isomerase homolog. PDI.

25

AAB08519.1 L39014 Zea mays
DESCRIPTION: protein disulfide isomerase. pdi. putative.

30

AAA19660.1 U11496 Triticum aestivum
DESCRIPTION: protein disulfide isomerase. PDI.

35

CAC21230.1 AJ277379 Triticum turgidum subsp. durum
DESCRIPTION: catalyzes formation of disulfide bonds. protein disulfide isomerase. Pdi.

40

CAC21228.1 AJ277377 Triticum turgidum subsp. durum
DESCRIPTION: catalyzes the formation of disulfide bonds. protein disulfide isomerase. Pdi.

45

AAA70345.1 L33251 Hordeum vulgare
DESCRIPTION: catalyze the formation of disulfide bonds. disulfide isomerase. PDI. putative.

5 AAA70344.1 L33250 *Hordeum vulgare*
 DESCRIPTION: catalyze the formation of disulfide bonds. disulfide
 isomerase. PDI. putative.

10 AAB05641.1 U41385 *Ricinus communis*
 DESCRIPTION: protein disulphide isomerase PDI. molecular chaperone.

15 CAA77575.1 Z11499 *Medicago sativa*
 DESCRIPTION: protein disulfide isomerase.

20 CAC21231.1 AJ277380 *Triticum turgidum* subsp. durum
 DESCRIPTION: catalyzes formation of disulfide bonds. protein disulfide
 isomerase. Pdi.

25 CAC21229.1 AJ277378 *Triticum turgidum* subsp. durum
 DESCRIPTION: catalyzes formation of disulfide bonds. protein disulfide
 isomerase. Pdi.

30 BAB18780.1 AB047268 *Cucumis sativus*
 DESCRIPTION: disulfide isomerase.

35 BAA92322.1 AB039278 *Oryza sativa*
 DESCRIPTION: protein disulfide isomerase. Pdi.

40 AAA70346.1 L33252 *Hordeum vulgare*
 DESCRIPTION: catalyze the formation of disulfide bonds. disulfide
 isomerase. PDI. putative.

45 CAA72092.1 Y11209 *Nicotiana tabacum*
 DESCRIPTION: protein disulfide-isomerase precursor. PDI.

AAG13988.1 AF298829 *Prunus avium*
 DESCRIPTION: putative protein disulfide-isomerase. PDI.

251

CAA61275.1 X88797 Eucalyptus gunnii
 DESCRIPTION: cinnamyl alcohol dehydrogenase. CAD1.

5

AAC06319.1 AF053084 Malus x domestica
 DESCRIPTION: putative cinnamyl alcohol dehydrogenase. CAD.

253

10 -----

CAB61745.1 AJ275311 Cicer arietinum
 DESCRIPTION: farnesylated protein.

15

AAD09515.1 U64917 Glycine max
 DESCRIPTION: putative metal-binding protein. GMFP7. farnesylated protein.

254

20 -----

BAB19757.1 AB052785 Glycine max
 DESCRIPTION: nitrate transporter NRT1-2. NRT1-2.

25

BAB19756.1 AB052784 Glycine max
 DESCRIPTION: nitrate transporter NRT1-1. NRT1-1.

30

BAB19760.1 AB052788 Glycine max
 DESCRIPTION: nitrate transporter NRT1-5. NRT1-5.

AAC32034.1 AF023472 Hordeum vulgare
 DESCRIPTION: peptide transporter. ptr1. PTR1; integral membrane protein.

35

AAD01600.1 AF016713 Lycopersicon esculentum
 DESCRIPTION: LeOPT1. LeOPT1. oligopeptide transporter.

40

BAB40113.1 AP003311 Oryza sativa
 DESCRIPTION: putative peptide transport protein. P0024G09.4. contains
 ESTs D40448(S2437),C71800(E0368),AU102190(E2393),
 AU055921(S20154),AU102191(E2393),AU055922(S20154),
 C98524(E0368),AU097146(S2437).

45

BAB16458.1 AP002483 *Oryza sativa*
DESCRIPTION: putative peptide transport protein. P0019D06.16. contains
ESTs D40448(S2437),C71800(E0368),AU102190(E2393),
AU055921(S20154),AU102191(E2393),AU055922(S20154),
5 C98524(E0368),AU097146(S2437).

CAA93316.1 Z69370 *Cucumis sativus*
DESCRIPTION: nitrite transporter. NiTR1.
10

AAK15441.1 AC037426 *Oryza sativa*
DESCRIPTION: putative nitrate transporter. OSJNBb0014I11.9.

15 AAG21898.1 AC026815 *Oryza sativa*
DESCRIPTION: putative peptide transport protein. OSJNBa0079L16.13.

20 CAC00544.1 AJ277084 *Nicotiana plumbaginifolia*
DESCRIPTION: ion transport. putative low-affinity nitrate transporter.
nrt1.1.

25 AAG46153.1 AC018727 *Oryza sativa*
DESCRIPTION: putative peptide transporter. OSJNBa0056G17.8.

30 CAC00545.1 AJ277085 *Nicotiana plumbaginifolia*
DESCRIPTION: ion transport. putative low-affinity nitrate transporter.
nrt1.2.

35 AAG21906.1 AC026815 *Oryza sativa*
DESCRIPTION: putative peptide transport protein. OSJNBa0079L16.9.

40 AAF20002.1 AF213936 *Prunus dulcis*
DESCRIPTION: amino acid/peptide transporter. PTR2. similar to
transporters of nitrogenous compounds.

45 AAF07875.1 AF140606 *Oryza sativa*
DESCRIPTION: nitrate transporter. NRT1.

BAB16322.1 AP002318 *Oryza sativa*
DESCRIPTION: putative peptide transporter-like protein. P0436E04.4.

5 BAB19758.1 AB052786 *Glycine max*
DESCRIPTION: putative nitrate transporter NRT1-3. NRT1-3.

10 AAA80582.1 U17987 *Brassica napus*
DESCRIPTION: putative nitrate transporter. RCH2 protein.

15 CAC07206.1 AJ278966 *Brassica napus*
DESCRIPTION: Low-affinity nitrate transporter. nitrate transporter. nrt1.

AAG46154.1 AC018727 *Oryza sativa*
DESCRIPTION: putative peptide transporter. OSJNBa0056G17.27.

20 AAB69642.1 AF000392 *Lotus japonicus*
DESCRIPTION: peptide transporter. LjNOD65.

25 BAB19759.1 AB052787 *Glycine max*
DESCRIPTION: putative nitrate transporter NRT1-4. NRT1-4.

30 AAD16016.1 AF080545 *Nepenthes alata*
DESCRIPTION: peptide transporter. PTR1.

35 AAD42860.1 AF154930 *Prunus dulcis*
DESCRIPTION: transporter-like protein. TLP1.

AAG13513.1 AC068924 *Oryza sativa*
DESCRIPTION: putative peptide transporter. OSJNBa0026L12.7.

40 255

AAB01567.1 L47672 *Picea glauca*
DESCRIPTION: EMB34. embryo-abundant protein.

45 257

AAB71743.1 U75345 *Chlamydomonas reinhardtii*
 DESCRIPTION: envelope protein. LIP-36G1. low CO2 inducible carrier
 protein LIP-36 with a molecular weight of 36 kDa.

5

AAB71744.1 U75346 *Chlamydomonas reinhardtii*
 DESCRIPTION: envelope protein. LIP-36G2. low CO2 inducible carrier
 protein LIP-36 with a molecular weight of 36 kDa.

10

BAA92520.1 AP001383 *Oryza sativa*
 DESCRIPTION: ESTs AU068633(C30614),AU068634(C30614) correspond to
 a
 region of the predicted gene. Similar to *Bos taurus* mitochondrial solute
 carrier protein. (AF049236).

15

BAB16462.1 AP002483 *Oryza sativa*
 DESCRIPTION: putative peroxisomal Ca-dependent solute carrier protein.
 P0019D06.21.

20

BAB40117.1 AP003311 *Oryza sativa*
 DESCRIPTION: putative peroxisomal Ca-dependent solute carrier protein.
 P0024G09.9.

25

CAA07568.1 AJ007580 *Ribes nigrum*
 DESCRIPTION: Mitochondrial carrier protein. prib7.

30

CAC27140.1 AJ132535 *Picea abies*
 DESCRIPTION: ADP, ATP carrier protein precursor.

35

CAA56325.1 X80023 *Triticum turgidum*
 DESCRIPTION: ATP/ADP carrier protein.

40

CAC12820.1 AJ299250 *Nicotiana tabacum*
 DESCRIPTION: mitochondrial 2-oxoglutarate/malate carrier protein. momc1.

45

AAG48999.1 AY013246 *Hordeum vulgare*
 DESCRIPTION: putative mitochondrial carrier protein. 635P2.1.

CAA05276.1 AJ002236 *Lycopersicon pimpinellifolium*
 DESCRIPTION: resistance gene. Hcr9-9E. Hcr9-9E.

5

AAC78591.1 AF053993 *Lycopersicon esculentum*
 DESCRIPTION: disease resistance protein. Cf-5.

10

AAC78596.1 AF053998 *Lycopersicon esculentum*
 DESCRIPTION: Hcr2-5D. Hcr2-5D. similar to *Lycopersicon pimpinellifolium*
 disease resistance protein Cf-2.2 encoded by the sequence presented in
 GenBank Accession Number U42445.

15

CAA05279.1 AJ002237 *Lycopersicon esculentum*
 DESCRIPTION: Hcr9-0. Hcr9-0. homologue of *Cladosporium fulvum* disease
 resistance gene Cf-9.

20

AAC78593.1 AF053995 *Lycopersicon esculentum*
 DESCRIPTION: Hcr2-0B. Hcr2-0B. similar to *Lycopersicon pimpinellifolium*
 disease resistance protein Cf-2.2 encoded by the sequence presented in
 GenBank Accession Number U42445.

25

AAA65235.1 U15936 *Lycopersicon pimpinellifolium*
 DESCRIPTION: Cf-9 precursor. Cf-9. this is the ninth resistance gene to
 disease caused by *Cladosporium fulvum* to be isolated.

30

CAA05274.1 AJ002236 *Lycopersicon pimpinellifolium*
 DESCRIPTION: resistance gene. Cf-9. Cf-9.

35

AAC78592.1 AF053994 *Lycopersicon esculentum*
 DESCRIPTION: Hcr2-0A. Hcr2-0A. similar to *Lycopersicon pimpinellifolium*
 disease resistance protein Cf-2.2 encoded by the sequence presented in
 GenBank Accession Number U42445.

40

AAC78595.1 AF053997 *Lycopersicon esculentum*
 DESCRIPTION: Hcr2-5B. Hcr2-5B. similar to *Lycopersicon pimpinellifolium*
 disease resistance protein Cf-2.2 encoded by the sequence presented in
 GenBank Accession Number U42445.

45

- 5 AAC78594.1 AF053996 *Lycopersicon pimpinellifolium*
 DESCRIPTION: Hcr2-2A. Hcr2-2A. similar to *Lycopersicon pimpinellifolium*
 disease resistance protein Cf-2.2 encoded by the sequence presented in
 GenBank Accession Number U42445.
- 10 BAA96776.1 AP002521 *Oryza sativa*
 DESCRIPTION: Similar to *Lycopersicon esculentum* disease resistance
 protein (AF053993).
- 15 BAB08215.1 AP002539 *Oryza sativa*
 DESCRIPTION: Similar to *Lycopersicon esculentum* disease resistance
 protein (AF053993).
- 20 CAA05268.1 AJ002235 *Lycopersicon hirsutum*
 DESCRIPTION: Resistance gene. Cf-4. Cf-4.
- 25 AAG21897.1 AC026815 *Oryza sativa*
 DESCRIPTION: putative disease resistance protein (3' partial).
 OSJNBa0079L16.21.
- 30 AAD50430.1 AF166121 *Hordeum vulgare*
 DESCRIPTION: Cf2/Cf5 disease resistance protein homolog. Big1. leucine
 rich repeat protein.
- 35 AAG21917.1 AC026815 *Oryza sativa*
 DESCRIPTION: putative disease resistance protein. OSJNBa0079L16.5.
- 40 AAG21909.1 AC026815 *Oryza sativa*
 DESCRIPTION: putative disease resistance protein. OSJNBa0079L16.3.
- 45 CAB55409.1 AL117265 *Oryza sativa*
 DESCRIPTION: zhb0001.1. Incomplete at 5'end, Similar to disease resistance
 protein; Method: conceptual translation with partial peptide sequencing.
- AAC49123.1 U37133 *Oryza sativa*

DESCRIPTION: receptor kinase-like protein. Xa21. Xa21 disease resistance gene.

- 5 AAC80225.1 U72723 *Oryza longistaminata*
DESCRIPTION: receptor kinase-like protein. Xa21. disease resistance gene.

259

- 10 CAB52689.1 AJ132224 *Lycopersicon esculentum*
DESCRIPTION: hexose transporter. ht2.

- 15 CAA09419.1 AJ010942 *Lycopersicon esculentum*
DESCRIPTION: hexose transporter protein.

- 20 BAB19864.1 AB052885 *Oryza sativa*
DESCRIPTION: monosaccharide transporter 3. OsMST3.

- 25 AAA18534.1 L21753 *Saccharum hybrid cultivar H65-7052*
DESCRIPTION: glucose transporter. putative.

- CAA47324.1 X66856 *Nicotiana tabacum*
DESCRIPTION: monosaccharid transporter. MST1.

- 30 AAB06594.1 U38651 *Medicago truncatula*
DESCRIPTION: sugar transporter.

- 35 AAA79761.1 L08196 *Ricinus communis*
DESCRIPTION: hexose transport. sugar carrier protein. RCSTC.

- 40 CAA04511.1 AJ001061 *Vitis vinifera*
DESCRIPTION: hexose uptake. hexose transporter.

- CAA70777.1 Y09590 *Vitis vinifera*
DESCRIPTION: hexose transporter.

- 45 AAC61852.1 AF061106 *Petunia x hybrida*

DESCRIPTION: putative monosaccharide transporter 1. pmt1. similar to hexose transporter protein; PMT1.

5 AAA79857.1 L08188 Ricinus communis

DESCRIPTION: hexose transport. hexose carrier protein. HEX6.

10 CAB06079.1 Z83829 Picea abies

DESCRIPTION: monosaccharide transporter. PaMst-1. PaMst-1.

15 BAB19863.1 AB052884 Oryza sativa

DESCRIPTION: monosaccharide transporter 2. OsMST2.

20 BAA83554.1 AP000399 Oryza sativa

DESCRIPTION: Similar to hexose carrier protein HEX6 & RCCHCP_1 (Q07423).

25 AAK31286.1 AC079890 Oryza sativa

DESCRIPTION: putative hexose carrier protein. OSJNBb0089A17.11.

CAA53192.1 X75440 Chlorella kessleri

DESCRIPTION: hexose transporter like protein. HUP3.

30 CAA68813.1 Y07520 Chlorella kessleri

DESCRIPTION: H(+)/hexose cotransporter (AA 1-533).

35 CAA39036.1 X55349 Chlorella kessleri

DESCRIPTION: H(+)/hexose-cotransporter. HUP1.

40 BAB19862.1 AB052883 Oryza sativa

DESCRIPTION: monosaccharide transporter 1. OsMST1.

AAA18533.1 L21752 Saccharum hybrid cultivar H65-7052

DESCRIPTION: glucose transporter. putative.

45 CAB52688.1 AJ132223 Lycopersicon esculentum

DESCRIPTION: hexose transporter. ht1.

5 AAD55054.1 AF173655 Beta vulgaris
DESCRIPTION: glucose transporter. Gt.

10 CAB52690.1 AJ132225 Lycopersicon esculentum
DESCRIPTION: hexose transporter. ht3.

AAA33875.1 L31352 Ricinus communis
DESCRIPTION: hexose transport. hexose carrier. Hex9. putative.

15 AAK13147.1 AC083945 Oryza sativa
DESCRIPTION: Putative sugar transporter. OSJNBa0058E19.22.

20 AAB68029.1 U64903 Beta vulgaris
DESCRIPTION: BvcDNA-397. putative sugar transporter; member of major
facilitative superfamily; integral membrane protein.

25 AAB68028.1 U64902 Beta vulgaris
DESCRIPTION: BvcDNA-205. putative sugar transporter; member of major
facilitative superfamily; integral membrane protein.

30 AAG43998.1 AF215837 Apium graveolens var. dulce
DESCRIPTION: mannitol transporter. Mat1.

35 AAF74568.1 AF215854 Zea mays
DESCRIPTION: transport of hexoses across the plastid inner envelope
membrane. hexose transporter. pGlcT.

40 AAF74567.1 AF215853 Solanum tuberosum
DESCRIPTION: transport of hexoses across the plastid inner envelope
membrane. hexose transporter. pGlcT.

45 AAF74566.1 AF215852 Nicotiana tabacum
DESCRIPTION: transport of hexoses across the plastid inner envelope
membrane. hexose transporter. pGlcT.

5 AAF74565.1 AF215851 *Spinacia oleracea*
 DESCRIPTION: transport of hexoses across the plastid inner envelope
 membrane. hexose transporter. pGlcT.

10 AAG46179.1 AC018727 *Oryza sativa*
 DESCRIPTION: putative sugar transporter protein. OSJNBa0056G17.3.

15 AAG00995.1 AF286906 *Mesembryanthemum crystallinum*
 DESCRIPTION: putative glucose translocator. metabolite transporter;
 targeted to plastid inner envelope membrane.

20 AAB53155.1 U43629 *Beta vulgaris*
 DESCRIPTION: putative sugar transporter. integral membrane protein.
 member of major facilitator superfamily.

25 AAB88879.1 AF000952 *Prunus armeniaca*
 DESCRIPTION: putative sugar transporter.

30 AAA33874.1 L31353 *Ricinus communis*
 DESCRIPTION: hexose transport. hexose carrier. Hex10. putative.

35 AAD37424.1 AF149282 *Phaseolus vulgaris*
 DESCRIPTION: hexose carrier protein 1. HCP1.

260 AAD45934.1 AF168773 *Betula pendula*
 DESCRIPTION: hexose transport protein. HEX2.

 40 AAA33915.1 L27821 *Oryza sativa*
 DESCRIPTION: receptor type serine/threonine kinase. protein kinase.

45 AAF34428.1 AF172282 *Oryza sativa*
 DESCRIPTION: receptor-like protein kinase. DUPR11.18.

BAA92954.1 AP001551 Oryza sativa
DESCRIPTION: Similar to Oryza sativa protein kinase (OSPK10) mRNA.
(L27821).

5

BAB07906.1 AP002835 Oryza sativa
DESCRIPTION: putative S-receptor kinase. P0417G05.14.

10 BAA94516.1 AP001800 Oryza sativa
DESCRIPTION: Similar to Zea mays S-domain receptor-like protein kinase
(AJ010166).

15 BAA94528.1 AP001800 Oryza sativa
DESCRIPTION: Similar to Arabidopsis thaliana chromosome 2 BAC T20K24;
putative receptor-like protein kinase (AC002392).

20 BAA94517.1 AP001800 Oryza sativa
DESCRIPTION: Similar to Zea mays S-domain receptor-like protein kinase
(AJ010166).

25 BAB07905.1 AP002835 Oryza sativa
DESCRIPTION: putative S-receptor kinase. P0417G05.13.

30 BAA94529.2 AP001800 Oryza sativa
DESCRIPTION: Similar to Zea mays S-domain receptor-like protein kinase
(AJ010166).

35 BAB07904.1 AP002835 Oryza sativa
DESCRIPTION: putative S-receptor kinase. P0417G05.12.

40 BAA94518.1 AP001800 Oryza sativa
DESCRIPTION: Similar to Arabidopsis thaliana chromosome 2 section 111 of
255; putative receptor-like protein kinase (AC002392).

45 CAA47962.1 X67733 Zea mays
DESCRIPTION: receptor-like protein kinase. PK1.

BAA83573.1 AP000399 *Oryza sativa*
DESCRIPTION: Similar to serine/threonine-specific protein kinase PK10 precursor (AL021811).

5

CAA73134.1 Y12531 *Brassica oleracea*
DESCRIPTION: serine/threonine kinase. BRLK.

10 CAA74662.1 Y14286 *Brassica oleracea*
DESCRIPTION: SFR3. extracellular S domain: 123-1346; transmembrane domain: 1347-1412; intracellular kinase domain: from 1413.

15 BAB17345.1 AP002747 *Oryza sativa*
DESCRIPTION: putative receptor kinase. P0698G03.29.

20 BAB17348.1 AP002747 *Oryza sativa*
DESCRIPTION: putative receptor kinase. P0698G03.32.

25 BAB17342.1 AP002747 *Oryza sativa*
DESCRIPTION: putative receptor kinase. P0698G03.26.

BAB39451.1 AP003338 *Oryza sativa*
DESCRIPTION: putative receptor kinase. OJ1212_B09.24.

30

BAB17126.1 AP002867 *Oryza sativa*
DESCRIPTION: putative receptor kinase. P0463F06.16.

35 BAB19337.1 AP003044 *Oryza sativa*
DESCRIPTION: putative protein kinase. P0038C05.10. contains ESTs AU056335(S20481),AU056336(S20481).

40 CAB51480.1 Y14600 *Sorghum bicolor*
DESCRIPTION: putative protein serine /threonine kinase. RLK1. accumulates in mesophyll cells.

45 BAB17339.1 AP002747 *Oryza sativa*
DESCRIPTION: putative receptor kinase. P0698G03.23.

AAB61708.1 U93048 *Daucus carota*
 DESCRIPTION: somatic embryogenesis receptor-like kinase. SERK.
 5

AAF78016.1 AF238472 *Oryza sativa*
 DESCRIPTION: receptor-like kinase. RLG15. protein kinase.
 10

AAD46420.1 AF100771 *Hordeum vulgare*
 DESCRIPTION: receptor-like kinase. Hv3ARK. similar to wheat ARK1AS.
 15

AAC49629.1 U51330 *Triticum aestivum*
 DESCRIPTION: rust resistance kinase Lr10. LRK10.
 20

BAB17139.1 AP002867 *Oryza sativa*
 DESCRIPTION: putative receptor kinase. P0463F06.31.
 25

BAB17331.1 AP002747 *Oryza sativa*
 DESCRIPTION: putative receptor kinase. P0698G03.12.
 30

AAC01746.1 AF044489 *Oryza sativa*
 DESCRIPTION: receptor-like protein kinase. drpk1.
 35

AAC27489.1 AF077130 *Oryza sativa*
 DESCRIPTION: receptor-like protein kinase.
 40

AAC02535.1 AF044260 *Oryza sativa*
 DESCRIPTION: receptor serine/threonine kinase. protein kinase.
 45

BAB39434.1 AP003338 *Oryza sativa*
 DESCRIPTION: receptor-like kinase. OJ1212_B09.1.
 45

AAF78020.1 AF238476 *Oryza sativa*
 DESCRIPTION: receptor-like kinase. RLG11. protein kinase.
 45

BAA92953.1 AP001551 *Oryza sativa*
DESCRIPTION: Similar to *Arabidopsis thaliana* chromosome 4 BAC clone
F10M6
; S-receptor kinase -like protein. (AL021811).

5

AAF78018.1 AF238474 *Oryza sativa*
DESCRIPTION: receptor-like kinase. RLG16. protein kinase.

10

AAD46917.1 AF164021 *Oryza sativa*
DESCRIPTION: receptor kinase.

15 BAB39438.1 AP003338 *Oryza sativa*
DESCRIPTION: putative receptor kinase. OJ1212_B09.7.

20 BAB39435.1 AP003338 *Oryza sativa*
DESCRIPTION: putative receptor kinase. OJ1212_B09.2.

25 BAB17129.1 AP002867 *Oryza sativa*
DESCRIPTION: putative receptor kinase. P0463F06.20.

BAB17321.1 AP002747 *Oryza sativa*
DESCRIPTION: putative receptor kinase. P0698G03.1.

30

AAF68398.1 AF237568 *Oryza sativa*
DESCRIPTION: receptor-like protein kinase. RLG2.

35 BAB39437.1 AP003338 *Oryza sativa*
DESCRIPTION: receptor-like kinase. OJ1212_B09.6.

40 AAF78019.1 AF238475 *Oryza sativa*
DESCRIPTION: receptor-like kinase. RLG17. protein kinase.

261

45 AAD09343.1 AF026538 *Hordeum vulgare*
DESCRIPTION: ABA-responsive protein.

263

BAA22813.1 D26015 Nicotiana tabacum

5 DESCRIPTION: aspartic protease activity. CND41, chloroplast nucleoid DNA binding protein. cnd41.

BAB21205.1 AP002913 Oryza sativa

10 DESCRIPTION: nucleoid DNA-binding protein cnd41-like protein.
P0480E02.11. contains ESTs AU166073(E31027),AU029516(E31027).

270

BAB12719.1 AP002746 Oryza sativa

15 DESCRIPTION: putative regulatory protein NPR1. P0671B11.35.

BAB16860.1 AP002537 Oryza sativa

20 DESCRIPTION: Arabidopsis thaliana regulatory protein NPR1 like protein.
P0001B06.13.

271

AAG35658.1 AF204925 Petroselinum crispum

25 DESCRIPTION: transcription factor WRKY4. WRKY4. binds to W box
(TTGACC)
elements.

30 BAA87058.1 AB028022 Nicotiana tabacum

DESCRIPTION: WIZZ. wizz. wound-induced transcription factor.

35 BAA86031.1 AB026890 Nicotiana tabacum

DESCRIPTION: transcription factor NtWRKY4.

AAD16139.1 AF096299 Nicotiana tabacum

40 DESCRIPTION: DNA-binding protein 2. WRKY2. transcription factor.

BAA77383.1 AB020590 Nicotiana tabacum

DESCRIPTION: transcription factor NtWRKY2.

45

AAF23898.1 AF193802 Oryza sativa

DESCRIPTION: zinc finger transcription factor WRKY1.

AAD55974.1 AF121353 Petroselinum crispum

5 DESCRIPTION: zinc-finger type transcription factor WRKY1. WRKY1.

CAB97004.1 AJ278507 Solanum tuberosum

10 DESCRIPTION: putative transcription factor. WRKY DNA binding protein.
WRKY1.

BAA82107.1 AB022693 Nicotiana tabacum

15 DESCRIPTION: transcription factor. NtWRKY1.

AAD32677.1 AF140554 Avena sativa

20 DESCRIPTION: DNA-binding protein WRKY1. wrky1. putative transcription
factor.

BAB16432.1 AB041520 Nicotiana tabacum

25 DESCRIPTION: WRKY transcription factor Nt-SubD48. Nt-SubD48.

AAD16138.1 AF096298 Nicotiana tabacum

30 DESCRIPTION: DNA-binding protein 1. WRKY1. transcription factor.

AAD32676.1 AF140553 Avena sativa

35 DESCRIPTION: DNA-binding protein WRKY3. wrky3. putative transcription
factor.

AAD27591.1 AF121354 Petroselinum crispum

40 DESCRIPTION: binds sequence specifically to W Boxes (TTGACC).
transcription factor. WRKY3. sequence specific DNA-binding protein.

AAF61864.1 AF193771 Nicotiana tabacum

45 DESCRIPTION: DNA-binding protein 4. WRKY4. transcription factor.

AAG35659.1 AF204926 Petroselinum crispum

DESCRIPTION: transcription factor WRKY5. WRKY5. binds to W box
(TTGACC)

elements.

5 AAF61863.1 AF193770 *Nicotiana tabacum*
DESCRIPTION: DNA-binding protein 3. WRKY3. transcription factor.

272

10 BAA07395.1 D38220 *Brassica napus*
DESCRIPTION: nitrate reductase.

15 BAA07394.1 D38219 *Brassica napus*
DESCRIPTION: nitrate reductase.

20 AAG30576.1 AF314093 *Ricinus communis*
DESCRIPTION: nitrate reductase. NIA.

CAA32217.1 X14059 *Nicotiana tabacum*
DESCRIPTION: nitrate reductase.

25 AAA33713.1 L13691 *Petunia x hybrida*
DESCRIPTION: nitrate reductase. putative.

30 CAA32218.1 X14060 *Lycopersicon esculentum*
DESCRIPTION: nitrate reductase.

35 AAA33712.1 L11563 *Petunia x hybrida*
DESCRIPTION: nitrate reductase apoenzyme. nia.

CAA32216.1 X14058 *Nicotiana tabacum*
DESCRIPTION: nitrate reductase.

40 CAA56696.1 X80670 *Lotus japonicus*
DESCRIPTION: nitrate reductase (NADH). NIA.

45 AAB52786.1 U95317 *Solanum tuberosum*
DESCRIPTION: NADH nitrate reductase. StNR3.

- 5 AAB18985.1 U76701 Solanum tuberosum
DESCRIPTION: NADH nitrate reductase. StNR2.
- 10 AAA95940.1 U01029 Phaseolus vulgaris
DESCRIPTION: nitrate reductase. PVNR2.
- 15 AAA34033.1 M32600 Spinacia oleracea
DESCRIPTION: NADH nitrate reductase.
- 20 CAA38031.1 X54097 Betula pendula
DESCRIPTION: nitrate reductase (NADH). nia1.
- 25 BAA13047.1 D86226 Spinacia oleracea
DESCRIPTION: nitrate reductase.
- 30 AAA33114.1 M33154 Cucurbita maxima
DESCRIPTION: nitrate reductase.
- 35 AAD19790.1 AF055369 Glycine max
DESCRIPTION: nitrate reductase. nr2.
- 40 CAA58909.1 X84103 Cichorium intybus
DESCRIPTION: nitrate reductase (NADH). nia.
- 45 AAA96813.1 U13987 Glycine max
DESCRIPTION: inducible nitrate reductase 2. INR2.
- CAA37672.1 X53603 Phaseolus vulgaris
DESCRIPTION: nitrate reductase.
- AAA96727.1 L23854 Glycine max
DESCRIPTION: nitrate reductase. INR1.

reductase.

- 5 AAB39553.1 U64308 *Agrostemma githago*
DESCRIPTION: nitrate reductase. agnr1. NADH; similar to agnr2 product
encoded by GenBank Accession Number U64309 and to agnr3 product encoded
by
GenBank Accession Number U64310.
- 10 AAA03202.1 M27821 *Zea mays*
DESCRIPTION: NADH:nitrate reductase; (EC 1.6.6.1).
- 15 AAA33483.1 M77792 *Zea mays*
DESCRIPTION: enzyme. nitrate reductase. NAR1S.
- 20 AAB39555.1 U64310 *Agrostemma githago*
DESCRIPTION: nitrate reductase. agnr3. NADH; similar to agnr1 product
encoded by GenBank Accession Number U64308 and agnr2 product encoded by
GenBank Accession Number U64309.
- 25 AAB39554.1 U64309 *Agrostemma githago*
DESCRIPTION: nitrate reductase. agnr2. NADH; similar to agnr1 product
encoded by GenBank Accession Number U64308 and agnr3 product encoded by
GenBank Accession Number U64310.
- 30 CAA33819.1 X15820 *Oryza sativa*
DESCRIPTION: nitrate reductase apoenzyme (AA 472-916); Protein sequence
is in conflict with the conceptual translation.
- 35 CAA33817.1 X15819 *Oryza sativa*
DESCRIPTION: nitrate reductase apoenzyme.
- 40 AAA33998.1 L23853 *Glycine max*
DESCRIPTION: nitrate reductase. mutant.
- 45 CAA58908.1 X84102 *Cichorium intybus*
DESCRIPTION: nitrate reductase (NADH). nia.

- CAA40090.1 X56771 *Chlorella vulgaris*
DESCRIPTION: nitrate reductase (NADH).
- 5 CAA45776.1 X64446 *Zea mays*
DESCRIPTION: nitrate reductase (NAD(P)H). nar.
- 10 AAD17694.1 AF077372 *Zea mays*
DESCRIPTION: possible reduction of Fe³⁺-chelates. cytochrome b5
reductase. NFR.
- 15 AAA96242.1 L40147 *Avena strigosa*
DESCRIPTION: nitrate reductase.
- 20 AAB20155.1 S61885 *Nicotiana plumbaginifolia*
DESCRIPTION: nitrate reductase heme domain. nitrate reductase heme
domain, NR. This sequence comes from fig3; NR.
- 25 AAA96245.1 L40151 *Hordeum pusillum*
DESCRIPTION: nitrate reductase.
- 30 AAA96247.1 L40153 *Hordeum stenostachys*
DESCRIPTION: nitrate reductase.
- 273
-
- 35 BAA07395.1 D38220 *Brassica napus*
DESCRIPTION: nitrate reductase.
- BAA07394.1 D38219 *Brassica napus*
DESCRIPTION: nitrate reductase.
- 40 AAA33713.1 L13691 *Petunia x hybrida*
DESCRIPTION: nitrate reductase. putative.
- 45 CAA32218.1 X14060 *Lycopersicon esculentum*
DESCRIPTION: nitrate reductase.

- 5 AAA33712.1 L11563 *Petunia x hybrida*
DESCRIPTION: nitrate reductase apoenzyme. nia.
- 10 AAG30576.1 AF314093 *Ricinus communis*
DESCRIPTION: nitrate reductase. NIA.
- 15 CAA32217.1 X14059 *Nicotiana tabacum*
DESCRIPTION: nitrate reductase.
- 20 CAA32216.1 X14058 *Nicotiana tabacum*
DESCRIPTION: nitrate reductase.
- 25 AAA33114.1 M33154 *Cucurbita maxima*
DESCRIPTION: nitrate reductase.
- AAB52786.1 U95317 *Solanum tuberosum*
DESCRIPTION: NADH nitrate reductase. StNR3.
- 30 AAB18985.1 U76701 *Solanum tuberosum*
DESCRIPTION: NADH nitrate reductase. StNR2.
- 35 AAA34033.1 M32600 *Spinacia oleracea*
DESCRIPTION: NADH nitrate reductase.
- 40 BAA13047.1 D86226 *Spinacia oleracea*
DESCRIPTION: nitrate reductase.
- 45 CAA38031.1 X54097 *Betula pendula*
DESCRIPTION: nitrate reductase (NADH). nia1.
- CAA56696.1 X80670 *Lotus japonicus*
DESCRIPTION: nitrate reductase (NADH). NIA.

- AAA95940.1 U01029 Phaseolus vulgaris
DESCRIPTION: nitrate reductase. PVNR2.
- 5 CAA58909.1 X84103 Cichorium intybus
DESCRIPTION: nitrate reductase (NADH). nia.
- 10 AAD19790.1 AF055369 Glycine max
DESCRIPTION: nitrate reductase. nr2.
- 15 AAA96813.1 U13987 Glycine max
DESCRIPTION: inducible nitrate reductase 2. INR2.
- 20 CAA40976.1 X57845 Hordeum vulgare
DESCRIPTION: nitrate reductase.
- 25 AAA96727.1 L23854 Glycine max
DESCRIPTION: nitrate reductase. INR1.
- 30 CAA37672.1 X53603 Phaseolus vulgaris
DESCRIPTION: nitrate reductase.
- 35 CAA33819.1 X15820 Oryza sativa
DESCRIPTION: nitrate reductase apoenzyme (AA 472-916); Protein sequence
is in conflict with the conceptual translation.
- 40 AAD38068.1 AF153448 Zea mays
DESCRIPTION: nitrate reductase. NR1.
- 45 CAA40975.1 X57844 Hordeum vulgare
DESCRIPTION: nitrate reductase. cDNA is 9bp short of atg.
- AAB93560.1 AF022780 Glycine max
DESCRIPTION: nitrate reductase. BCNR-A.
- AAA62316.1 U20450 Zea mays

DESCRIPTION: nitrate reductase.

CAA42739.1 X60173 Hordeum vulgare
5 DESCRIPTION: nitrate reductase (NAD(P)H). nar7.

AAF17595.1 AF203033 Chlamydomonas reinhardtii
10 DESCRIPTION: nitrate reductase. NIT1.

CAA45497.1 X64136 Volvox carteri
DESCRIPTION: nitrate reductase (NADH). nitA.

15 AAC49460.1 U39931 Chlorella vulgaris
DESCRIPTION: nitrate reductase.

20 AAC49459.1 U39930 Chlorella vulgaris
DESCRIPTION: nitrate reductase.

CAA29497.1 X06134 Nicotiana tabacum
25 DESCRIPTION: nitrate reductase.

AAA18377.1 U08029 Spinacia oleracea
30 DESCRIPTION: reduces nitrate to nitrite with NADH. NADH:nitrate
reductase.

AAB39553.1 U64308 Agrostemma githago
35 DESCRIPTION: nitrate reductase. agnr1. NADH; similar to agnr2 product
encoded by GenBank Accession Number U64309 and to agnr3 product encoded
by
GenBank Accession Number U64310.

40 AAA03202.1 M27821 Zea mays
DESCRIPTION: NADH:nitrate reductase; (EC 1.6.6.1).

AAA33483.1 M77792 Zea mays
45 DESCRIPTION: enzyme. nitrate reductase. NAR1S.

- 5 AAB39555.1 U64310 *Agrostemma githago*
DESCRIPTION: nitrate reductase. agnr3. NADH; similar to agnr1 product
encoded by GenBank Accession Number U64308 and agnr2 product encoded by
GenBank Accession Number U64309.
- 10 AAB39554.1 U64309 *Agrostemma githago*
DESCRIPTION: nitrate reductase. agnr2. NADH; similar to agnr1 product
encoded by GenBank Accession Number U64308 and agnr3 product encoded by
GenBank Accession Number U64310.
- 15 CAA33817.1 X15819 *Oryza sativa*
DESCRIPTION: nitrate reductase apoenzyme.
- 20 CAA58908.1 X84102 *Cichorium intybus*
DESCRIPTION: nitrate reductase (NADH). nia.
- 25 AAA33998.1 L23853 *Glycine max*
DESCRIPTION: nitrate reductase. mutant.
- 30 CAA40090.1 X56771 *Chlorella vulgaris*
DESCRIPTION: nitrate reductase (NADH).
- 35 CAA45776.1 X64446 *Zea mays*
DESCRIPTION: nitrate reductase (NAD(P)H). nar.
- 40 AAD17694.1 AF077372 *Zea mays*
DESCRIPTION: possible reduction of Fe³⁺-chelates. cytochrome b5
reductase. NFR.
- 45 AAA96242.1 L40147 *Avena strigosa*
DESCRIPTION: nitrate reductase.
- AAA96250.1 L40149 *Hordeum chilense*
DESCRIPTION: nitrate reductase.

AAA96245.1 L40151 *Hordeum pusillum*
DESCRIPTION: nitrate reductase.

5 AAA96247.1 L40153 *Hordeum stenostachys*
DESCRIPTION: nitrate reductase.

274

10 AAC39318.1 AF029858 *Sorghum bicolor*
DESCRIPTION: second multifunctional cytochrome P450 in the biosynthetic
pathway of the cyanogenic glucoside dhurrin. Catalyzes the conversion of
p-hydroxyphenylacetaldoxime to p-hydroxymandelonitrile. cytochrome P450
CYP71E1. CYP71E1. No EST#s identified.

15

BAB40323.1 AB037244 *Asparagus officinalis*
DESCRIPTION: cytochrome P450. ASPI-1.

20

AAA32913.1 M32885 *Persea americana*
DESCRIPTION: cytochrome P-450LXXIA1 (cyp71A1).

25 BAB40324.1 AB037245 *Asparagus officinalis*
DESCRIPTION: cytochrome P450. ASPI-2.

30 AAA19701.1 L24438 *Thlaspi arvense*
DESCRIPTION: cytochrome P450.

35 CAA71513.1 Y10489 *Glycine max*
DESCRIPTION: putative cytochrome P450.

AAB94589.1 AF022460 *Glycine max*
DESCRIPTION: CYP83D1p. CYP83D1. cytochrome P450 monooxygenase.

40

AAB94588.1 AF022459 *Glycine max*
DESCRIPTION: CYP71D10p. CYP71D10. cytochrome P450 monooxygenase.

45 AAB61965.1 U48435 *Solanum chacoense*
DESCRIPTION: putative cytochrome P450.

- CAA70575.1 Y09423 *Nepeta racemosa*
DESCRIPTION: cytochrome P450. CYP71A5.
- 5
- CAA71517.1 Y10493 *Glycine max*
DESCRIPTION: putative cytochrome P450.
- 10
- AAD47832.1 AF166332 *Nicotiana tabacum*
DESCRIPTION: cytochrome P450.
- 15
- AAK38084.1 AF321860 *Lolium rigidum*
DESCRIPTION: putative cytochrome P450.
- 20
- AAB94584.1 AF022157 *Glycine max*
DESCRIPTION: capable of catalyzing the metabolism of phenylurea herbicides. CYP71A10. CYP71A10. cytochrome P450 monooxygenase.
- 25
- AAF27282.1 AF122821 *Capsicum annuum*
DESCRIPTION: cytochrome P450. PepCYP.
- 30
- AAK38083.1 AF321859 *Lolium rigidum*
DESCRIPTION: putative cytochrome P450.
- 35
- CAA50312.1 X70981 *Solanum melongena*
DESCRIPTION: P450 hydroxylase. CYPEG2.
- 40
- CAB56503.1 AJ238612 *Catharanthus roseus*
DESCRIPTION: cytochrome P450.
- 45
- AAK38087.1 AF321863 *Lolium rigidum*
DESCRIPTION: putative cytochrome P450.

DESCRIPTION: flavonoid 3'-hydroxylase. Ht1. cytochrome P450; CYP75B2.

AAG14963.1 AF214009 Brassica napus

5 DESCRIPTION: cytochrome p450-dependent monooxygenase. BNF5H3.

AAD37433.1 AF150881 Lycopersicon esculentum x Lycopersicon peruvianum

10 DESCRIPTION: catalyzes the hydroxylation of ferulic acid to
5-hydroxyferulic acid. ferulate-5-hydroxylase. CYP84. cytochrome
P450-dependent monooxygenase; F5H; FAH1.

BAB39252.1 AP002968 Oryza sativa

15 DESCRIPTION: putative cytochrome P450. P0416G11.1.

AAK38088.1 AF321864 Lolium rigidum

20 DESCRIPTION: putative cytochrome P450.

CAA65580.1 X96784 Nicotiana tabacum

25 DESCRIPTION: cytochrome P450. hsr515.

AAG14961.1 AF214007 Brassica napus

DESCRIPTION: cytochrome p450-dependent monooxygenase. BNF5H1.

30 AAG14962.1 AF214008 Brassica napus

DESCRIPTION: cytochrome p450-dependent monooxygenase. BNF5H2.

AAB17562.1 U72654 Eustoma grandiflorum

35 DESCRIPTION: flavonoid 3'5'-hydroxylase. F3'5'H. cytochrome P450; CYP75.

279

AAA34122.1 M84466 Nicotiana tabacum

40 DESCRIPTION: phenylalanine ammonia lyase. tpal.

BAA22948.1 AB008200 Nicotiana tabacum

45 DESCRIPTION: phenylalanine ammonia-lyase. palB.

- AAA34176.1 M90692 *Lycopersicon esculentum*
DESCRIPTION: phenylalanine ammonia-lyase. PAL5.
- 5 AAF40224.1 AF237955 *Rubus idaeus*
DESCRIPTION: phenylalanine ammonia-lyase 2. PAL2. PAL;
phenylpropanoid;
multigene; flavonoid.
- 10 CAA37129.1 X52953 *Glycine max*
DESCRIPTION: phenylalanine ammonia-lyase. PAL1.
- 15 CAA68036.1 X99705 *Triticum aestivum*
DESCRIPTION: phenylalanine ammonia-lyase. PAL.
- 20 AAA33389.1 M29232 *Ipomoea batatas*
DESCRIPTION: phenylalanine ammonia-lyase.
- 25 AAA34179.2 M83314 *Lycopersicon esculentum*
DESCRIPTION: deamination of phenylalanine to coumarate. phenylalanine
ammonia lyase. pal.
- 30 BAA21643.1 D30656 *Populus kitakamiensis*
DESCRIPTION: phenylalanine ammonia-lyase.
- 35 AAB67733.1 U43338 *Citrus limon*
DESCRIPTION: phenylalanine ammonia-lyase. pal6.
- 40 BAA95629.1 AB042520 *Catharanthus roseus*
DESCRIPTION: phenylalanine ammonia lyase.
- 45 BAA05643.1 D26596 *Camellia sinensis*
DESCRIPTION: phenylalanine ammonia-lyase.
- CAA73065.1 Y12461 *Helianthus annuus*
DESCRIPTION: phenylalanine ammonia lyase. PAL.

- BAA24929.1 D83076 *Lithospermum erythrorhizon*
DESCRIPTION: phenylalanine ammonia-lyase.
- 5 BAA24928.1 D83075 *Lithospermum erythrorhizon*
DESCRIPTION: phenylalanine ammonia-lyase.
- 10 BAA00885.1 D10001 *Pisum sativum*
DESCRIPTION: phenylalanine ammonia-lyase.
- 15 AAA84889.1 U39792 *Pinus taeda*
DESCRIPTION: phenylalanine ammonia-lyase. lpPAL.
- 20 CAA61198.1 X87946 *Oryza sativa*
DESCRIPTION: phenylalanine ammonia-lyase. ZB8.
- CAA41169.1 X58180 *Medicago sativa*
DESCRIPTION: phenylalanine ammonia-lyase. PAL.
- 25 BAA00887.1 D10003 *Pisum sativum*
DESCRIPTION: phenylalanine ammonia-lyase. PAL2.
- 30 BAA00886.1 D10002 *Pisum sativum*
DESCRIPTION: phenylalanine ammonia-lyase. PAL1.
- 35 AAA17993.1 M91192 *Trifolium subterraneum*
DESCRIPTION: phenylalanine ammonia-lyase. PAL1.
- 40 AAA33805.1 L11747 *Populus x generosa*
DESCRIPTION: phenylalanine ammonia lyase. PAL.
- AAC78457.1 AF036948 *Prunus avium*
DESCRIPTION: phenylalanine ammonia-lyase. PAL1.
- 45 BAA23367.1 D85850 *Daucus carota*

DESCRIPTION: phenylalanine ammonia-lyase. gDcPAL1.

5 CAB42793.1 AJ238753 Citrus clementina x Citrus reticulata
DESCRIPTION: phenylalanine-ammonia lyase. pal1.

10 AAA99500.1 L36822 Stylosanthes humilis
DESCRIPTION: phenylalanine ammonia lyase. PAL17.1.

CAA55075.1 X78269 Nicotiana tabacum
DESCRIPTION: phenylalanine ammonia-lyase.

15 BAA22963.1 D17467 Nicotiana tabacum
DESCRIPTION: phenylalanine ammonia-lyase. TOBPAL1.

20 BAA22947.1 AB008199 Nicotiana tabacum
DESCRIPTION: phenylalanine ammonia-lyase. palA.

25 CAA57057.1 X81159 Petroselinum crispum
DESCRIPTION: phenylalanine ammonia-lyase 3. PAL3. tetramere subunit.

30 AAG49585.1 AF325496 Ipomoea nil
DESCRIPTION: phenylalanine ammonia-lyase.

CAA57056.1 X81158 Petroselinum crispum
DESCRIPTION: phenylalanine ammonia-lyase 2. PAL2. deaminase subunit.

35 CAB42794.1 AJ238754 Citrus clementina x Citrus reticulata
DESCRIPTION: phenylalanine-ammonia lyase. pal2.

40 CAA05251.1 AJ002221 Digitalis lanata
DESCRIPTION: phenylalanine ammonia lyase.

45 BAA07860.1 D43802 Populus kitakamiensis
DESCRIPTION: phenylalanine ammonia-lyase.

- CAB60719.1 AJ250836 *Cicer arietinum*
DESCRIPTION: phenylpropanoid pathway. phenylalanine ammonia-lyase. pal.
- 5 CAA68256.1 X99997 *Bromheadia finlaysoniana*
DESCRIPTION: phenylalanine ammonia-lyase. pal.
- 10 AAK15640.1 AF326116 *Agastache rugosa*
DESCRIPTION: phenylalanine ammonia-lyase. PAL.
- 15 CAA34226.1 X16099 *Oryza sativa* subsp. japonica
DESCRIPTION: phenylalanine ammonia-lyase.
- 20 AAF40223.1 AF237954 *Rubus idaeus*
DESCRIPTION: phenylalanine ammonia-lyase 1. PAL1. PAL;
phenylpropanoid;
multigene; flavonoid.
- 25 BAA11459.1 D78640 *Ipomoea batatas*
DESCRIPTION: Phenylalanine Ammonia-Lyase.
- 30 BAA06337.1 D30657 *Populus kitakamiensis*
DESCRIPTION: phenylalanine ammonia-lyase.
- AAD45384.1 AF165998 *Vigna unguiculata*
DESCRIPTION: phenylalanine ammonia-lyase.
- 35 CAA53733.1 X76130 *Cucumis melo*
DESCRIPTION: phenylalanine ammonia-lyase. pal.
- 40 AAA51873.1 U16130 *Persea americana*
DESCRIPTION: phenylalanine ammonia lyase. PAL.
- 45 BAB19128.1 AB041361 *Dianthus caryophyllus*
DESCRIPTION: phenylalanine ammonia-lyase. Dcpal1.

- CAA34715.1 X16772 *Petroselinum crispum*
 DESCRIPTION: phenylalanine ammonia-lyase (AA 137 - 716) (1 is 3rd base in codon).
- 5
- BAA07861.1 D43803 *Populus kitakamiensis*
 DESCRIPTION: phenylalanine ammonia-lyase.
- 10 280
-
- AAG43550.1 AF211532 *Nicotiana tabacum*
 DESCRIPTION: Avr9/Cf-9 rapidly elicited protein 132. ACRE132. similar to RING finger proteins.
- 15
- AAK00436.1 AC060755 *Oryza sativa*
 DESCRIPTION: putative zinc finger protein. OSJNBa0003O19.23.
- 20
- BAA78746.1 AB023482 *Oryza sativa*
 DESCRIPTION: Similar to Arabidopsis thaliana RING-H2 finger protein RHX1a mRNA, partial cds.(AF079184).
- 25
- CAA74911.1 Y14573 *Hordeum vulgare*
 DESCRIPTION: ring finger protein. putative.
- 30
- AAG46117.1 AC073166 *Oryza sativa*
 DESCRIPTION: putative ring finger protein. OSJNBb0064P21.7.
- 35
- BAA96875.1 AB045121 *Oryza sativa*
 DESCRIPTION: RING finger 1. RRF1.
- 40
- BAA90357.1 AP001080 *Oryza sativa*
 DESCRIPTION: EST AU070319(S10788) corresponds to a region of the predicted gene. Similar to RING-H2 finger protein RHA2b (AC006200).
- 45
- BAA90806.1 AP001168 *Oryza sativa*
 DESCRIPTION: ESTs C26000(C11448),AU082130(C11448) correspond to a region

of the predicted gene.; Similar to mRNA for zinc-finger protein (Z36749).

286

5 AAG14454.1 AF283706 *Tulipa gesneriana*
DESCRIPTION: auxin-induced protein TGSAUR12. SAUR12. small auxin
upregulated RNA.

10 AAG14456.1 AF283708 *Tulipa gesneriana*
DESCRIPTION: auxin-induced protein TGSAUR22. SAUR22. small auxin
upregulated RNA.

15 AAG14455.1 AF283707 *Tulipa gesneriana*
DESCRIPTION: auxin-induced protein TGSAUR21. SAUR21. small auxin
upregulated RNA.

20 AAC08401.1 AF053564 *Mesembryanthemum crystallinum*
DESCRIPTION: auxin-induced protein. similar to auxin-induced proteins
from soybean.

290

25 AAB65498.1 U73856 *Chlamydomonas reinhardtii*
DESCRIPTION: carbonic anhydrase, alpha type. CAH3.

30 AAC49983.1 U40871 *Chlamydomonas reinhardtii*
DESCRIPTION: intracellular carbonic anhydrase, alpha type. CAH3.

35 AAF04292.2 AF190735 *Dunaliella salina*
DESCRIPTION: carbonic anhydrase. CA.

40 AAC49378.1 U53811 *Dunaliella salina*
DESCRIPTION: carbonic anhydrase. dca.

45 AAF22644.1 AF183939 *Dunaliella salina*
DESCRIPTION: duplicated carbonic anhydrase. DCA1. DCA; carbonic
anhydrase
gene family member; salt-inducible; intra-duplicated.

AAD51633.1 AF170173 *Acetabularia acetabulum*
 DESCRIPTION: putative carbonic anhydrase 2. CA2. AaCA2.

5

AAD51634.1 AF170174 *Acetabularia acetabulum*
 DESCRIPTION: putative carbonic anhydrase 1. CA1. AaCA1.

10

AAD51635.1 AF170175 *Acetabularia acetabulum*
 DESCRIPTION: putative carbonic anhydrase 1. CA1. AaCA1.

15

BAA14232.1 D90206 *Chlamydomonas reinhardtii*
 DESCRIPTION: carbonic anhydrase.

20

BAA28217.1 AB013804 *Chlorella sorokiniana*
 DESCRIPTION: soluble carbonic anhydrase precursor. CAH1.

301

AAG03089.2 AC073405 *Oryza sativa*
 DESCRIPTION: similar to an Arabidopsis putative P-type transporting
 ATPase (AC010926).

25

BAA89544.1 AP001072 *Oryza sativa*
 DESCRIPTION: Similar to chromaffin granule ATPase II homolog. (U75321).

30

BAA88191.1 AP000836 *Oryza sativa*
 DESCRIPTION: Similar to chromaffin granule ATPase II homolog (U75321).

35

BAA90510.2 AP001111 *Oryza sativa*
 DESCRIPTION: rice EST AU030811, similar to rice Ca²⁺-ATPase (U82966).

40

AAD11618.1 AF050496 *Lycopersicon esculentum*
 DESCRIPTION: Ca²⁺-ATPase. LCA1B; alternative transcript.

45

AAA34138.1 M96324 *Lycopersicon esculentum*
 DESCRIPTION: The calcium ATPase is a calcium ion pump. Ca²⁺-ATPase.
 LCA1.

5 AAD11617.1 AF050495 *Lycopersicon esculentum*
DESCRIPTION: Ca²⁺-ATPase. LCA1A; alternative transcript.

AAAF73985.1 AF096871 *Zea mays*
DESCRIPTION: calcium pump. calcium ATPase. cap1.

10 AAD31896.1 AF145478 *Mesembryanthemum crystallinum*
DESCRIPTION: calcium ATPase.

15 AAG28436.1 AF195029 *Glycine max*
DESCRIPTION: plasma membrane Ca²⁺-ATPase. SCA2.

20 CAA63790.1 X93592 *Dunaliella bioculata*
DESCRIPTION: P-type ATPase. cal. calcium pumping; CA1.

AAG28435.1 AF195028 *Glycine max*
DESCRIPTION: plasma membrane Ca²⁺-ATPase. SCA1.
25

CAA68234.1 X99972 *Brassica oleracea*
DESCRIPTION: calmodulin-stimulated calcium-ATPase.

30 AAB58910.1 U82966 *Oryza sativa*
DESCRIPTION: Ca²⁺-ATPase.

35 CAB69824.1 AJ271439 *Prunus persica*
DESCRIPTION: plasma membrane H⁺ ATPase. PPA1.

40 AAB60276.1 U09989 *Zea mays*
DESCRIPTION: H(+)-transporting ATPase. Mha1.

BAA01058.1 D10207 *Oryza sativa*
DESCRIPTION: H-ATPase. OSA1.
45

CAC29435.1 AJ310523 *Vicia faba*
DESCRIPTION: P-type H⁺-ATPase. vha4. predominantly expressed in flowers.

5 AAD20330.1 AF110268 *Oryza sativa*
DESCRIPTION: plasma membrane proton-ATPase gene OSA3.

10 AAA34098.1 M80490 *Nicotiana plumbaginifolia*
DESCRIPTION: plasma membrane H⁺ ATPase. pma3.

15 AAB84203.1 AF029257 *Kosteletzkya virginica*
DESCRIPTION: plasma membrane H⁺-ATPase.

CAC28224.1 AJ286749 *Sesbania rostrata*
DESCRIPTION: p-type H⁺-ATPase. ha5.

20 AAD46188.1 AF156691 *Nicotiana plumbaginifolia*
DESCRIPTION: plasma membrane proton ATPase. pma9.

25 AAA34173.1 M60166 *Lycopersicon esculentum*
DESCRIPTION: H⁺-ATPase. LHA1.

30 AAA34094.1 M80489 *Nicotiana plumbaginifolia*
DESCRIPTION: plasma membrane H⁺ ATPase. pma1.

35 AAA34052.1 M27888 *Nicotiana plumbaginifolia*
DESCRIPTION: H⁺-translocating ATPase.

CAC28221.1 AJ286746 *Sesbania rostrata*
DESCRIPTION: p-type H⁺-ATPase. ha2.

40 CAA54045.1 X76535 *Solanum tuberosum*
DESCRIPTION: H(+)-transporting ATPase. PHA2.

45 BAA06629.1 D31843 *Oryza sativa*
DESCRIPTION: plasma membrane H⁺-ATPase. OSA2.

CAA64406.1 X94936 Phaseolus vulgaris
 DESCRIPTION: H(+)-transporting ATPase. BHA-2.

5

AAF98344.1 AF275745 Lycopersicon esculentum
 DESCRIPTION: plasma membrane H+-ATPase. LHA2. P-type ion pump.

10

AAD55399.1 AF179442 Lycopersicon esculentum
 DESCRIPTION: plasma membrane H+-ATPase isoform LHA2. LHA2.

15 CAA54046.1 X76536 Solanum tuberosum
 DESCRIPTION: H(+)-transporting ATPase. PHA1.

302

20 CAA70575.1 Y09423 Nepeta racemosa
 DESCRIPTION: cytochrome P450. CYP71A5.

25 CAA70576.1 Y09424 Nepeta racemosa
 DESCRIPTION: cytochrome P450. CYP71A6.

30 CAA50312.1 X70981 Solanum melongena
 DESCRIPTION: P450 hydroxylase. CYPEG2.

AAA32913.1 M32885 Persea americana
 DESCRIPTION: cytochrome P-450LXXIA1 (cyp71A1).

35 BAA03635.1 D14990 Solanum melongena
 DESCRIPTION: Cytochrome P-450EG4.

40 CAA50645.1 X71654 Solanum melongena
 DESCRIPTION: P450 hydroxylase.

45 CAA83941.1 Z33875 Mentha x piperita
 DESCRIPTION: cytochrome P-450 oxidase.

CAA71513.1 Y10489 Glycine max
DESCRIPTION: putative cytochrome P450.

5

AAB94584.1 AF022157 Glycine max
DESCRIPTION: capable of catalyzing the metabolism of phenylurea
herbicides. CYP71A10. CYP71A10. cytochrome P450 monooxygenase.

10

AAB61965.1 U48435 Solanum chacoense
DESCRIPTION: putative cytochrome P450.

15

AAB69644.1 AF000403 Lotus japonicus
DESCRIPTION: putative cytochrome P450. LjNP450.

20

BAB40324.1 AB037245 Asparagus officinalis
DESCRIPTION: cytochrome P450. ASPI-2.

25

AAD47832.1 AF166332 Nicotiana tabacum
DESCRIPTION: cytochrome P450.

30

AAB61964.1 U48434 Solanum chacoense
DESCRIPTION: putative cytochrome P450.

BAB40323.1 AB037244 Asparagus officinalis
DESCRIPTION: cytochrome P450. ASPI-1.

35

CAA71514.1 Y10490 Glycine max
DESCRIPTION: putative cytochrome P450.

40

AAB94588.1 AF022459 Glycine max
DESCRIPTION: CYP71D10p. CYP71D10. cytochrome P450 monooxygenase.

45

AAF27282.1 AF122821 Capsicum annuum
DESCRIPTION: cytochrome P450. PepCYP.

CAA50313.1 X70982 Solanum melongena
DESCRIPTION: P450 hydroxylase. CYPEG3.

5 AAA19701.1 L24438 Thlaspi arvense
DESCRIPTION: cytochrome P450.

10 BAA12159.1 D83968 Glycine max
DESCRIPTION: Cytochrome P-450 (CYP93A1).

15 AAK38082.1 AF321858 Lolium rigidum
DESCRIPTION: putative cytochrome P450.

20 BAB40322.1 AB036772 Triticum aestivum
DESCRIPTION: cytochrome P450. N-1.

CAA71516.1 Y10492 Glycine max
DESCRIPTION: putative cytochrome P450.

25 CAA65580.1 X96784 Nicotiana tabacum
DESCRIPTION: cytochrome P450. hsr515.

30 AAK38083.1 AF321859 Lolium rigidum
DESCRIPTION: putative cytochrome P450.

35 AAK38084.1 AF321860 Lolium rigidum
DESCRIPTION: putative cytochrome P450.

40 CAA71517.1 Y10493 Glycine max
DESCRIPTION: putative cytochrome P450.

CAA72196.1 Y11368 Zea mays
DESCRIPTION: cytochrome p450. cyp71c4.

45 CAA57425.1 X81831 Zea mays

DESCRIPTION: cytochrome P-50. CYP71C4. family CYP71, subfamily CYP71C.

5 AAC39318.1 AF029858 Sorghum bicolor
DESCRIPTION: second multifunctional cytochrome P450 in the biosynthetic pathway of the cyanogenic glucoside dhurrin. Catalyzes the conversion of p-hydroxyphenylacetaldoxime to p-hydroxymandelonitrile. cytochrome P450 CYP71E1. CYP71E1. No EST#s identified.

10

AAD56282.1 AF155332 Petunia x hybrida
DESCRIPTION: flavonoid 3'-hydroxylase. Ht1. cytochrome P450; CYP75B2.

15

CAB56503.1 AJ238612 Catharanthus roseus
DESCRIPTION: cytochrome P450.

20 AAK38087.1 AF321863 Lolium rigidum
DESCRIPTION: putative cytochrome P450.

25 CAA57421.1 X81827 Zea mays
DESCRIPTION: cytochrome P450. CYP71C1. family CYP71, subfamily CYP71C.

30 CAA57422.1 X81828 Zea mays
DESCRIPTION: cytochrome P450. CYP71C1. family CYP71, subfamily CYP71C.

35 BAB39252.1 AP002968 Oryza sativa
DESCRIPTION: putative cytochrome P450. P0416G11.1.

40 BAA13076.1 D86351 Glycine max
DESCRIPTION: cytochrome P-450 (CYP93A2).

AAB94589.1 AF022460 Glycine max
DESCRIPTION: CYP83D1p. CYP83D1. cytochrome P450 monooxygenase.

45 AAD38930.1 AF135485 Glycine max

DESCRIPTION: cytochrome P450 monooxygenase CYP93D1. CYP93E1.

CAA57423.1 X81829 Zea mays

5 DESCRIPTION: cytochrome P450. CYP71C2. family CYP71, subfamily CYP71C.

CAA72208.1 Y11404 Zea mays

10 DESCRIPTION: cytochrome p450. cyp71c2.

AAG44132.1 AF218296 Pisum sativum

15 DESCRIPTION: cytochrome P450. P450 isolog.

AAK38088.1 AF321864 Lolium rigidum

20 DESCRIPTION: putative cytochrome P450.

CAA64635.1 X95342 Nicotiana tabacum

25 DESCRIPTION: cytochrome P450. hsr515. hypersensitivity-related gene.

303

25 -----

AAC49826.1 U71604 Catharanthus roseus

30 DESCRIPTION: involved in the second to last step in vindoline biosynthesis. desacetoxyvindoline 4-hydroxylase. CRSD4H. 2-oxoglutarate dependent dioxygenase.

AAB97311.1 AF008597 Catharanthus roseus

35 DESCRIPTION: desacetoxyvindoline-4-hydroxylase. CRSD4H. 2-oxoglutarate dependent dioxygenase; involved in the second to last step in vindoline biosynthesis.

AAC49827.1 U71605 Catharanthus roseus

40 DESCRIPTION: involved in the second to last step in vindoline biosynthesis. desacetoxyvindoline 4-hydroxylase. CRSD4H. 2-oxoglutarate dependent dioxygenase.

BAA95828.1 AP002069 Oryza sativa

45 DESCRIPTION: ESTs D47168(S12332),D46350(S10967) correspond to a region of

the predicted gene. Similar to *Prunus armeniaca*
ethylene-forming-enzyme-like dioxygenase. (U97530).

5 BAA37127.1 AB012203 *Lactuca sativa*
DESCRIPTION: 2-oxoglutarate-dependent dioxygenase. gibberelin 20-oxidase.
Ls20ox1.

10 CAA54557.1 X77368 *Solanum melongena*
DESCRIPTION: dioxygenase. DIOX.

BAA81862.1 AB026295 *Oryza sativa*
15 DESCRIPTION: Similar to leucoanthocyanidin dioxygenase.(AI440611).

304

20 AAF61647.1 AF190634 *Nicotiana tabacum*
DESCRIPTION: UDP-glucose:salicylic acid glucosyltransferase. SA-GTase.

BAA89009.1 AB027455 *Petunia x hybrida*
25 DESCRIPTION: anthocyanin 5-O-glucosyltransferase. PH1.

AAF17077.1 AF199453 *Sorghum bicolor*
DESCRIPTION: UDP-glucose glucosyltransferase.
UDP-glucose:p-hydroxymandelonitrile-o- glucosyltransferase.
30

AAF98390.1 AF287143 *Brassica napus*
DESCRIPTION: catalyzes the transfer of glucose from UDP-glucose to
35 sinapate and some other hydroxycinnamates (4-coumarate, caffeate,
ferulate). UDP-glucose:sinapate glucosyltransferase. SGT1. SGT.

BAA36423.1 AB013598 *Verbena x hybrida*
40 DESCRIPTION: UDP-glucose:anthocyanin 5-O-glucosyltransferase. HGT8.

AAK16181.1 AC079887 *Oryza sativa*
DESCRIPTION: putative glucosyltransferase. OSJNBa0040E01.16.

45 BAA36421.1 AB013596 *Perilla frutescens*

DESCRIPTION: UDP-glucose:anthocyanin 5-O-glucosyltransferase. PF3R4.

- 5 BAB07962.1 AP002524 *Oryza sativa*
DESCRIPTION: putative anthocyanin 5-O-glucosyltransferase. P0406H10.16.
contains ESTs AU067881(C10481),AU067882(C10481).
- 10 AAK16178.1 AC079887 *Oryza sativa*
DESCRIPTION: putative glucosyltransferase. OSJNBa0040E01.5.
- 15 BAA93039.1 AB033758 *Citrus unshiu*
DESCRIPTION: limonoid UDP-glucosyltransferase. LGTase.
- 20 AAK16172.1 AC079887 *Oryza sativa*
DESCRIPTION: putative glucosyltransferase. OSJNBa0040E01.14.
- BAA36422.1 AB013597 *Perilla frutescens*
DESCRIPTION: UDP-glucose:anthocyanin 5-O-glucosyltransferase homologue.
PF3R6.
- 25 BAB17182.1 AP002843 *Oryza sativa*
DESCRIPTION: putative UTP-glucose glucosyltransferase. P0407B12.19.
- 30 BAA12737.1 D85186 *Gentiana triflora*
DESCRIPTION: UDP-glucose:flavonoid-3-glucosyltransferase.
- 35 AAG25643.1 AF303396 *Phaseolus vulgaris*
DESCRIPTION: UDP-glucosyltransferase HRA25. putative; defense associated.
- 40 AAB48444.1 U82367 *Solanum tuberosum*
DESCRIPTION: UDP-glucose glucosyltransferase.
- 45 BAA19659.1 AB002818 *Perilla frutescens*
DESCRIPTION: flavonoid 3-O-glucosyltransferase. UDP glucose.
- CAA54612.1 X77462 *Manihot esculenta*

DESCRIPTION: UTP-glucose glucosyltransferase. CGT5.

BAA89008.1 AB027454 *Petunia x hybrida*

5 DESCRIPTION: anthocyanidin 3-O-glucosyltransferase. PGT8.

AAK16175.1 AC079887 *Oryza sativa*

10 DESCRIPTION: putative glucosyltransferase. OSJNBa0040E01.15.

BAA83484.1 AB031274 *Scutellaria baicalensis*

DESCRIPTION: UDP-glucose: flavonoid 7-O-glucosyltransferase. ufgt.

15 AAB36652.1 U32643 *Nicotiana tabacum*

DESCRIPTION: immediate-early salicylate-induced glucosyltransferase.
IS10a.

20 AAK28304.1 AF346432 *Nicotiana tabacum*

DESCRIPTION: phenylpropanoid:glucosyltransferase 2. togt2.
glucosyltransferase.

25 AAB36653.1 U32644 *Nicotiana tabacum*

DESCRIPTION: immediate-early salicylate-induced glucosyltransferase.
IS5a.

30 AAD04166.1 AF101972 *Phaseolus lunatus*

DESCRIPTION: catalyzes formation of O-glucosylzeatin from zeatin and
UDPG; catalyzes formation of O-xylosylzeatin from zeatin and UDPX. zeatin
O-glucosyltransferase. ZOG1. cytokinin O-glucosyltransferase.

35 AAD21086.1 AF127218 *Forsythia x intermedia*

DESCRIPTION: adds glucose residue to position 3 of flavonoid compounds.
flavonoid 3-O-glucosyltransferase. UFGT.

40 CAA54611.1 X77461 *Manihot esculenta*

DESCRIPTION: UTP-glucose glucosyltransferase. CGT2.

45 AAK28303.1 AF346431 *Nicotiana tabacum*

DESCRIPTION: phenylpropanoid:glucosyltransferase 1. togt1.
glucosyltransferase.

5 CAA54609.1 X77459 Manihot esculenta
DESCRIPTION: UTP-glucose glucosyltransferase. CGT1.

10 CAA54613.1 X77463 Manihot esculenta
DESCRIPTION: UTP-glucose glucosyltransferase. CGT6.

15 BAB41026.1 AB047099 Vitis vinifera
DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. FIUFGT2.

20 BAB41024.1 AB047097 Vitis vinifera
DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. AIUFGT2.

25 BAB41022.1 AB047095 Vitis vinifera
DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. RuUFGT2.

30 BAB41017.1 AB047090 Vitis labrusca x Vitis vinifera
DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. KyUFGT1.
The
gene was derived from one of the parents V. labruscana cv. Ishiharawase.

35 BAB41020.1 AB047093 Vitis vinifera
DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. ItUFGT2.

40 CAA59450.1 X85138 Lycopersicon esculentum
DESCRIPTION: twi1. homologous to glucosyltransferases.

45 BAB41025.1 AB047098 Vitis vinifera
DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. FIUFGT1.

45 BAB41023.1 AB047096 Vitis vinifera
DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. AIUFGT1.

BAB41018.1 AB047091 Vitis labrusca x Vitis vinifera
 DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. KyUFGT2.
 The
 gene originated in one of the parents V. vinifera cv. Centennial.
 5
 306

 AAB06458.1 U64806 Brassica napus
 DESCRIPTION: pathogenesis-related protein PR1. Ypr1.
 10
 AAB01666.1 U21849 Brassica napus
 DESCRIPTION: PR-1a. LSC94.
 15
 AAB09587.1 U70666 Brassica napus
 DESCRIPTION: pathogenesis-related protein PR1. Ypr1.
 20
 CAA47374.1 X66942 Nicotiana tabacum
 DESCRIPTION: prb-1b. PRB-1B.
 25
 AAK30143.1 AF348141 Capsicum annuum
 DESCRIPTION: pathogenesis-related protein PR-1 precursor.
 30
 CAA36790.1 X52555 Nicotiana tabacum
 DESCRIPTION: PR-1 protein (AA 1-184).
 35
 CAA35666.1 X17681 Nicotiana tabacum
 DESCRIPTION: pathogenesis-related protein 1b (AA 1-168).
 40
 CAA31010.1 X12487 Nicotiana tabacum
 DESCRIPTION: PR1c preprotein.
 45
 CAA29023.1 X05454 Nicotiana tabacum
 DESCRIPTION: PR-1c protein.
 CAA32228.1 X14065 Nicotiana tabacum
 DESCRIPTION: PRP 1 precursor (AA -23 to 154).

- CAA27183.1 X03465 *Nicotiana tabacum*
DESCRIPTION: PR-1b precursor; (aa -30-138).
- 5 CAA35665.1 X17680 *Nicotiana tabacum*
DESCRIPTION: pathogenesis-related protein 1b (AA 1-168).
- 10 BAA14221.1 D90197 *Nicotiana tabacum*
DESCRIPTION: PR1b protein precursor.
- 15 CAA48672.1 X68738 *Lycopersicon esculentum*
DESCRIPTION: P1(p14) protein. pTE28.1.
- 20 CAA81229.1 Z26320 *Hordeum vulgare*
DESCRIPTION: pathogenesis-related protein. pathogenesis-related protein.
- AAA03616.1 M69248 *Lycopersicon esculentum*
DESCRIPTION: pathogenesis-related protein P6. P6.
- 25 CAA70042.1 Y08804 *Lycopersicon esculentum*
DESCRIPTION: PR protein. PR1b1.
- 30 AAB05225.1 U49241 *Nicotiana glutinosa*
DESCRIPTION: pathogenesis-related protein-1.
- 35 CAA31009.1 X12486 *Nicotiana tabacum*
DESCRIPTION: PR1b preprotein.
- AAC25629.1 U82200 *Zea mays*
DESCRIPTION: pathogenesis related protein-1. PR-1.
- 40 AAF78528.1 AF195237 *Pyrus pyrifolia*
DESCRIPTION: pathogenesis-related protein. PR-1b.
- 45 AAD33696.1 AF136636 *Glycine max*
DESCRIPTION: PR1a precursor. PR1a.

- CAA79703.1 Z21494 *Hordeum vulgare*
DESCRIPTION: Pathogenesis-related protein 1.
5
- CAA52894.1 X74940 *Hordeum vulgare*
DESCRIPTION: PR-1b pathogenesis related protein (Hv-8).
10
- CAA81234.1 Z26333 *Hordeum vulgare*
DESCRIPTION: pathogenesis-related protein. pathogenesis-related protein.
15
- CAA81230.1 Z26321 *Hordeum vulgare*
DESCRIPTION: pathogenesis-related protein. pathogenesis-related protein.
20
- CAA04881.1 AJ001627 *Lycopersicon esculentum*
DESCRIPTION: pathogenesis-related protein. PR1d.
25
- CAA07473.1 AJ007348 *Triticum aestivum*
DESCRIPTION: pathogenesis-related protein 1.1. PR-1.1.
30
- CAA07474.1 AJ007349 *Triticum aestivum*
DESCRIPTION: pathogenesis-related protein 1.2. PR-1.2.
35
- CAA50596.1 X71592 *Lycopersicon esculentum*
DESCRIPTION: PR-1a1.
40
- CAA70070.1 Y08844 *Lycopersicon esculentum*
DESCRIPTION: PR protein. PR1a2.
45
- CAA38223.1 X54325 *Zea mays*
DESCRIPTION: pathogenesis-related protein. PRms.
- AAF78527.1 AF195236 *Pyrus pyrifolia*
DESCRIPTION: pathogenesis-related proteins. PR-1a.

CAC03571.1 AJ278436 *Oryza sativa*
DESCRIPTION: defence response. PR1a protein. Pr1a.

5 AAG44566.1 AF251277 *Oryza sativa* subsp. *japonica*
DESCRIPTION: acidic PR-1 type pathogenesis-related protein PR-1a. PR-1a.
induced by pathogen attack.

10 AAC06244.1 AF053343 *Capsicum annuum*
DESCRIPTION: PR-1 protein precursor. pathogen-induced PR1 protein.

CAA56174.1 X79778 *Medicago truncatula*
15 DESCRIPTION: PR-1.

307

20 AAF06347.1 AF195654 *Vitis vinifera*
DESCRIPTION: SCUTL2. thaumatin-like protein.

BAA28872.1 AB006009 *Pyrus pyrifolia*
25 DESCRIPTION: thaumatin-like protein precursor. PsTL1.

AAB38064.1 U32440 *Prunus avium*
DESCRIPTION: thaumatin-like protein precursor.

30 BAA95017.1 AB031870 *Cestrum elegans*
DESCRIPTION: thaumatin-like protein. CETLP.

35 BAA74546.2 AB000834 *Nicotiana tabacum*
DESCRIPTION: thaumatin-like protein SE39b.

40 AAC36740.1 AF090143 *Malus x domestica*
DESCRIPTION: thaumatin-like protein precursor Mdt11. MDTL1.
pathogenesis-related.

45 CAC10270.1 AJ243427 *Malus x domestica*
DESCRIPTION: thaumatin-like protein. tl. allergen, pathogenesis-related.

- 5 AAB95118.1 U71244 *Brassica rapa*
DESCRIPTION: pathogenesis-related group 5 protein. BFTP. thaumatin-like protein; PR-5.
- 10 CAC09477.1 AL442113 *Oryza sativa*
DESCRIPTION: thaumatin-like protein. H0806H05.10.
- 15 CAB62167.1 AJ242828 *Castanea sativa*
DESCRIPTION: antifungal. thaumatin-like protein. tl1.
- 20 CAA06927.1 AJ006233 *Nicotiana tabacum*
DESCRIPTION: putative thaumatin-like protein precursor.
- 25 AAF06346.1 AF195653 *Vitis vinifera*
DESCRIPTION: SCUTL1. thaumatin-like protein.
- 30 AAB02259.1 U57787 *Avena sativa*
DESCRIPTION: permatin precursor. thaumatin-like protein.
- 35 AAD55090.1 AF178653 *Vitis riparia*
DESCRIPTION: thaumatin. osmotin; pathogenesis-related protein.
- 40 CAA10492.1 AJ131731 *Pseudotsuga menziesii*
DESCRIPTION: Thaumatin-like protein. 5A1A.16.
- 45 CAA09228.1 AJ010501 *Cicer arietinum*
DESCRIPTION: thaumatin-like protein PR-5b.
- 40 BAA95165.1 AB029918 *Nicotiana tabacum*
DESCRIPTION: pistil transmitting tissue specific thaumatin (SE39b)-like protein. SE39b.
- 45 AAF82264.1 AF227324 *Vitis vinifera*
DESCRIPTION: thaumatin-like protein.

CAB85636.1 AJ237998 *Vitis vinifera*
DESCRIPTION: putative thaumatin-like protein. Tl2.

5

AAB53368.1 U77657 *Oryza sativa*
DESCRIPTION: pathogenesis-related thaumatin-like protein.

10 AAB61590.1 AF003007 *Vitis vinifera*
DESCRIPTION: VVTL1. osmotin-like protein, PR-5 protein; thaumatin-like protein.

15 AAB53367.1 U77656 *Oryza sativa*
DESCRIPTION: pathogenesis-related thaumatin-like protein.

20 CAB85637.1 AJ237999 *Vitis vinifera*
DESCRIPTION: putative thaumatin-like protein. Tl1. alternative name grip 51.

308

25 BAA14143.1 D90115 *Armoracia rusticana*
DESCRIPTION: peroxidase isozyme.

30 BAA14144.1 D90116 *Armoracia rusticana*
DESCRIPTION: peroxidase isozyme.

35 BAA11853.1 D83225 *Populus nigra*
DESCRIPTION: peroxidase.

CAA66035.1 X97349 *Populus balsamifera* subsp. *trichocarpa*
DESCRIPTION: signal for ER. peroxidase.

40

CAA66036.1 X97350 *Populus balsamifera* subsp. *trichocarpa*
DESCRIPTION: signal for ER. peroxidase.

45 BAA11852.1 D83224 *Populus nigra*
DESCRIPTION: peroxidase.

AAB41811.1 L36157 *Medicago sativa*
 DESCRIPTION: peroxidase. pxdC. amino acid feature: conserved domains, aa
 123 .. 129, 191 .. 198; amino acid feature: heme-binding domain, aa 68 ..
 5 73.

CAA62225.1 X90692 *Medicago sativa*
 DESCRIPTION: peroxidase1A. prx1A.
 10

AAB41810.1 L36156 *Medicago sativa*
 DESCRIPTION: peroxidase. pxdA. amino acid feature: conserved motifs, aa
 181 .. 188; amino acid feature: heme-binding domain, aa 60 .. 65.
 15

AAD37430.1 AF149280 *Phaseolus vulgaris*
 DESCRIPTION: peroxidase 5 precursor. FBP5. secretory peroxidase.
 20

CAB94692.1 AJ242742 *Ipomoea batatas*
 DESCRIPTION: Removal of H₂O₂, oxidation of toxic reductants, defence
 response toward wounding. peroxidase. pod.
 25

AAA34108.1 J02979 *Nicotiana tabacum*
 DESCRIPTION: lignin-forming peroxidase precursor (EC 1.11.1.7).
 30

CAA40796.1 X57564 *Armoracia rusticana*
 DESCRIPTION: peroxidase. peroxidase precursor.
 35

BAA01877.1 D11102 *Populus kitakamiensis*
 DESCRIPTION: peroxidase. prxA1.
 40

BAA01992.1 D11396 *Nicotiana tabacum*
 DESCRIPTION: 'peroxidase'.
 45

CAB67121.1 Y19023 *Lycopersicon esculentum*
 DESCRIPTION: peroxidase. cevi-1.
 45

CAA50597.1 X71593 *Lycopersicon esculentum*

DESCRIPTION: peroxidase. CEVI-1.

5 AAD43561.1 AF155124 *Gossypium hirsutum*
DESCRIPTION: bacterial-induced peroxidase precursor. Perx_Goshiko.

10 BAA92500.1 AP001383 *Oryza sativa*
DESCRIPTION: ESTs D39300(R3292),AU030751(E60187) correspond to a
region
of the predicted gene. Similar to peroxidase ATP6a. (X98774).

15 AAF63027.1 AF244924 *Spinacia oleracea*
DESCRIPTION: hydrogen peroxide catabolism. peroxidase prx15 precursor.
type III peroxidase.

20 AAB02554.1 L37790 *Stylosanthes humilis*
DESCRIPTION: cationic peroxidase.

25 AAB06183.1 M37636 *Arachis hypogaea*
DESCRIPTION: cationic peroxidase. PNC1.

30 CAA59487.1 X85230 *Triticum aestivum*
DESCRIPTION: peroxidase. pox4.

BAA94962.1 AB042103 *Asparagus officinalis*
DESCRIPTION: peroxidase. AspPOX1.

35 AAF63026.1 AF244923 *Spinacia oleracea*
DESCRIPTION: hydrogen peroxide catabolism. peroxidase prx14 precursor.
type III peroxidase.

40 CAB99487.1 AJ276227 *Hordeum vulgare*
DESCRIPTION: defence against plant pathogens. peroxidase. prx8.

45 CAA71492.1 Y10466 *Spinacia oleracea*
DESCRIPTION: peroxidase. prxr5.

CAB65334.1 AJ250121 *Picea abies*
DESCRIPTION: peroxidase. SPI2 protein. spi2.

5

AAA33121.1 M32742 *Cucumis sativus*
DESCRIPTION: peroxidase (CuPer2).

10 CAA39486.1 X56011 *Triticum aestivum*
DESCRIPTION: peroxidase.

15 BAA92422.1 AP001366 *Oryza sativa*
DESCRIPTION: ESTs AU081576(R0541),AU032412(R4029) correspond to a
region
of the predicted gene. Similar to *A.thaliana* mRNA for peroxidase ATP18a.
(X98804).

20

BAA92497.1 AP001383 *Oryza sativa*
DESCRIPTION: ESTs AU081576(R0541),AU032412(R4029) correspond to a
region
of the predicted gene. Similar to peroxidase ATP18a. (X98804).

25

CAA59485.1 X85228 *Triticum aestivum*
DESCRIPTION: peroxidase. POX2.

30

CAA76680.1 Y17192 *Cucurbita pepo*
DESCRIPTION: peroxidase. aprx. type III peroxidase.

309

35

BAA85400.1 AP000615 *Oryza sativa*
DESCRIPTION: similar to OsMlo-h1. (Z95353).

40 CAB06083.1 Z83834 *Hordeum vulgare*
DESCRIPTION: Mlo. Mlo.

45 CAA74909.1 Y14573 *Hordeum vulgare*
DESCRIPTION: Mlo protein. Mlo.

AAG46114.1 AC073166 *Oryza sativa*
DESCRIPTION: putative Mlo (pathogen resistance) protein.
OSJNBb0064P21.5.

5

CAA06487.1 AJ005341 *Linum usitatissimum*
DESCRIPTION: MLO. homolog.

10 310

AAC63113.1 AF000307 *Brassica napus*
DESCRIPTION: steroid sulfotransferase 3. BnST3.

15

AAC63112.1 AF000306 *Brassica napus*
DESCRIPTION: steroid sulfotransferase 2. BnST2.

20

AAC63111.1 AF000305 *Brassica napus*
DESCRIPTION: steroid sulfotransferase 1. BnST1.

25

AAA61638.1 U10275 *Flaveria bidentis*
DESCRIPTION: O-sulfation of position 3 of flavonols. flavonol
3-sulfotransferase.

30

AAA33342.2 M84135 *Flaveria chloraefolia*
DESCRIPTION: flavonol 3-sulfotransferase.

35

AAA87399.1 U10277 *Flaveria bidentis*
DESCRIPTION: transfers sulfate group into flavonol. sulfotransferase-like
flavonol.

40

AAA33343.1 M84136 *Flaveria chloraefolia*
DESCRIPTION: O-sulfation of position 4' of flavonol. flavonol
4'-sulfotransferase.

312

45

AAD22970.1 AF124148 *Glycine max*
DESCRIPTION: trehalase 1 GMTRE1. expressed constitutively in many tissues
of soybean at a low level; similar to the *Arabidopsis thaliana* trehalase

precursor encoded by CenBank Accession Number AC002343.

5 AAG13442.1 AC051634 *Oryza sativa*
DESCRIPTION: putative trehalase. OSJNBb0018B10.19.

10 CAB50901.1 AJ238651 *Medicago truncatula*
DESCRIPTION: trehalase. TRE1 protein. tre1.
313

15 BAA19928.1 AB003491 *Oryza sativa*
DESCRIPTION: tryptophan synthase B. trpB.

20 AAA33491.1 M76685 *Zea mays*
DESCRIPTION: tryptophan synthase beta-subunit. TSB2.

25 AAB97526.1 AF042321 *Camptotheca acuminata*
DESCRIPTION: tryptophan synthase beta. TSB.

30 AAB97087.1 AF042320 *Camptotheca acuminata*
DESCRIPTION: tryptophan synthase beta subunit.

35 AAA33490.1 M76684 *Zea mays*
DESCRIPTION: tryptophan synthase beta-subunit. TSB1.

AAC25986.1 AF047024 *Chlamydomonas reinhardtii*
DESCRIPTION: tryptophan synthase beta. MAA7.
314

40 AAG42689.1 AF271384 *Zea mays*
DESCRIPTION: putative tryptophan synthase alpha. TSAlike.

45 CAA54131.1 X76713 *Zea mays*
DESCRIPTION: tryptophan synthase, alpha subunit. trpA.

AAG42688.1 AF271383 *Zea mays*

DESCRIPTION: putative tryptophan synthase alpha. TSAlike.

315

5 AAB97526.1 AF042321 *Camptotheca acuminata*
DESCRIPTION: tryptophan synthase beta. TSB.

10 AAB97087.1 AF042320 *Camptotheca acuminata*
DESCRIPTION: tryptophan synthase beta subunit.

15 BAA19928.1 AB003491 *Oryza sativa*
DESCRIPTION: tryptophan synthase B. trpB.

20 AAA33491.1 M76685 *Zea mays*
DESCRIPTION: tryptophan synthase beta-subunit. TSB2.

AAA33490.1 M76684 *Zea mays*
DESCRIPTION: tryptophan synthase beta-subunit. TSB1.

25 AAC25986.1 AF047024 *Chlamydomonas reinhardtii*
DESCRIPTION: tryptophan synthase beta. MAA7.

316

30 AAA33967.1 M76981 *Glycine max*
DESCRIPTION: vegetative storage protein. vspA.

35 BAA23563.1 D50094 *Phaseolus vulgaris*
DESCRIPTION: pod storage protein.

40 BAA19152.1 AB000585 *Phaseolus vulgaris*
DESCRIPTION: pod storage protein. PSP.

AAA34020.1 M20037 *Glycine max*
DESCRIPTION: vegetative storage protein.

45 AAA34022.1 M76980 *Glycine max*

DESCRIPTION: vegetative storage protein. vspB.

AAA34021.1 M20038 Glycine max

5 DESCRIPTION: vegetative storage protein.

321

BAA87043.1 AB035183 Ipomoea batatas

10 DESCRIPTION: N-hydroxycinnamoyl/benzoyltransferase. hcbt.

CAB06427.1 Z84383 Dianthus caryophyllus

15 DESCRIPTION: phytoalexin biosynthesis. anthranilate
N-hydroxycinnamoyl/benzoyltransferase.

CAB06429.1 Z84385 Dianthus caryophyllus

20 DESCRIPTION: phytoalexin biosynthesis. anthranilate
N-hydroxycinnamoyl/benzoyltransferase.

CAB06430.1 Z84386 Dianthus caryophyllus

25 DESCRIPTION: phytoalexin biosynthesis. anthranilate
N-hydroxycinnamoyl/benzoyltransferase.

CAB11466.1 Z98758 Dianthus caryophyllus

30 DESCRIPTION: carnation phytoalexin biosynthesis. anthranilate
N-hydroxycinnamoyl/benzoyltransferase.

CAB06538.1 Z84571 Dianthus caryophyllus

35 DESCRIPTION: phytoalexin biosynthesis. anthranilate
N-hydroxycinnamoyl/benzoyltransferase.

CAB06428.1 Z84384 Dianthus caryophyllus

40 DESCRIPTION: phytoalexin biosynthesis. anthranilate
N-hydroxycinnamoyl/benzoyltransferase.

323

BAB12694.1 AP002746 Oryza sativa

45 DESCRIPTION: putative zinc finger transcription factor. P0671B11.10.
contains ESTs AU098331(E31537),C91783(E31537).

 BAB03447.1 AP002817 Oryza sativa

5 DESCRIPTION: ESTs C96615(C10106),C26336(C12127),D21959(C10106)
 correspond
 to a region of the predicted gene. Similar to Arabidopsis thaliana DNA
 chromosome 4, BAC clone T6K21; NAM (no apical meristem) - like protein
 (AL021889).

10

BAA92400.1 AP001366 Oryza sativa

DESCRIPTION: ESTs C96615(C10106),C26336(C12127),D21959(C10106)
 correspond
 15 to a region of the predicted gene. Similar to NAM (AL021889).

BAB16335.1 AP002818 Oryza sativa

DESCRIPTION: putative NAM protein. P0436E04.18. contains ESTs
 20 E10793(C19698),E10793(C99379).

BAB16328.1 AP002818 Oryza sativa

DESCRIPTION: putative NAM protein. P0436E04.11. contains ESTs
 25 R4069(AU032425),R4069(AU082730).

CAA63102.2 X92205 Petunia x hybrida

DESCRIPTION: apical meristem formation. NAM.

30

CAA63101.1 X92204 Petunia x hybrida

DESCRIPTION: apical meristem formation. NAM.

35

AAK13151.1 AC078829 Oryza sativa

DESCRIPTION: putative NAM (no apical meristem) protein.
 OSJNBa0026012.6.

40

BAB19365.1 AP002542 Oryza sativa

DESCRIPTION: putative NAM (no apical meristem) protein. P0679C08.4.

45

BAA84803.1 AP000559 Oryza sativa

DESCRIPTION: Similar to NAM like protein (AC005310).

-
- 5 CAB51836.1 AJ243961 *Oryza sativa*
DESCRIPTION: Putitive Ser/Thr protein kinase. I1332.7.
- 10 BAB18292.1 AP002860 *Oryza sativa*
DESCRIPTION: putative receptor-like protein kinase. P0409B08.19.
- 15 BAB39873.1 AP002882 *Oryza sativa*
DESCRIPTION: putative protein kinase. P0439B06.8. contains ESTs
AU056701(S20808),AU056702(S20808).
- 20 BAB21240.1 AP002953 *Oryza sativa*
DESCRIPTION: Putative protein kinase. P0426D06.20. contains ESTs
C22359(C11461),C22360(C11461).
- 25 AAA33000.1 M76647 *Brassica oleracea*
DESCRIPTION: receptor protein kinase. SKR6.
- 30 CAA74661.1 Y14285 *Brassica oleracea*
DESCRIPTION: SFR1. extracellular S domain: 8-1342; transmembrane domain:
1343-1411; intracellular kinase domain: 1412-2554.
- 35 CAB89179.1 AJ245479 *Brassica napus* subsp. *napus*
DESCRIPTION: ser /thr kinase. S-locus receptor kinase. srk.
- 40 AAA33008.1 M97667 *Brassica napus*
DESCRIPTION: serine/threonine kinase receptor.
- 45 AAA62232.1 U00443 *Brassica napus*
DESCRIPTION: S-receptor kinase. protein contains an immunoglobulin-like
domain.
- BAA87853.1 AP000816 *Oryza sativa*
DESCRIPTION: EST AU030604(E51294) corresponds to a region of the
predicted gene. Similar to putative NAK-like Ser/Thr protein kinase.

(AF001308).

- CAA73134.1 Y12531 Brassica oleracea
5 DESCRIPTION: serine/threonine kinase. BRLK.
- BAA92836.1 AB032473 Brassica oleracea
10 DESCRIPTION: S18 S-locus receptor kinase. SRK18.
- AAK21965.1 AY028699 Brassica napus
DESCRIPTION: receptor protein kinase PERK1.
- 15 BAA23676.1 AB000970 Brassica rapa
DESCRIPTION: receptor kinase 1. BcRK1.
- 20 CAA73133.1 Y12530 Brassica oleracea
DESCRIPTION: serine /threonine kinase. ARLK.
- CAA67145.1 X98520 Brassica oleracea
25 DESCRIPTION: receptor-like kinase. SFR2.
- AAK00425.1 AC069324 Oryza sativa
30 DESCRIPTION: Putative protein kinase. OSJNBa0071K19.11.
- AAG03090.1 AC073405 Oryza sativa
DESCRIPTION: Similar to an Arabidopsis somatic embryogenesis
35 receptor-like kinase (AC007504).
- CAB41878.1 Y18259 Brassica oleracea
DESCRIPTION: SRK5 protein. SRK5. receptor-like kinase.
- 40 AAD21872.1 AF078082 Phaseolus vulgaris
DESCRIPTION: receptor-like protein kinase homolog RK20-1.
- 45 BAA21132.1 D88193 Brassica rapa
DESCRIPTION: S-receptor kinase. SRK9 (B.c).

- BAA07577.2 D38564 Brassica rapa
DESCRIPTION: receptor protein kinase SRK12.
- 5 BAA07576.1 D38563 Brassica rapa
DESCRIPTION: receptor protein kinase SRK8.
- 10 AAG59657.1 AC084319 Oryza sativa
DESCRIPTION: putative protein kinase. OSJNBa0004B24.20.
- 15 BAB03429.1 AP002817 Oryza sativa
DESCRIPTION: EST C22619(S11214) corresponds to a region of the predicted gene. Similar to Arabidopsis thaliana chromosome 2, BAC clone T17D12; putative protein kinase (AC006587).
- 20 BAB07999.1 AP002525 Oryza sativa
DESCRIPTION: putative protein kinase. P0462H08.22. contains EST C22619(S11214).
- 327

- 25 AAC04717.1 AF034131 Gossypium hirsutum
DESCRIPTION: putative MYB-like transcription factor. MYB-like DNA-binding domain protein. CmY-G. similar to MYB A encoded by GenBank Accession Number L04497.
- 30
- BAA23340.1 D88620 Oryza sativa
DESCRIPTION: transfactor. OSMYB4. Osmyb4.
- 35 AAK19611.1 AF336278 Gossypium hirsutum
DESCRIPTION: BNLGHi233. bnlghi6233. similar to myb.
- 40 AAA33482.1 M37153 Zea mays
DESCRIPTION: c1 locus myb homologue; putative.
- 45 AAK09326.1 AF320613 Zea mays
DESCRIPTION: activates anthocyanin transcription. anthocyanin regulatory C1. c1. transcription factor.

AAG43545.1 AF211527 *Nicotiana tabacum*
 DESCRIPTION: Avr9/Cf-9 rapidly elicited protein 1. ACRE1. similar to
 5 EREBP transcription factors.

CAC12822.1 AJ299252 *Nicotiana tabacum*
 DESCRIPTION: AP2 domain-containing transcription factor. ap2.
 10

BAA78738.1 AB023482 *Oryza sativa*
 DESCRIPTION: EST AU055776(S20048) corresponds to a region of the
 predicted gene.; Similar to *Arabidopsis thaliana* AP2 domain containing
 15 protein RAP2.10 mRNA, partial cds.(AF003103).

AAC14323.1 AF058827 *Nicotiana tabacum*
 DESCRIPTION: TSI1. Tsi1. contains putative AP2 DNA-binding domain;
 20 similar to Pti6.

BAA97122.1 AB016264 *Nicotiana sylvestris*
 DESCRIPTION: ERF (EREBP); ethylene-responsive element binding factor for
 25 basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive
 element binding factor. nserf2.

CAB93940.1 AJ238740 *Catharanthus roseus*
 DESCRIPTION: putative transcription factor. AP2-domain DNA-binding
 30 protein. orca2.

BAA76734.1 AB024575 *Nicotiana tabacum*
 35 DESCRIPTION: ethylene responsive element binding factor.

CAB96900.1 AJ251250 *Catharanthus roseus*
 DESCRIPTION: transcription factor. AP2-domain DNA-binding protein. orca3.
 40

CAB96899.1 AJ251249 *Catharanthus roseus*
 DESCRIPTION: transcription factor. AP2-domain DNA-binding protein. orca3.
 45

AAF63205.1 AF245119 *Mesembryanthemum crystallinum*

DESCRIPTION: AP2-related transcription factor. CDBP. stress induced transcription factor.

- 5 AAC24587.1 AF071893 *Prunus armeniaca*
DESCRIPTION: AP2 domain containing protein. AP2DCP.
- 10 BAA94514.2 AP001800 *Oryza sativa*
DESCRIPTION: Similar to *Arabidopsis thaliana* chromosome 4, BAC clone F9D16; putative Ap2 domain protein (AL035394).
- 15 BAA97124.1 AB016266 *Nicotiana sylvestris*
DESCRIPTION: ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf4.
- 20 BAA07321.1 D38123 *Nicotiana tabacum*
DESCRIPTION: ERF1. ethylene-responsive transcription factor.
- 25 BAB16083.1 AB036883 *Oryza sativa*
DESCRIPTION: transcriptional repressor. osERF3. osERF3. ERF protein family ERF3 associated repression domain.
- 30 BAB03248.1 AB037183 *Oryza sativa*
DESCRIPTION: ERF protein transcriptional repressor. ethylene responsive element binding factor3. osERF3.
- 35 BAA97123.1 AB016265 *Nicotiana sylvestris*
DESCRIPTION: ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf3.
- 40 AAF23899.1 AF193803 *Oryza sativa*
DESCRIPTION: transcription factor EREBP1. EREBP/AP2-like transcription factor.
- 45 AAK31271.1 AC079890 *Oryza sativa*
DESCRIPTION: putative transcriptional factor. OSJNBb0089A17.22.

AAC62619.1 AF057373 *Nicotiana tabacum*
DESCRIPTION: transcription factor. ethylene response element binding
5 protein 1. EREBP1.

AAG43548.1 AF211530 *Nicotiana tabacum*
DESCRIPTION: Avr9/Cf-9 rapidly elicited protein 111A. ACRE111A. similar
10 to EREBP transcription factors.

BAA90812.1 AP001168 *Oryza sativa*
DESCRIPTION: Similar to mRNA for DREB1A (AB007787).
15

AAG43549.1 AF211531 *Nicotiana tabacum*
DESCRIPTION: Avr9/Cf-9 rapidly elicited protein 111B. ACRE111B. similar
20 to EREBP transcription factors.

BAA99376.1 AP002526 *Oryza sativa*
DESCRIPTION: ESTs AU093391(E60370),AU091593(C60458),
AU093392(E60370)
25 correspond to a region of the predicted gene. Similar to Arabidopsis
thaliana BAC F21J9; AP2 domain protein. (AC000103).

AAK01089.1 AF298231 *Hordeum vulgare*
DESCRIPTION: CBF3-like protein BCBF3. BCBF3. AP2 domain protein; DRE
30 binding factor.

AAG59618.1 AF239616 *Hordeum vulgare*
DESCRIPTION: CRT/DRE-binding factor. CBF.
35

AAG59619.1 AF243384 *Oryza sativa*
DESCRIPTION: CRT/DRE binding factor. CBF. DREB.
40

AAK01088.1 AF298230 *Hordeum vulgare*
DESCRIPTION: CBF1-like protein BCBF1. BCBF1. AP2 domain protein;
putative
45 DRE binding factor.

AAC49567.1 U41466 Zea mays

DESCRIPTION: Glossy15. Glossy15. AP2 DNA-binding domain protein; similar

- 5 to the Arabidopsis floral homeotic gene APETALA2; maize AP2-domain regulator of leaf epidermal traits; homeotic regulator of leaf epidermal cell identity; allele: W64A; putative transcription factor.

330

10

AAC67571.1 AF060884 Brassica napus

DESCRIPTION: desiccation protein. Cdes. induced by dehydration.

- 15 AAA61564.1 U08108 Glycine max

DESCRIPTION: putative desiccation protectant protein, homolog of Lea14, GenBank Accession Number M88321.

- 20 AAA18543.1 M88322 Gossypium hirsutum

DESCRIPTION: probable desiccation protectant. Group 4 late embryogenesis-abundant protein. Lea14-A. This CDS is colinear and 66% identical with that in cDNA clone pcC27-45 from Craterostigma plantagineum desiccated leaves (Piatkowski et al., 1990, Plant Physiol. 94: 1682-1688).; putative.

25

AAA18542.1 M88321 Gossypium hirsutum

DESCRIPTION: probable desiccation protectant. Group 4 late embryogenesis-abundant protein. Lea14-A. putative.

30

AAD25354.1 AF115314 Glycine max

DESCRIPTION: possible desiccation protectant. seed maturation protein PM22. PM22. similar to desiccation protectant protein encoded by GenBank Accession Number U08108; late embryogenesis abundant protein; LEA protein.

35

AAF64451.1 AF239929 Euphorbia esula

DESCRIPTION: late-embryogenesis abundant protein. similar to desiccation protectant protein and late-embryogenesis abundant protein LEA14.

40

AAB96796.1 U77719 Lycopersicon esculentum

DESCRIPTION: ethylene-responsive late embryogenesis-like protein. ER5. LEA-like protein; drought-inducible; ABA-inducible; putative desiccation

45

protectant protein; similar to cotton Lea14A product encoded by GenBank
Accession Number M88321.

345

5

AAF61647.1 AF190634 *Nicotiana tabacum*
DESCRIPTION: UDP-glucose:salicylic acid glucosyltransferase. SA-GTase.

10

BAA36423.1 AB013598 *Verbena x hybrida*
DESCRIPTION: UDP-glucose:anthocyanin 5-O-glucosyltransferase. HGT8.

15

BAA89009.1 AB027455 *Petunia x hybrida*
DESCRIPTION: anthocyanin 5-O-glucosyltransferase. PH1.

20

BAA36421.1 AB013596 *Perilla frutescens*
DESCRIPTION: UDP-glucose:anthocynin 5-O-glucosyltransferase. PF3R4.

25

BAA93039.1 AB033758 *Citrus unshiu*
DESCRIPTION: limonoid UDP-glucosyltransferase. LGTase.

BAA36422.1 AB013597 *Perilla frutescens*
DESCRIPTION: UDP-glucose:anthocyanin 5-O-glucosyltransferase homologue.
PF3R6.

30

AAF98390.1 AF287143 *Brassica napus*
DESCRIPTION: catalyzes the transfer of glucose from UDP-glucose to
sinapate and some other hydroxycinnamates (4-coumarate, caffeate,
ferulate). UDP-glucose:sinapate glucosyltransferase. SGT1. SGT.

35

BAB07962.1 AP002524 *Oryza sativa*
DESCRIPTION: putative anthocyanin 5-O-glucosyltransferase. P0406H10.16.
contains ESTs AU067881(C10481),AU067882(C10481).

40

AAF17077.1 AF199453 *Sorghum bicolor*
DESCRIPTION: UDP-glucose glucosyltransferase.
UDP-glucose:p-hydroxymandelonitrile-o- glucosyltransferase.

45

AAK16172.1 AC079887 *Oryza sativa*
DESCRIPTION: putative glucosyltransferase. OSJNBa0040E01.14.

5 AAB36653.1 U32644 *Nicotiana tabacum*
DESCRIPTION: immediate-early salicylate-induced glucosyltransferase.
IS5a.

10 AAK28303.1 AF346431 *Nicotiana tabacum*
DESCRIPTION: phenylpropanoid:glucosyltransferase 1. togt1.
glucosyltransferase.

15 BAA83484.1 AB031274 *Scutellaria baicalensis*
DESCRIPTION: UDP-glucose: flavonoid 7-O-glucosyltransferase. ufgt.

20 AAK16181.1 AC079887 *Oryza sativa*
DESCRIPTION: putative glucosyltransferase. OSJNBa0040E01.16.

25 AAD21086.1 AF127218 *Forsythia x intermedia*
DESCRIPTION: adds glucose residue to position 3 of flavonoid compounds.
flavonoid 3-O-glucosyltransferase. UFGT.

30 AAB36652.1 U32643 *Nicotiana tabacum*
DESCRIPTION: immediate-early salicylate-induced glucosyltransferase.
IS10a.

35 AAK28304.1 AF346432 *Nicotiana tabacum*
DESCRIPTION: phenylpropanoid:glucosyltransferase 2. togt2.
glucosyltransferase.

40 CAA59450.1 X85138 *Lycopersicon esculentum*
DESCRIPTION: twi1. homologous to glucosyltransferases.

AAK16178.1 AC079887 *Oryza sativa*
DESCRIPTION: putative glucosyltransferase. OSJNBa0040E01.5.

45 AAK16175.1 AC079887 *Oryza sativa*

DESCRIPTION: putative glucosyltransferase. OSJNBa0040E01.15.

AAK16180.1 AC079887 *Oryza sativa*

5 DESCRIPTION: putative glucosyltransferase. OSJNBa0040E01.21.

CAB56231.1 Y18871 *Dorotheanthus bellidiformis*

10 DESCRIPTION: betanidin-5-O-glucosyltransferase.

BAA12737.1 D85186 *Gentiana triflora*

DESCRIPTION: UDP-glucose:flavonoid-3-glucosyltransferase.

AAG25643.1 AF303396 *Phaseolus vulgaris*

15 DESCRIPTION: UDP-glucosyltransferase HRA25. putative; defense associated.

BAB41017.1 AB047090 *Vitis labrusca* x *Vitis vinifera*

20 DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. KyUFGT1.
The
gene was derived from one of the parents *V. labruscana* cv. Ishiharawase.

25 AAB81683.1 AF000372 *Vitis vinifera*

DESCRIPTION: UDP glucose:flavonoid 3-o-glucosyltransferase.

30 BAB41020.1 AB047093 *Vitis vinifera*

DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. ItUFGT2.

BAB41022.1 AB047095 *Vitis vinifera*

35 DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. RuUFGT2.

BAB41019.1 AB047092 *Vitis vinifera*

40 DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. ItUFGT1.

AAB81682.1 AF000371 *Vitis vinifera*

DESCRIPTION: UDP glucose:flavonoid 3-o-glucosyltransferase.

45 BAB41025.1 AB047098 *Vitis vinifera*

DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. FIUFGT1.

BAB41023.1 AB047096 *Vitis vinifera*

5 DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. AIUFGT1.

BAB41021.1 AB047094 *Vitis vinifera*

10 DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. RuUFGT1.

BAB41026.1 AB047099 *Vitis vinifera*

15 DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. FIUFGT2.

BAB41024.1 AB047097 *Vitis vinifera*

DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. AIUFGT2.

20 BAB41018.1 AB047091 *Vitis labrusca* x *Vitis vinifera*

DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. KyUFGT2.
The
gene originated in one of the parents *V. vinifera* cv. Centennial.

25 BAB17182.1 AP002843 *Oryza sativa*

DESCRIPTION: putative UTP-glucose glucosyltransferase. P0407B12.19.

30 BAA19659.1 AB002818 *Perilla frutescens*

DESCRIPTION: flavonoid 3-O-glucosyltransferase. UDP glucose.

BAA89008.1 AB027454 *Petunia x hybrida*

35 DESCRIPTION: anthocyanidin 3-O-glucosyltransferase. PGT8.

BAB17176.1 AP002843 *Oryza sativa*

40 DESCRIPTION: putative UTP-glucose glucosyltransferase. P0407B12.13.

AAB86473.1 AF028237 *Ipomoea purpurea*

DESCRIPTION: UDP glucose: flavonoid 3-O-glucosyltransferase. UF3GT-FL1.

45 350

- CAA44216.1 X62343 *Nicotiana tabacum*
DESCRIPTION: cinnamyl-alcohol dehydrogenase. CAD14.
- 5 BAA03099.1 D13991 *Aralia cordata*
DESCRIPTION: cinnamyl alcohol dehydrogenase. cadac1.
- 10 CAA79622.1 Z19568 *Populus deltoides*
DESCRIPTION: lignin biosynthesis. cinnamyl alcohol dehydrogenase.
- 15 CAC07423.1 AJ295837 *Populus balsamifera* subsp. *trichocarpa*
DESCRIPTION: lignin monomer biosynthesis. cinnamyl alcohol dehydrogenase.
cad.
- 20 AAF43140.1 AF217957 *Populus tremuloides*
DESCRIPTION: cinnamyl alcohol dehydrogenase. CAD.
- 25 CAA44217.1 X62344 *Nicotiana tabacum*
DESCRIPTION: cinnamyl-alcohol dehydrogenase. CAD19.
- CAA79625.1 Z19573 *Medicago sativa*
DESCRIPTION: lignin biosynthesis. cinnamyl alcohol dehydrogenase.
- 30 AAC35845.1 AF083332 *Medicago sativa*
DESCRIPTION: cinnamyl-alcohol dehydrogenase. MsaCad2.
- 35 AAC07987.1 AF038561 *Eucalyptus globulus*
DESCRIPTION: catalyses the reduction of cinnamaldehydes to the
corresponding cinnamyl alcohols as the last step in the production of
lignin monomers. cinnamyl alcohol dehydrogenase. CAD.
- 40 CAA46585.1 X65631 *Eucalyptus gunnii*
DESCRIPTION: cinnamyl-alcohol dehydrogenase. cad.
- 45 AAG15553.1 AF294793 *Eucalyptus saligna*
DESCRIPTION: cinnamyl alcohol dehydrogenase. cad. CAD.

CAA53211.1 X75480 Eucalyptus gunnii
DESCRIPTION: cinnamyl-alcohol dehydrogenase. CAD.

5

AAB70908.1 AF010290 Lolium perenne
DESCRIPTION: cinnamyl alcohol dehydrogenase. CAD.

10 CAA74070.1 Y13733 Zea mays
DESCRIPTION: cinnamyl alcohol dehydrogenase. cad.

15 CAA06687.1 AJ005702 Zea mays
DESCRIPTION: cinnamyl alcohol dehydrogenase. cad.

20 CAA13177.1 AJ231135 Saccharum officinarum
DESCRIPTION: lignin biosynthesis. cinnamyl alcohol dehydrogenase. cad.

BAA19487.1 D86590 Zinnia elegans
DESCRIPTION: cinnamyl alcohol dehydrogenase. ZCAD1.

25 CAA51226.1 X72675 Picea abies
DESCRIPTION: cinnamyl-alcohol dehydrogenase.

30 CAA05097.1 AJ001926 Picea abies
DESCRIPTION: cinnamyl alcohol dehydrogenase. cad8.

35 CAA05096.1 AJ001925 Picea abies
DESCRIPTION: cinnamyl alcohol dehydrogenase. cad7.

40 CAA05095.1 AJ001924 Picea abies
DESCRIPTION: cinnamyl alcohol dehydrogenase. cad2.

AAB38774.1 U62394 Pinus radiata
DESCRIPTION: cinnamyl alcohol dehydrogenase. CAD.

45 AAC31166.1 AF060491 Pinus radiata

DESCRIPTION: cinnamyl alcohol dehydrogenase. CAD.

- CAA86073.1 Z37992 Pinus taeda
5 DESCRIPTION: cinnamyl alcohol dehydrogenase.
- CAA86072.1 Z37991 Pinus taeda
10 DESCRIPTION: cinnamyl alcohol dehydrogenase.
- BAA04046.1 D16624 Eucalyptus botryoides
DESCRIPTION: cinnamyl alcohol dehydrogenase. Cad1:Eb:1.
- 15 AAD10327.1 U63534 Fragaria x ananassa
DESCRIPTION: catalyzes the reduction of cinnamylaldehydes leading to
monolignols. cinnamyl alcohol dehydrogenase. CAD. involved with lignin
biosynthesis.
- 20 AAK28509.1 AF320110 Fragaria x ananassa
DESCRIPTION: cinnamyl alcohol dehydrogenase.
- 25 AAB38503.1 U79770 Mesembryanthemum crystallinum
DESCRIPTION: cinnamyl-alcohol dehydrogenase Eli3.
- 30 AAC35846.1 AF083333 Medicago sativa
DESCRIPTION: cinnamyl-alcohol dehydrogenase. MsaCad1.
- 35 AAA74882.1 L36823 Stylosanthes humilis
DESCRIPTION: cinnamyl-alcohol dehydrogenase. CAD1.
- AAF23409.1 AF207552 Brassica napus
40 DESCRIPTION: cinnamyl alcohol dehydrogenase. CAdA-1.
- AAC15467.1 U24561 Apium graveolens
DESCRIPTION: converts mannitol to mannose. mannitol dehydrogenase. Mtd.
1-oxidoreductase; induced with sodium salicylate; similar to the plant
45 defense gene ELI3 in Arabidopsis thaliana, PIR Accession Number S28044; EC
number unassigned; MTD.

DESCRIPTION: caleosin. 27 kDa calcium-binding protein.

CAA61981.1 X89891 *Oryza sativa*

5 DESCRIPTION: EFA27 for EF hand, abscisic acid, 27kD. efa27.

CAB71337.1 AJ250283 *Hordeum vulgare*

10 DESCRIPTION: putative calcium binding EF-hand protein. bci-4.

CAB42585.1 AJ238627 *Chlorella protothecoides*

DESCRIPTION: putative Ca⁺⁺ binding protein. dee112.

15 353

AAF60316.1 AF236108 *Glycine max*

20 DESCRIPTION: putative purple acid phosphatase precursor. PAP. type 5 acid phosphatase.

AAF60315.1 AF236107 *Ipomoea batatas*

25 DESCRIPTION: putative purple acid phosphatase precursor. PAP. type 5 acid phosphatase.

AAF60317.1 AF236109 *Phaseolus vulgaris*

30 DESCRIPTION: putative purple acid phosphatase precursor. PAP. type 5 acid phosphatase.
359

CAA55039.1 X78203 *Hyoscyamus muticus*

35 DESCRIPTION: glutathione transferase.

AAB65163.1 AF002692 *Solanum commersonii*

40 DESCRIPTION: glutathione S-transferase, class-phi. GST1. low temperature induced.

CAA96431.1 Z71749 *Nicotiana plumbaginifolia*

DESCRIPTION: glutathione S-transferase.

45

BAA01394.1 D10524 *Nicotiana tabacum*

DESCRIPTION: glutathione S-transferase. parB.

5 AAA33930.1 M84968 *Silene vulgaris*
DESCRIPTION: glutathione-S-transferase.

10 AAA33931.1 M84969 *Silene vulgaris*
DESCRIPTION: glutathione-S-transferase.

15 AAF65767.1 AF242309 *Euphorbia esula*
DESCRIPTION: glutathione S-transferase. putative auxin-binding GST.

AAF61392.1 AF133894 *Persea americana*
DESCRIPTION: glutathione S-transferase. GTH.

20 CAB38119.1 AJ010296 *Zea mays*
DESCRIPTION: Glutathione transferase III(b). gst3b.

25 CAB38118.1 AJ010295 *Zea mays*
DESCRIPTION: Glutathione transferase III(a). gst3a.

30 BAB39935.1 AP002914 *Oryza sativa*
DESCRIPTION: putative glutathione S-transferase. P0493G01.17.

AAG34811.1 AF243376 *Glycine max*
DESCRIPTION: glutathione S-transferase GST 21.

35 BAB39941.1 AP002914 *Oryza sativa*
DESCRIPTION: putative glutathione S-transferase. P0493G01.23.

40 CAA09190.1 AJ010451 *Alopecurus myosuroides*
DESCRIPTION: glutathione transferase. GST2a.

45 CAA09192.1 AJ010453 *Alopecurus myosuroides*
DESCRIPTION: glutathione transferase. GST2c.

- CAA09193.1 AJ010454 *Alopecurus myosuroides*
DESCRIPTION: glutathione transferase. GST2d.
- 5 AAG34814.1 AF243379 *Glycine max*
DESCRIPTION: glutathione S-transferase GST 24.
- 10 CAA09191.1 AJ010452 *Alopecurus myosuroides*
DESCRIPTION: glutathione transferase. GST2b.
- 15 BAB39939.1 AP002914 *Oryza sativa*
DESCRIPTION: putative glutathione S-transferase. P0493G01.21.
- 20 AAG32476.1 AF309383 *Oryza sativa* subsp. *japonica*
DESCRIPTION: putative glutathione S-transferase OsGSTF4.
- AAG34812.1 AF243377 *Glycine max*
DESCRIPTION: glutathione S-transferase GST 22.
- 25 BAB39929.1 AP002914 *Oryza sativa*
DESCRIPTION: putative glutathione transferase. P0493G01.7.
- 30 CAA39487.1 X56012 *Triticum aestivum*
DESCRIPTION: glutathione transferase. gstA1.
- 35 AAD56395.1 AF184059 *Triticum aestivum*
DESCRIPTION: glutathione S-transferase. GST1.
- BAB39940.1 AP002914 *Oryza sativa*
DESCRIPTION: putative glutathione S-transferase. P0493G01.22.
- 40 CAA68993.1 Y07721 *Petunia x hybrida*
DESCRIPTION: conjugates glutathione to anthocyanin to facilitate transport to the vacuole. glutathione S-transferase. an9 locus.
- 45

- AAA33469.1 M16902 Zea mays
DESCRIPTION: glutathione S-transferase I.
- 5 AAG32477.1 AF309384 Oryza sativa subsp. japonica
DESCRIPTION: putative glutathione S-transferase OsGSTF3.
- 10 AAA33470.1 M16901 Zea mays
DESCRIPTION: glutathione S-transferase I.
- 15 AAA20585.1 U12679 Zea mays
DESCRIPTION: glutathione S-transferase IV. GSTIV.
- 20 CAA56047.1 X79515 Zea mays
DESCRIPTION: glutathione transferase. GST27.
- 25 CAA39480.1 X56004 Triticum aestivum
DESCRIPTION: glutathione transferase. gstA2.
- 30 AAC64007.1 AF062403 Oryza sativa
DESCRIPTION: glutathione S-transferase II.
- 35 BAB39927.1 AP002914 Oryza sativa
DESCRIPTION: putative glutathione S-transferase. P0493G01.1. contains
ESTs AU031696(R0596),C97559(C60386),C28218(C60386), D28287(R0596).
- 40 AAG32475.1 AF309382 Oryza sativa subsp. japonica
DESCRIPTION: putative glutathione S-transferase OsGSTF5.
- 45 AAG34823.1 AF244680 Zea mays
DESCRIPTION: glutathione S-transferase GST 15.
- AAG34817.1 AF244674 Zea mays
DESCRIPTION: glutathione S-transferase GST 9.
- CAA05354.1 AJ002380 Oryza sativa

DESCRIPTION: glutathione S-transferase. Rgst I.

AAG34820.1 AF244677 Zea mays

5 DESCRIPTION: glutathione S-transferase GST 11.

AAG34821.1 AF244678 Zea mays

10 DESCRIPTION: glutathione S-transferase GST 13.

CAB66333.1 AJ279691 Betula pendula

DESCRIPTION: glutathione-S-transferase. gst.

AAG34818.1 AF244675 Zea mays

15 DESCRIPTION: glutathione S-transferase GST 10.

AAG34816.1 AF244673 Zea mays

20 DESCRIPTION: glutathione S-transferase GST 8.

AAG34822.1 AF244679 Zea mays

25 DESCRIPTION: glutathione S-transferase GST 14.

CAA05355.1 AJ002381 Oryza sativa

30 DESCRIPTION: glutathione S-transferase. Rgst II.

360

AAA33710.1 L16977 Petunia x hybrida

35 DESCRIPTION: glutamate decarboxylase. gad.

AAA33709.1 L16797 Petunia x hybrida

DESCRIPTION: glutamate decarboxylase. gad.

AAC24195.1 AF020425 Nicotiana tabacum

40 DESCRIPTION: calmodulin binding protein. glutamate decarboxylase isozyme
1. NtGAD1. calcium-calmodulin-dependent enzyme.

45 AAB40608.1 U54774 Nicotiana tabacum

DESCRIPTION: glutamate decarboxylase. NtGAD1. calmodulin regulated enzyme; calmodulin-binding protein.

5 AAK18620.1 AF352732 *Nicotiana tabacum*

DESCRIPTION: converts glutamate to gamma-aminobutyric acid. glutamate decarboxylase isozyme 3. GAD; GAD3; NtGAD3; calcium/calmodulin-dependent enzyme.

10

AAC39483.1 AF020424 *Nicotiana tabacum*

DESCRIPTION: glutamate decarboxylase isozyme 2. NtGAD2. calcium-calmodulin-dependent enzyme.

15

BAB32870.1 AB056062 *Oryza sativa*

DESCRIPTION: glutamate decarboxylase. GAD.

20

BAB32868.1 AB056060 *Oryza sativa*

DESCRIPTION: glutamate decarboxylase. GAD.

25 BAB32869.1 AB056061 *Oryza sativa*

DESCRIPTION: glutamate decarboxylase. GAD.

30 BAB32871.1 AB056063 *Oryza sativa*

DESCRIPTION: glutamate decarboxylase. GAD.

35 CAA56812.1 X80840 *Lycopersicon esculentum*

DESCRIPTION: homology to pyroxidal-5'-phosphate-dependant glutamate decarboxylases; putative start codon.

40 CAA50719.1 X71900 *Lycopersicon esculentum*

DESCRIPTION: histidine decarboxylase. hdc. pyridoxal 5'-phosphate dependant.

362

45 AAG13467.1 AC026758 *Oryza sativa*

DESCRIPTION: putative proline oxidase. OSJNBa0015J15.31.

AAD48490.1 AF171226 Brassica napus
DESCRIPTION: proline dehydrogenase. pdh.

5 363

AAA33967.1 M76981 Glycine max
DESCRIPTION: vegetative storage protein. vspA.

10

AAA34022.1 M76980 Glycine max
DESCRIPTION: vegetative storage protein. vspB.

15 AAA34021.1 M20038 Glycine max
DESCRIPTION: vegetative storage protein.

20 BAA23563.1 D50094 Phaseolus vulgaris
DESCRIPTION: pod storage protein.

25 BAA19152.1 AB000585 Phaseolus vulgaris
DESCRIPTION: pod storage protein. PSP.

AAA34020.1 M20037 Glycine max
DESCRIPTION: vegetative storage protein.

30 364

AAB86939.1 AF030387 Oryza sativa
DESCRIPTION: NOI protein.

35 AAC03022.1 AF045033 Zea mays
DESCRIPTION: nitrate-induced NOI protein.

40 AAB86937.1 AF030385 Zea mays
DESCRIPTION: nitrate-induced NOI protein.

366

45 AAF75824.1 AF101788 Pinus taeda
DESCRIPTION: phytocyanin homolog.

- 5 AAC32448.1 U76296 *Spinacia oleracea*
 DESCRIPTION: plantacyanin. member of a strictly plant-specific family of mononuclear blue copper proteins known as phytoeyanins, which are further classified into three distinct subfamilies: Uclacyanins, Stellacyanins, and Plantacyanins; member of the subfamily of Plantacyanins; non-glycosylated.
- 10 AAC32421.1 U65511 *Cucumis sativus*
 DESCRIPTION: putative oxygen activation and/or lignin formation. stellacyanin. member of a strictly plant-specific family of mononuclear blue copper proteins known as phytoeyanins, which are further classified into three distinct subfamilies: Uclacyanins, Stellacyanins, and Plantacyanins; member of the subfamily of Stellacyanins; similar to Rhus vernicifera stellacyanin: SwissProt Accession Number P00302; similar to umecyanin: SwissProt Accession Number P42849; similar to mavicyanin; SwissProt Accession Number P80728; similar to BCB encoded by GenBank Accession Number Z15058; similar to F18A8.9, encoded by GenBank Accession Number AC003105; similar to F7F1.27 encoded by GenBank Accession Number AC004669; similar to F9D12.16 encoded by GenBank Accession Number AF077407; glycoprotein.
- 25 AAF66243.1 AF243181 *Lycopersicon esculentum*
 DESCRIPTION: plantacyanin. naturally occurring cupredoxin with a Val residue in the position of the axial ligand Met; member of the plantacyanin subfamily of a strictly plant-specific family of mononuclear blue copper proteins known as phytoeyanins.
- 35 BAA90481.1 AB035146 *Ipomoea nil*
 DESCRIPTION: phytoeyanin-related protein.
- 367

- 40 AAD11617.1 AF050495 *Lycopersicon esculentum*
 DESCRIPTION: Ca²⁺-ATPase. LCA1A; alternative transcript.
- 45 AAA34138.1 M96324 *Lycopersicon esculentum*
 DESCRIPTION: The calcium ATPase is a calcium ion pump. Ca²⁺-ATPase. LCA1.

- AAD11618.1 AF050496 *Lycopersicon esculentum*
DESCRIPTION: Ca²⁺-ATPase. LCA1B; alternative transcript.
- 5 CAA63790.1 X93592 *Dunaliella bioculata*
DESCRIPTION: P-type ATPase. ca1. calcium pumping; CA1.
- 10 AAF73985.1 AF096871 *Zea mays*
DESCRIPTION: calcium pump. calcium ATPase. cap1.
- 15 AAB58910.1 U82966 *Oryza sativa*
DESCRIPTION: Ca²⁺-ATPase.
- 20 AAG28435.1 AF195028 *Glycine max*
DESCRIPTION: plasma membrane Ca²⁺-ATPase. SCA1.
- AAG28436.1 AF195029 *Glycine max*
DESCRIPTION: plasma membrane Ca²⁺-ATPase. SCA2.
- 25 AAB49042.1 U54690 *Dunaliella acidophila*
DESCRIPTION: plasma membrane proton ATPase. dha1. DaDHA1; proton pump.
- 30 AAB35314.2 S79323 *Vicia faba*
DESCRIPTION: plasma membrane H⁽⁺⁾-ATPase precursor. plasma membrane H⁽⁺⁾-ATPase. This sequence comes from Fig. 1; conceptual translation presented here differs from translation in publication.
- 35 CAB85495.1 AJ132892 *Medicago truncatula*
DESCRIPTION: proton pump. H⁺-ATPase. ha1.
- 40 CAB85494.1 AJ132891 *Medicago truncatula*
DESCRIPTION: proton pump. H⁺-ATPase. ha1.
- 45 AAB17186.1 U72148 *Lycopersicon esculentum*
DESCRIPTION: plasma membrane H⁺-ATPase. LHA4. plasma membrane proton

pumping ATPase.

- 5 CAC29436.1 AJ310524 *Vicia faba*
DESCRIPTION: P-type H⁺-ATPase. ha5. predominantly expressed in guard cells and flowers.
- 10 AAB41898.1 U84891 *Mesembryanthemum crystallinum*
DESCRIPTION: plasma membrane proton pump. H⁺-transporting ATPase. PMA.
- 15 CAC29435.1 AJ310523 *Vicia faba*
DESCRIPTION: P-type H⁺-ATPase. vha4. predominantly expressed in flowers.
- 20 AAF98344.1 AF275745 *Lycopersicon esculentum*
DESCRIPTION: plasma membrane H⁺-ATPase. LHA2. P-type ion pump.
369

- 25 BAB17726.1 AB050900 *Raphanus sativus*
DESCRIPTION: asparagine synthetase. Asn1.
- 30 CAA59138.1 X84448 *Brassica oleracea*
DESCRIPTION: asparagine synthase (glutamine-hydrolysing).
- 35 AAC16325.1 AF061740 *Elaeagnus umbellata*
DESCRIPTION: asparagine synthetase. AS.
- 40 CAA08913.1 AJ009952 *Phaseolus vulgaris*
DESCRIPTION: asparagine synthesis. asparagine synthetase type II. as2.
- 45 AAF02775.1 AF190728 *Helianthus annuus*
DESCRIPTION: asparagine synthetase. HAS1.
- AAC49613.1 U77678 *Glycine max*
DESCRIPTION: catalyzes the ATP-dependent transfer of the amide group of glutamine to aspartate producing asparagine and glutamate. asparagine synthetase 2. AS2.

- 5 AAB81011.1 U89923 *Medicago sativa*
 DESCRIPTION: asparagine synthetase.
- 10 AAC09952.1 U55874 *Glycine max*
 DESCRIPTION: asparagine synthetase.
- 15 CAA61589.1 X89409 *Lotus japonicus*
 DESCRIPTION: asparagine synthase (glutamine-hydrolyzing). AS.
- 20 CAA67889.1 X99552 *Asparagus officinalis*
 DESCRIPTION: asparagine synthetase.
- 25 AAF74755.1 AF263432 *Helianthus annuus*
 DESCRIPTION: asparagine synthetase. HAS1.1.
- 30 AAD05035.1 AF014057 *Triphysaria versicolor*
 DESCRIPTION: asparagine synthetase. AS. glutamine-hydrolyzing.
- 35 AAD05034.1 AF014056 *Triphysaria versicolor*
 DESCRIPTION: asparagine synthetase. AS. glutamine-hydrolyzing.
- 40 AAD05033.1 AF014055 *Triphysaria versicolor*
 DESCRIPTION: asparagine synthetase. AS. glutamine-hydrolyzing.
- 45 CAA96526.1 Z72354 *Vicia faba*
 DESCRIPTION: synthesis of asparagine from aspartate and glutamine.
 asparagine synthetase. VfAS1.
- CAA48141.1 X67958 *Asparagus officinalis*
 DESCRIPTION: asparagine synthase (glutamine-hydrolyzing).

CAA58052.1 X82849 Zea mays
DESCRIPTION: asparragine synthetase. AS.

5 AAB91481.1 AF037363 Helianthus annuus
DESCRIPTION: asparagine synthetase.

10 CAA73762.1 Y13321 Pisum sativum
DESCRIPTION: asparagine synthetase 1. AS1.

15 CAA73763.1 Y13322 Pisum sativum
DESCRIPTION: asparagine synthetase 2. AS2.

20 BAA96452.1 AB021793 Pyrus pyrifolia
DESCRIPTION: asparagine synthetase. PPFRU32.

25 AAA73943.1 L23833 Glycine max
DESCRIPTION: production of phosphoribosylamine using glutamine and
phosphoribosylpyrophosphate as substrates. glutamine
phosphoribosylpyrophosphate amidotransferase.

370

30 AAG21985.1 AF271636 Zea mays
DESCRIPTION: lysine ketoglutarate reductase/saccharopine dehydrogenase.
LKRS DH. bifunctional enzyme; LKR/SDH; lysine 2-oxoglutarate
reductase/saccharopine dehydrogenase.

35 AAC18622.2 AF003551 Zea mays
DESCRIPTION: lysine-ketoglutarate reductase/saccharopine dehydrogenase
bifunctional enzyme.

40 AAG28387.1 AF191667 Brassica oleracea
DESCRIPTION: lysine-ketoglutarate reductase/saccharopine dehydrogenase.

45 AAG28386.1 AF191666 Brassica napus
DESCRIPTION: lysine-ketoglutarate reductase/saccharopine dehydrogenase.

AAB97685.1 AF042184 Brassica napus
DESCRIPTION: lysine-ketoglutarate reductase/saccharopine dehydrogenase.

5

AAG14462.1 AF293461 Brassica napus
DESCRIPTION: lysine-ketoglutarate reductase. LKR.

371

10

CAB62537.1 AJ012583 Hevea brasiliensis
DESCRIPTION: pseudo-hevein.

15

AAA33357.1 M36986 Hevea brasiliensis
DESCRIPTION: hevein (HEV1) precursor.

20

CAA05978.1 AJ003196 Hevea brasiliensis
DESCRIPTION: N-acetyl-D-glucosamine/N-acetyl-D-neuraminic acid binding
lectin. prohevein.

25

AAF61435.1 AF137352 Pisum sativum
DESCRIPTION: pre-hevein-like protein. PHLP. stress-induced; the coding
region is putative in the 5' end.

372

30

AAG28503.1 AF196966 Citrus sinensis
DESCRIPTION: hexokinase.

35

AAF18584.1 AF118132 Spinacia oleracea
DESCRIPTION: chloroplast outer envelope hexokinase 1. Hxk1.

40

AAF18585.1 AF118133 Nicotiana tabacum
DESCRIPTION: chloroplast outer envelope hexokinase 1. Hxk1.

45

AAF14186.1 AF106068 Solanum tuberosum
DESCRIPTION: hexokinase 2.

AAG35735.1 AF208543 Lycopersicon esculentum

DESCRIPTION: hexokinase. Hxk2.

CAA63966.1 X94302 Solanum tuberosum
5 DESCRIPTION: hexokinase. hxk.

BAA99425.1 AP002743 Oryza sativa
10 DESCRIPTION: putative chloroplast outer envelope hexokinase 1.
P0710E05.10.

374

AAC83688.2 AF083343 Nicotiana tabacum
15 DESCRIPTION: 101 kDa heat shock protein. HSP101.

AAF01280.1 AF174433 Triticum aestivum
20 DESCRIPTION: heat shock protein 101. HSP101. ClpB family member.

AAD33606.1 AF133840 Zea mays
25 DESCRIPTION: heat shock protein HSP101. HSP101. 101 kDa protein.

AAD25223.1 AF077337 Zea mays
30 DESCRIPTION: heat shock protein 101. HSP101. ClpB/Hsp100 protein
homolog;
101 kDa heat shock protein.

AAF91178.1 AF203700 Phaseolus lunatus
35 DESCRIPTION: ClpB. clpB. heat shock protein HSP100.

AAD22629.1 AF097363 Triticum aestivum
40 DESCRIPTION: heat shock protein 101. Hsp101a.

AAC83689.2 AF083344 Triticum aestivum
45 DESCRIPTION: 101 kDa heat shock protein. HSP101.

AAD26530.1 AF083327 Zea mays
DESCRIPTION: 101 kDa heat shock protein. HSP101. similar to HSP100/ClpB;
HSP104.

-
- 5 CAA04611.1 AJ001208 *Brassica juncea*
DESCRIPTION: APS reductase. apsr8. putative mitochondrial or plastidic transit peptide.
- 10 CAA04610.1 AJ001207 *Brassica juncea*
DESCRIPTION: APS reductase. apsr2. putative mitochondrial or plastidic transit peptide.
- 15 AAB05871.2 U63784 *Catharanthus roseus*
DESCRIPTION: reduction of adenylyl sulfate (APS). PAPS-reductase-like protein. par2neu.
- 20 CAB65911.1 AJ249831 *Lemna minor*
DESCRIPTION: APR reducing enzyme, sulphur assimilation. adenosine 5'-phosphosulphate reductase. lapr.
- 25 AAF18999.1 AF212155 *Allium cepa*
DESCRIPTION: APS-reductase.
- 30 AAC26855.1 AF069951 *Enteromorpha intestinalis*
DESCRIPTION: catalyzes the formation of sulfite and 5'-AMP from APS and reduced glutathione. 5'-adenylylsulfate reductase. EAPR1; sulfate assimilation enzyme; similar to *Escherichia coli* 3'-phosphoadenosine, 5'-phosphosulfate (PAPS) reductase encoded by cysH.
- 35 AAD02069.1 AF036939 *Chlamydomonas reinhardtii*
DESCRIPTION: redox-regulator of 5'UTR psbA mRNA binding complex and translation. protein disulfide isomerase. localized to ER and chloroplast.
- 40 AAC49896.1 AF027727 *Chlamydomonas reinhardtii*
DESCRIPTION: involved in the redox-regulated binding of chloroplast poly(A)-binding protein to the 5'-UTR of psbA mRNA; regulates chloroplast translational activation. protein disulfide isomerase RB60. PDI.
- 45 376
-

- AAC62017.1 AF077547 *Brassica juncea*
DESCRIPTION: arginine decarboxylase.
- 5 AAF26434.1 AF220097 *Brassica juncea*
DESCRIPTION: arginine decarboxylase.
- 10 AAF26435.1 AF220098 *Brassica juncea*
DESCRIPTION: arginine decarboxylase.
- 15 AAB60880.1 AF002017 *Dianthus caryophyllus*
DESCRIPTION: arginine decarboxylase. gCARADC8.
- 20 AAF42972.1 AF127241 *Nicotiana tabacum*
DESCRIPTION: arginine decarboxylase 2. ADC2.
- BAA25685.1 AB012873 *Nicotiana sylvestris*
DESCRIPTION: arginine decarboxylase. NsADC-1.
- 25 CAA85773.1 Z37540 *Pisum sativum*
DESCRIPTION: arginine decarboxylase.
- 30 CAB64599.1 AJ251898 *Datura stramonium*
DESCRIPTION: polyamine biosynthesis. arginine decarboxylase 1. adc1.
- 35 AAD09204.1 U35367 *Glycine max*
DESCRIPTION: arginine decarboxylase.
- 40 BAA84799.1 AP000559 *Oryza sativa*
DESCRIPTION: ESTs C99670(E21043),C99671(E21043),
AU078262(R10938),AU078261(R10938),D15282(C0402) correspond to a
region of
the predicted gene.; Similar to arginine decarboxylase (U52851).
- 45 AAB67887.1 U63832 *Dianthus caryophyllus*
DESCRIPTION: arginine decarboxylase. ADC.

AAF42971.1 AF127240 *Nicotiana tabacum*
DESCRIPTION: arginine decarboxylase 1. ADC1.

5

AAF42970.1 AF127239 *Nicotiana tabacum*
DESCRIPTION: arginine decarboxylase 1. ADC1.

10 AAC68511.1 AF045666 *Theobroma cacao*
DESCRIPTION: arginine decarboxylase. spe2.

CAA65585.1 X96791 *Vitis vinifera*
15 DESCRIPTION: arginine decarboxylase. ADC.

AAA61347.1 L16582 *Lycopersicon esculentum*
20 DESCRIPTION: decarboxylation of L-arginine. arginine decarboxylase.

AAC68530.1 AF045685 *Arabidopsis arenosa*
DESCRIPTION: arginine decarboxylase. spe2.

25 AAC68529.1 AF045684 *Capsella bursa-pastoris*
DESCRIPTION: arginine decarboxylase. spe2.

30 AAC68525.1 AF045680 *Arabis drummondii*
DESCRIPTION: arginine decarboxylase. spe2.

AAC68526.1 AF045681 *Barbarea vulgaris*
35 DESCRIPTION: arginine decarboxylase. spe2.

AAC68535.1 AF045690 *Nasturtium officinale*
40 DESCRIPTION: arginine decarboxylase. spe2.

AAC68534.1 AF045689 *Thellungiella salsuginea*
DESCRIPTION: arginine decarboxylase. spe2.

45 AAC68533.1 AF045688 *Thlaspi arvense*

DESCRIPTION: arginine decarboxylase. spe2.

5 AAC68532.1 AF045687 *Stanleya pinnata*
DESCRIPTION: arginine decarboxylase. spe2.

10 AAC68531.1 AF045686 *Sisymbrium altissimum*
DESCRIPTION: arginine decarboxylase. spe2.

AAC68510.1 AF045665 *Aethionema grandiflora*
DESCRIPTION: arginine decarboxylase. spe2.

15 AAC68528.1 AF045683 *Brassica oleracea*
DESCRIPTION: arginine decarboxylase. spe2.

20 AAC68519.1 AF045674 *Arabidopsis arenosa*
DESCRIPTION: arginine decarboxylase. spe2.

25 AAC68527.1 AF045682 *Brassica nigra*
DESCRIPTION: arginine decarboxylase. spe2.

30 AAC68523.1 AF045678 *Thellungiella salsuginea*
DESCRIPTION: arginine decarboxylase. spe2.

AAC68514.1 AF045669 *Arabis drummondii*
DESCRIPTION: arginine decarboxylase. spe2.

35 AAC68524.1 AF045679 *Nasturtium officinale*
DESCRIPTION: arginine decarboxylase. spe2.

40 AAC68522.1 AF045677 *Thlaspi arvense*
DESCRIPTION: arginine decarboxylase. spe2.

45 AAC68513.1 AF045668 *Polanisia dodecandra*
DESCRIPTION: arginine decarboxylase. spe2.

- AAC68518.1 AF045673 *Capsella bursa-pastoris*
DESCRIPTION: arginine decarboxylase. spe2.
- 5 AAC68515.1 AF045670 *Barbarea vulgaris*
DESCRIPTION: arginine decarboxylase. spe2.
- 10 AAC68521.1 AF045676 *Stanleya pinnata*
DESCRIPTION: arginine decarboxylase. spe2.
- 15 AAC68520.1 AF045675 *Sisymbrium altissimum*
DESCRIPTION: arginine decarboxylase. spe2.
- 20 AAC68517.1 AF045672 *Brassica oleracea*
DESCRIPTION: arginine decarboxylase. spe2.
- 25 AAC68516.1 AF045671 *Brassica nigra*
DESCRIPTION: arginine decarboxylase. spe2.
- 30 AAC68512.1 AF045667 *Carica papaya*
DESCRIPTION: arginine decarboxylase. spe2.
- 35 CAA40137.1 X56802 *Avena sativa*
DESCRIPTION: arginine decarboxylase. spel.
- 40 AAD24801.1 AF132498 *Brassica napus*
DESCRIPTION: arginine decarboxylase. ADC.
- 45 BAA21617.1 AB005880 *Nicotiana tabacum*
DESCRIPTION: arginine decarboxylase.
- AAB82607.1 AF026809 *Ipomoea nil*
DESCRIPTION: arginine decarboxylase. adc.
- 377
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AAG22606.1 AF258809 Lycopersicon esculentum
DESCRIPTION: aldehyde oxidase. AO2. molybdenum cofactor-binding enzyme.

5

BAA23226.1 D88451 Zea mays
DESCRIPTION: aldehyde oxidase. zmAO-1.

10 AAG22607.1 AF258810 Lycopersicon esculentum
DESCRIPTION: aldehyde oxidase. AO3. molybdenum cofactor-binding enzyme.

15 AAG22605.1 AF258808 Lycopersicon esculentum
DESCRIPTION: aldehyde oxidase. AO1. molybdenum cofactor-binding enzyme.

20 BAA23227.1 D88452 Zea mays
DESCRIPTION: aldehyde oxidase-2. zmAO-2. putative.

25 AAB41742.1 U82559 Lycopersicon esculentum
DESCRIPTION: aldehyde oxidase 1 homolog. TAO1. has sequence properties of
the molybdenum cofactor containing the hydroxylase genes aldehyde oxidase and xanthine dehydrogenase; belongs to a multigene family.

30

AAG22608.1 AF259793 Lycopersicon esculentum
DESCRIPTION: aldehyde oxidase. AO1. molybdenum cofactor-binding enzyme.

35

AAB41741.1 U82558 Lycopersicon esculentum
DESCRIPTION: aldehyde oxidase 1 homolog. TAO1. has sequence properties of
the molybdenum cofactor containing the hydroxylase genes aldehyde oxidase and xanthine dehydrogenase; belongs to a multigene family.

40

378

45 BAB21211.1 AP002913 Oryza sativa
DESCRIPTION: putative DNA binding protein RAV2. P0480E02.17.

BAB21218.1 AP002913 *Oryza sativa*
DESCRIPTION: putative DNA binding protein RAV2. P0480E02.24.

5

BAA90643.1 AP001129 *Oryza sativa*
DESCRIPTION: Similar to *Arabidopsis thaliana* chromosome II BAC F11F19
genomic sequence, putative DNA-binding protein RAV2. (AC007017).

10

BAA85426.1 AP000616 *Oryza sativa*
DESCRIPTION: similar to putative DNA-binding protein RAV2 (AC007017).

380

15

CAB65369.1 AJ250832 *Pisum sativum*
DESCRIPTION: germin-like protein. ger1.

20

AAF03355.1 AF132671 *Nicotiana plumbaginifolia*
DESCRIPTION: nectarin I precursor. NEC1. germin-like protein.

25

AAD38298.1 AC007789 *Oryza sativa*
DESCRIPTION: putative oxalate oxidase (germin protein).
OSJNBa0049B20.25.

30

BAB18339.1 AP002865 *Oryza sativa*
DESCRIPTION: putative germin protein. P0034C11.30. contains EST
C97263(C53484).

35

BAA25197.1 AB012138 *Lycopersicon esculentum*
DESCRIPTION: adaptation to Mn-deficiency. germin-like protein. Mdip1.

40

AAC78470.1 AF067731 *Solanum tuberosum*
DESCRIPTION: germin-like protein. OXAOXA. similar to oxalate oxidase.

45

AAC04835.1 AF032974 *Oryza sativa*
DESCRIPTION: germin-like protein 4. GER4. similar to wheat and barley
oxalate oxidase.

BAB39980.1 AP003020 Oryza sativa
DESCRIPTION: probable germin protein 4. P0498A12.8. contains ESTs
AU101991(S4037),AU070167(R0031).

5

BAB39965.1 AP003018 Oryza sativa
DESCRIPTION: probable germin protein 4. OSJNBa0004B13.19. contains
ESTs
AU101991(S4037),AU070167(R0031).

10

AAC04833.1 AF032972 Oryza sativa
DESCRIPTION: germin-like protein 2. GER2. similar to wheat and barley
oxalate oxidase.

15

AAG00425.1 AF250933 Hordeum vulgare
DESCRIPTION: germin A. GerA. apoplastic protein; contains prepeptide for
targeting into the cell wall.

20

AAD43972.1 AF141879 Oryza sativa
DESCRIPTION: germin-like protein 2 precursor. RGLP2. similar to barley
epidermis/papilla-specific oxalate oxidase-like protein.

25

AAD43973.1 AF141880 Oryza sativa
DESCRIPTION: germin-like protein 1 precursor. RGLP1. similar to barley
epidermis/papilla-specific oxalate oxidase-like protein.

30

AAD43971.1 AF141878 Oryza sativa
DESCRIPTION: germin-like protein 1 precursor. RGLP1. similar to barley
epidermis/papilla-specific oxalate oxidase-like protein.

35

CAB55559.1 AJ237943 Triticum aestivum
DESCRIPTION: germin-like protein. glp2b.

40

CAB55558.1 AJ237942 Triticum aestivum
DESCRIPTION: germin-like protein. glp2a.

45

AAC04837.1 AF032976 Oryza sativa
DESCRIPTION: germin-like protein 6. GER6. similar to wheat and barley

oxalate oxidase.

- 5 AAC04832.1 AF032971 *Oryza sativa*
DESCRIPTION: germin-like protein 1. GER1. similar to wheat and barley
oxalate oxidase.
- 10 CAA63659.1 X93171 *Hordeum vulgare*
DESCRIPTION: oxalate oxidase-like protein or germin-like protein.
- 15 CAB55394.1 AL117264 *Oryza sativa*
DESCRIPTION: zwh0010.1. similar to Arabidopsis germin-like protein 6
(AF032976); Method: conceptual translation with partial peptide
sequencing.
- 20 AAB97470.1 AF042489 *Oryza sativa*
DESCRIPTION: germin-like protein 16. glp16.
- 25 AAC25777.1 AF072694 *Oryza sativa*
DESCRIPTION: germin-like protein 7. GER7. similar to wheat and barley
oxalate oxidase.
- 30 AAG00427.1 AF250935 *Hordeum vulgare*
DESCRIPTION: germin F. GerF. apoplastic protein; contains prepeptide for
targeting into the cell wall.
- 35 AAG00426.1 AF250934 *Hordeum vulgare*
DESCRIPTION: germin B. GerB. apoplastic protein; contains prepeptide for
targeting into the cell wall.
- 40 BAA78563.1 AB024338 *Atriplex lentiformis*
DESCRIPTION: germin-like protein.
- 45 AAA20245.1 U01963 *Hordeum vulgare*
DESCRIPTION: germin subunit.
- AAG00428.1 AF250936 *Hordeum vulgare*

DESCRIPTION: germin D. GerD. apoplastic protein; contains prepeptide for targeting into the cell wall.

5 AAC99473.1 AF039201 *Pinus caribaea*
DESCRIPTION: germin-like protein. PcGER1.

10 AAC04834.1 AF032973 *Oryza sativa*
DESCRIPTION: germin-like protein 3. GER3. similar to wheat and barley oxalate oxidase.

15 AAA34271.1 M63224 *Triticum aestivum*
DESCRIPTION: germin. germin 9f-3.8.

20 AAC05146.1 AF049065 *Pinus radiata*
DESCRIPTION: germin-like protein. PRGer1.

25 AAA34268.1 M21962 *Triticum aestivum*
DESCRIPTION: germin protein precursor.

30 AAA34270.1 M63223 *Triticum aestivum*
DESCRIPTION: germin. germin 9f-2.8.

35 CAA71052.1 Y09917 *Triticum aestivum*
DESCRIPTION: germin homolog. pSBGer3.

AAG00429.1 AF250937 *Hordeum vulgare*
DESCRIPTION: germin E. GerE. apoplastic protein.

40 BAA86880.1 AB028454 *Barbula unguiculata*
DESCRIPTION: germin-like protein.

CAB65370.1 AJ250833 *Pisum sativum*
DESCRIPTION: germin-like protein. ger2a. 1st variant of this clone.

45 AAA33030.1 M93041 *Mesembryanthemum crystallinum*

DESCRIPTION: germin-like protein. germin-like protein.

CAB65371.1 AJ250834 Pisum sativum

5 DESCRIPTION: germin-like protein. ger2b. 2nd variant of the clone PsGER2.

CAA71050.1 Y09915 Triticum aestivum

10 DESCRIPTION: germin homolog. pSBGer1.

CAA71051.1 Y09916 Triticum aestivum

DESCRIPTION: germin homolog. pSBGer2.

15

AAA86365.1 U21743 Brassica napus

DESCRIPTION: germin-like protein. similar to product encoded by GenBank
Accession Number X84786.

20

CAC34417.1 AJ311624 Pisum sativum

DESCRIPTION: Germin-like protein. glp3.

389

25

CAA04703.1 AJ001370 Olea europaea

DESCRIPTION: cytochrome b5. cytb5-2.

30

AAA32990.1 M87514 Brassica oleracea

DESCRIPTION: cytochrome b-5. cytochrome b-5.

CAA50575.1 X71441 Nicotiana tabacum

35 DESCRIPTION: cytochrome b5.

CAA53366.1 X75670 Oryza sativa

40 DESCRIPTION: cytochrome b5.

CAA04702.1 AJ001369 Olea europaea

DESCRIPTION: cytochrome b5. cytb5-1.

45

AAA62621.1 L22209 Cuscuta reflexa

DESCRIPTION: associated with cytokinin-induced haustoria formation in
Cuscuta reflexa. cytochrome b5.

5 AAC49701.1 U79011 *Borago officinalis*
DESCRIPTION: haem-binding protein. cytochrome b5.

10 CAA56318.1 X80008 *Nicotiana tabacum*
DESCRIPTION: cytochrome b5.

15 CAA48240.1 X68140 *Nicotiana tabacum*
DESCRIPTION: cytochrome b5.

20 AAD10774.1 AF098510 *Petunia x hybrida*
DESCRIPTION: involved in anthocyanin biosynthesis. cytochrome b5 DIF-F.
diff. required for full activity of flavonoid 3',5' hydroxylase.

25 AAF60299.1 AF233640 *Petunia x hybrida*
DESCRIPTION: involved in anthocyanin biosynthesis. cytochrome b5 DIF-F.
diff.

30 CAA11033.1 AJ222981 *Physcomitrella patens*
DESCRIPTION: delta6-acyl-lipid desaturase. des6. des6 represents a fusion
between a C-terminal desaturase with a cytochrome b5-related part and a
N-terminal extension.

392

35 AAK28303.1 AF346431 *Nicotiana tabacum*
DESCRIPTION: phenylpropanoid:glucosyltransferase 1. togt1.
glucosyltransferase.

40 AAB36653.1 U32644 *Nicotiana tabacum*
DESCRIPTION: immediate-early salicylate-induced glucosyltransferase.
IS5a.

45 BAB17061.1 AP002523 *Oryza sativa*
DESCRIPTION: putative glucosyl transferase. P0013F10.7. contains EST
C73149(E2992).

5 AAB36652.1 U32643 *Nicotiana tabacum*
DESCRIPTION: immediate-early salicylate-induced glucosyltransferase.
IS10a.

10 AAK28304.1 AF346432 *Nicotiana tabacum*
DESCRIPTION: phenylpropanoid:glucosyltransferase 2. togt2.
glucosyltransferase.

15 BAB17059.1 AP002523 *Oryza sativa*
DESCRIPTION: putative glucosyl transferase. P0013F10.5.

20 BAB17060.1 AP002523 *Oryza sativa*
DESCRIPTION: putative glucosyl transferase. P0013F10.6.

CAA59450.1 X85138 *Lycopersicon esculentum*
DESCRIPTION: twi1. homologous to glucosyltransferases.

25 CAB56231.1 Y18871 *Dorotheanthus bellidiformis*
DESCRIPTION: betanidin-5-O-glucosyltransferase.

30 BAA83484.1 AB031274 *Scutellaria baicalensis*
DESCRIPTION: UDP-glucose: flavonoid 7-O-glucosyltransferase. ufgt.

35 AAB48444.1 U82367 *Solanum tuberosum*
DESCRIPTION: UDP-glucose glucosyltransferase.

BAA36410.1 AB012114 *Vigna mungo*
DESCRIPTION: UDP-glycose:flavonoid glycosyltransferase. UFGlyT.

40 CAA54610.1 X77460 *Manihot esculenta*
DESCRIPTION: UTP-glucose glucosyltransferase. CGT4.

45 CAB88666.1 AJ400861 *Cicer arietinum*
DESCRIPTION: flavonoid glycosyltransferase. putative UDP-glycose.

- AAK16180.1 AC079887 *Oryza sativa*
 DESCRIPTION: putative glucosyltransferase. OSJNBa0040E01.21.
 5
- AAD51778.1 AF116858 *Phaseolus vulgaris*
 DESCRIPTION: utilizes UDPX as the sugar donor and catalyzes the formation
 of O-xylosylzeatin from zeatin. zeatin O-xylosyltransferase. ZOX1.
 10
- AAD04166.1 AF101972 *Phaseolus lunatus*
 DESCRIPTION: catalyzes formation of O-glucosylzeatin from zeatin and
 UDPG; catalyzes formation of O-xylosylzeatin from zeatin and UDPX. zeatin
 O-glucosyltransferase. ZOG1. cytokinin O-glucosyltransferase.
 15
- BAA89009.1 AB027455 *Petunia x hybrida*
 DESCRIPTION: anthocyanin 5-O-glucosyltransferase. PH1.
 20
- CAC09351.1 AL442007 *Oryza sativa*
 DESCRIPTION: putative glucosyltransferase. H0212B02.7.
 25
- AAB62270.1 AF006081 *Solanum berthaultii*
 DESCRIPTION: UDPG glucosyltransferase. PLGT.
 30
- AAK16172.1 AC079887 *Oryza sativa*
 DESCRIPTION: putative glucosyltransferase. OSJNBa0040E01.14.
 35
- AAF61647.1 AF190634 *Nicotiana tabacum*
 DESCRIPTION: UDP-glucose:salicylic acid glucosyltransferase. SA-GTase.
 40
- CAA54612.1 X77462 *Manihot esculenta*
 DESCRIPTION: UTP-glucose glucosyltransferase. CGT5.
 45
- AAK16181.1 AC079887 *Oryza sativa*
 DESCRIPTION: putative glucosyltransferase. OSJNBa0040E01.16.
- AAK16178.1 AC079887 *Oryza sativa*

DESCRIPTION: putative glucosyltransferase. OSJNBa0040E01.5.

BAA36412.1 AB012116 Vigna mungo

5 DESCRIPTION: UDP-glucose:flavonoid glucosyltransferase. UFGlyT.

AAK16175.1 AC079887 Oryza sativa

10 DESCRIPTION: putative glucosyltransferase. OSJNBa0040E01.15.

AAF98390.1 AF287143 Brassica napus

15 DESCRIPTION: catalyzes the transfer of glucose from UDP-glucose to sinapate and some other hydroxycinnamates (4-coumarate, caffeate, ferulate). UDP-glucose:sinapate glucosyltransferase. SGT1. SGT.

BAA36423.1 AB013598 Verbena x hybrida

20 DESCRIPTION: UDP-glucose:anthocyanin 5-O-glucosyltransferase. HGT8.

AAF17077.1 AF199453 Sorghum bicolor

25 DESCRIPTION: UDP-glucose glucosyltransferase.
UDP-glucose:p-hydroxymandelonitrile-o- glucosyltransferase.

BAA93039.1 AB033758 Citrus unshiu

30 DESCRIPTION: limonoid UDP-glucosyltransferase. LGTase.

BAB17176.1 AP002843 Oryza sativa

DESCRIPTION: putative UTP-glucose glucosyltransferase. P0407B12.13.

35 BAB17182.1 AP002843 Oryza sativa

DESCRIPTION: putative UTP-glucose glucosyltransferase. P0407B12.19.

BAA89008.1 AB027454 Petunia x hybrida

40 DESCRIPTION: anthocyanidin 3-O-glucosyltransferase. PGT8.

CAA54558.1 X77369 Solanum melongena

45 DESCRIPTION: glycosyl transferase. GT.

- CAA54611.1 X77461 *Manihot esculenta*
DESCRIPTION: UTP-glucose glucosyltransferase. CGT2.
- 5 CAA54609.1 X77459 *Manihot esculenta*
DESCRIPTION: UTP-glucose glucosyltransferase. CGT1.
- 10 BAA12737.1 D85186 *Gentiana triflora*
DESCRIPTION: UDP-glucose:flavonoid-3-glucosyltransferase.
- 15 AAD21086.1 AF127218 *Forsythia x intermedia*
DESCRIPTION: adds glucose residue to position 3 of flavonoid compounds.
flavonoid 3-O-glucosyltransferase. UFGT.
- 20 AAG25643.1 AF303396 *Phaseolus vulgaris*
DESCRIPTION: UDP-glucosyltransferase HRA25. putative; defense associated.
- 25 BAA36411.1 AB012115 *Vigna mungo*
DESCRIPTION: UDP-glycose:flavonoid glycosyltransferase. UFGlyT.
- 30 BAA19155.1 AB000623 *Nicotiana tabacum*
DESCRIPTION: glucosyl transferase. JIGT.
- 35 AAD55985.1 AF165148 *Petunia x hybrida*
DESCRIPTION: catalyzes the penultimate step of flavonol
glucosylgalactoside biosynthesis from UDP-galactose and flavonol aglycones
in petunia pollen. UDP-galactose:flavonol 3-O-galactosyltransferase.
F3galtase.
- 40 CAA54613.1 X77463 *Manihot esculenta*
DESCRIPTION: UTP-glucose glucosyltransferase. CGT6.
- 45 BAA36421.1 AB013596 *Perilla frutescens*
DESCRIPTION: UDP-glucose:anthocynin 5-O-glucosyltransferase. PF3R4.
- 45 BAA19659.1 AB002818 *Perilla frutescens*
DESCRIPTION: flavonoid 3-O-glucosyltransferase. UDP glucose.

AAB81683.1 AF000372 *Vitis vinifera*
 DESCRIPTION: UDP glucose:flavonoid 3-o-glucosyltransferase.
 5

BAB41025.1 AB047098 *Vitis vinifera*
 DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. FIUFGT1.

10 BAB41023.1 AB047096 *Vitis vinifera*
 DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. AIUFGT1.

393
 15 -----
 CAB56756.1 AJ011589 *Pisum sativum*
 DESCRIPTION: 5,10-methylenetetrahydrofolate dehydrogenase:
 5,10-methenyltetrahydrofolate cyclohydrolase. bifunctional enzyme.

20 AAD01907.1 AF030516 *Pisum sativum*
 DESCRIPTION: 5,10-methylenetetrahydrofolate
 dehydrogenase-5,10-methenyltetrahydrofolate cyclohydrolase. bifunctional
 protein; 31.3 kDa protein.

25 AAG48834.1 AC084218 *Oryza sativa*
 DESCRIPTION: similar to *Pisum sativum* methylenetetrahydrofolate
 dehydrogenase (NADP+) (EC 1.5.1.5) (AF030516).

30 406

 AAD46491.1 AF135014 *Zea mays*
 DESCRIPTION: dihydrolipoamide S-acetyltransferase. pyruvate dehydrogenase
 35 complex E2 subunit.

BAA90623.1 AP001129 *Oryza sativa*
 DESCRIPTION: ESTs AU033004(S0924),C74754(E50863) correspond to a
 40 region
 of the predicted gene.; Similar to Rat mRNA for dihydrolipoamide
 acetyltransferase. (D10655).

45 BAA77024.1 AB026124 *Lithospermum erythrorhizon*
 DESCRIPTION: dihydrolipoamide acetyltransferase.

407

AAF69017.1 AF261654 *Dianthus caryophyllus*

5 DESCRIPTION: ethylene-insensitive 3-like protein 1. EIL1. EIN3-like protein.

CAC09582.1 AJ298994 *Fagus sylvatica*

10 DESCRIPTION: gibberellic acid (GA3)-induced. ethylene insensitive (EIN3/EIL)-like transcription regulator. ein11.

AAG00419.1 AF247568 *Nicotiana tabacum*

15 DESCRIPTION: EIN3. component in ethylene signal transduction pathway.

408

AAC15870.1 AF002016 *Cucurbita* sp.

20 DESCRIPTION: acyl CoA oxidase homolog.

AAF14635.1 AF202987 *Petroselinum crispum*

25 DESCRIPTION: acyl-CoA oxidase. ACO. peroxisomal acyl-CoA oxidase.

AAB67883.1 U66299 *Phalaenopsis* sp. 'True Lady'

30 DESCRIPTION: acyl-CoA oxidase homolog.

AAC32108.1 AF051203 *Picea mariana*

35 DESCRIPTION: acyl-CoA oxidase homolog. Sb06. similar to *Phalaenopsis* sp. acyl-CoA oxidase homolog encoded by GenBank Accession Number U66299.

CAA04688.1 AJ001341 *Hordeum vulgare*

40 DESCRIPTION: putative acyl-CoA oxidase.

BAB08201.1 AP002539 *Oryza sativa*

45 DESCRIPTION: ESTs AU056822(S20908),C26441(C12328), C28477(C61243) correspond to a region of the predicted gene. Similar to *Arabidopsis thaliana* putative acyl-coA dehydrogenase (AF049236).

BAA96762.1 AP002521 *Oryza sativa*

DESCRIPTION: ESTs AU056822(S20908),C26441(C12328), C28477(C61243) correspond to a region of the predicted gene. Similar to Arabidopsis thaliana putative acyl-coA dehydrogenase (AF049236).

5

CAB55555.1 AJ010946 Pisum sativum
DESCRIPTION: auxin binding protein (ABP44). abp44/ivdh. has both auxin binding capability and enzymatic activity; isovaleryl-CoA Dehydrogenase.

10

CAB55554.1 AJ010945 Pisum sativum
DESCRIPTION: auxin binding protein (ABP44). abp44/ivdh. has both auxin binding capability and enzymatic activity; Isovaleryl-CoA Dehydrogenase.

15

CAC08233.1 AJ278987 Solanum tuberosum
DESCRIPTION: leucine catabolism. isovaleryl-CoA dehydrogenase. ivd1.

20

CAC08234.1 AJ278988 Solanum tuberosum
DESCRIPTION: leucine catabolism. isovaleryl-CoA dehydrogenase. ivd2.

25

AAF02449.1 AF127432 Picea abies
DESCRIPTION: acyl-CoA oxidase homolog. Sb06.

30

AAF02451.1 AF127434 Picea abies
DESCRIPTION: acyl-CoA oxidase homolog. Sb06.

35

AAF02450.1 AF127433 Picea abies
DESCRIPTION: acyl-CoA oxidase homolog. Sb06.

40

AAC32152.1 AF051733 Picea mariana
DESCRIPTION: acyl-CoA oxidase homolog. Sb06.

45

CAA58874.1 X84055 Hordeum vulgare
DESCRIPTION: mammalian acyl CoA oxidase homologous. cdr29. putative.

 CAB64356.1 AJ251511 *Populus tremula* x *Populus tremuloides*
 DESCRIPTION: mitochondrial oxidase. alternative oxidase. aox1.

5

AAC60576.1 S71335 Mitochondrion *Nicotiana tabacum*
 DESCRIPTION: alternative oxidase. Aox1. This sequence comes from Fig. 1;
 AOX.

10

CAA56163.1 X79768 *Nicotiana tabacum*
 DESCRIPTION: alternative oxidase. aox.

15

CAA48653.1 X68702 *Glycine max*
 DESCRIPTION: alternative oxidase. aox1. putative.

20

AAC35354.1 AF083880 *Glycine max*
 DESCRIPTION: alternative oxidase precursor. Aox1. AOX1; terminal oxidase
 of mitochondrial electron transport chain.

25

BAB21500.1 AB055060 *Catharanthus roseus*
 DESCRIPTION: alternative oxidase.

30

BAA23803.1 AB009395 *Catharanthus roseus*
 DESCRIPTION: alternative oxidase.

35

BAA86963.1 AB007452 *Oryza sativa*
 DESCRIPTION: alternative oxidase. Aox1(Ao1-1).

40

BAA28773.1 AB004864 *Oryza sativa*
 DESCRIPTION: alternative oxidase. AOX1a.

BAA28772.1 AB004813 *Oryza sativa*
 DESCRIPTION: alternative oxidase. AOX1a.

45

CAA78823.1 Z15117 *Sauromatum guttatum*
 DESCRIPTION: salicylic acid-inducible alternative oxidase. aox1.

- 5 AAA34048.1 M60330 Sauromatum guttatum
DESCRIPTION: alternative oxidase protein. aox1.
- AAD51707.1 AF174004 Triticum aestivum
DESCRIPTION: alternative oxidase.
- 10 CAA55892.1 X79329 Mangifera indica
DESCRIPTION: alternative oxidase. AOMI 1.
- 15 CAB72441.1 AJ271889 Populus tremula x Populus tremuloides
DESCRIPTION: mitochondrial oxidase. alternative oxidase. aox1b.
- 20 AAB97285.1 U87906 Glycine max
DESCRIPTION: alternative oxidase. Aox2.
- 25 BAA28771.1 AB004813 Oryza sativa
DESCRIPTION: alternative oxidase. AOX1b.
- BAA28774.1 AB004865 Oryza sativa
DESCRIPTION: alternative oxidase. AOX1b.
- 30 AAB97286.1 U87907 Glycine max
DESCRIPTION: alternative oxidase. Aox3.
- 35 AAB97839.1 AF040566 Zea mays
DESCRIPTION: alternative oxidase. Aox.
- 40 AAG33634.1 AF314255 Chlamydomonas reinhardtii
DESCRIPTION: alternative oxidase 2. AOX2.
- 45 AAG02081.1 AF285187 Chlamydomonas reinhardtii
DESCRIPTION: alternative oxidase. AOX2.

- AAG33633.1 AF314254 *Chlamydomonas reinhardtii*
DESCRIPTION: alternative oxidase 1. AOX1.
- 5 AAC05743.2 AF047832 *Chlamydomonas reinhardtii*
DESCRIPTION: alternative oxidase. AOX1.
- 10 BAA23725.1 AB009087 *Chlamydomonas* sp. W80
DESCRIPTION: alternative oxidase.
- 15 AAC34192.1 S81466 *Glycine max*
DESCRIPTION: alternative oxidase Aox1 precursor. Aox1. This sequence comes from Fig. 1.
- 20 AAG18450.1 AF302932 *Lycopersicon esculentum*
DESCRIPTION: plastid quinol oxidase.
- 25 AAG18449.1 AF302931 *Lycopersicon esculentum*
DESCRIPTION: plastid quinol oxidase.
- AAG02287.1 AF177980 *Lycopersicon esculentum*
DESCRIPTION: plastid terminal oxidase. PTOX.
- 30 AAG02286.1 AF177979 *Lycopersicon esculentum*
DESCRIPTION: plastid terminal oxidase. PTOX.
- 35 AAG02288.1 AF177981 *Capsicum annuum*
DESCRIPTION: plastid terminal oxidase. PTOX.
- 40 AAB36072.1 S81470 *Glycine max*
DESCRIPTION: Aox2. Aox2. alternative oxidase 2; This sequence comes from Fig. 1.
- 45 AAC35554.2 AF085174 *Oryza sativa*
DESCRIPTION: oxidase. IM1.

- AAG00450.1 AF274001 *Triticum aestivum*
DESCRIPTION: oxidase. IM1.
- 410
- 5 -----
- CAA69600.1 Y08292 *Nicotiana plumbaginifolia*
DESCRIPTION: NADH glutamate dehydrogenase. GDH A.
- 10 CAB94836.1 AJ277949 *Nicotiana plumbaginifolia*
DESCRIPTION: NADH glutamate dehydrogenase. gdhA.
- 15 CAC18730.1 AJ303070 *Vitis vinifera*
DESCRIPTION: NADH glutamate dehydrogenase. gdhA.
- 20 CAA60507.1 X86924 *Vitis vinifera*
DESCRIPTION: glutamate dehydrogenase. GDH.
- 25 BAA08445.1 D49475 *Zea mays*
DESCRIPTION: glutamate dehydrogenase.
- AAB51596.1 U93561 *Zea mays*
DESCRIPTION: glutamate dehydrogenase. GDH1. wild type.
- 30 AAB51595.1 U93560 *Zea mays*
DESCRIPTION: glutamate dehydrogenase mutant. GDH1. mutant allele.
- 35 CAB94837.1 AJ277950 *Nicotiana plumbaginifolia*
DESCRIPTION: NADH-glutamate dehydrogenase. gdhB.
- 40 CAA09478.1 AJ011096 *Asparagus officinalis*
DESCRIPTION: glutamate dehydrogenase. gdhb.
- 45 CAA69601.2 Y08293 *Nicotiana plumbaginifolia*
DESCRIPTION: NADH glutamate dehydrogenase. GDH B.
- AAB39508.1 U48695 *Lycopersicon esculentum*

DESCRIPTION: glutamate dehydrogenase. legdh1.

CAA09456.1 AJ011006 *Asparagus officinalis*
5 DESCRIPTION: NADH glutamate dehydrogenase. gdhA.

CAA41635.1 X58831 *Chlorella sorokiniana*
10 DESCRIPTION: glutamate dehydrogenase (NADP+). gdhANC. There are other
coding exons before the first exon given for this gene.

CAA41636.1 X58832 *Chlorella sorokiniana*
15 DESCRIPTION: glutamate dehydrogenase (NADP+). gdhANC.
412

CAA65456.2 X96681 *Oryza sativa*
20 DESCRIPTION: transcription factor. DNA-binding protein. Oshox1.
homeodomain leucine zipper gene.

AAK00416.1 AC069324 *Oryza sativa*
25 DESCRIPTION: Putative DNA-binding protein. OSJNBa0071K19.2.

BAA05622.1 D26573 *Daucus carota*
30 DESCRIPTION: transcriptional regulator. DNA-binding protein. homeodomain
at nt 585-764; leucine zipper at nt 765-851.

BAA05625.1 D26576 *Daucus carota*
35 DESCRIPTION: transcriptional regulator. DNA-binding protein. homeodomain
at nt 300-479; leucine zipper at nt 480-587.

BAA21017.1 D26578 *Daucus carota*
40 DESCRIPTION: transcriptional regulator. DNA-binding protein. homeodomain
at nt 761-940; leucine zipper at nt 941-1048.

BAA05624.1 D26575 *Daucus carota*
45 DESCRIPTION: transcriptional regulator. DNA-binding protein. homeodomain
at nt 520-699; leucine zipper at nt 700-805.

BAA05623.1 D26574 *Daucus carota*
 DESCRIPTION: transcriptional regulator. DNA-binding protein. homeodomain
 at nt 498-677; leucine zipper at nt 678-785.

5 414

 BAA95814.1 AP002069 *Oryza sativa*
 DESCRIPTION: ESTs AU082579(S2069),D40238(S2069) correspond to a
 region of
 10 the predicted gene. Similar to *Arabidopsis thaliana* vesicle-associated
 membrane protein 7C; synaptobrevin 7C. (AF025332).

415

 15 CAA45025.1 X63431 *Rauvolfia mannii*
 DESCRIPTION: strictosidine synthase. str1.

CAA68725.1 Y00756 *Rauvolfia serpentina*
 20 DESCRIPTION: strictosidine synthase.

CAA44208.1 X62334 *Rauvolfia serpentina*
 25 DESCRIPTION: strictosidine synthase. str1.

CAA37671.1 X53602 *Catharanthus roseus*
 DESCRIPTION: strictosidine synthase precursor.

30 CAA71255.1 Y10182 *Catharanthus roseus*
 DESCRIPTION: strictosidine synthase. str1.

35 CAA43936.1 X61932 *Catharanthus roseus*
 DESCRIPTION: strictosidine synthase. sss.

AA775751.1 AF261141 *Lycopersicon esculentum*
 40 DESCRIPTION: putative strictosidine synthase.

CAB53484.1 AJ245900 *Oryza sativa*
 45 DESCRIPTION: CAA303711.1 protein. q3037.11. Similar to strictosidine
 synthase 3 precursor.

418

AAG22607.1 AF258810 Lycopersicon esculentum

5 DESCRIPTION: aldehyde oxidase. AO3. molybdenum cofactor-binding enzyme.

AAG22606.1 AF258809 Lycopersicon esculentum

10 DESCRIPTION: aldehyde oxidase. AO2. molybdenum cofactor-binding enzyme.

AAG22605.1 AF258808 Lycopersicon esculentum

15 DESCRIPTION: aldehyde oxidase. AO1. molybdenum cofactor-binding enzyme.

BAA23227.1 D88452 Zea mays

20 DESCRIPTION: aldehyde oxidase-2. zmAO-2. putative.

BAA23226.1 D88451 Zea mays

25 DESCRIPTION: aldehyde oxidase. zmAO-1.

AAB41742.1 U82559 Lycopersicon esculentum

30 DESCRIPTION: aldehyde oxidase 1 homolog. TAO1. has sequence properties of the molybdenum cofactor containing the hydroxylase genes aldehyde oxidase and xanthine dehydrogenase; belongs to a multigene family.

AAG22608.1 AF259793 Lycopersicon esculentum

35 DESCRIPTION: aldehyde oxidase. AO1. molybdenum cofactor-binding enzyme.

AAB41741.1 U82558 Lycopersicon esculentum

40 DESCRIPTION: aldehyde oxidase 1 homolog. TAO1. has sequence properties of the molybdenum cofactor containing the hydroxylase genes aldehyde oxidase and xanthine dehydrogenase; belongs to a multigene family.

421

45

BAA13635.1 D88530 Spinacia oleracea

DESCRIPTION: serine acetyltransferase.

5 BAA13634.1 D88529 *Spinacia oleracea*
DESCRIPTION: serine acetyltransferase.

10 BAA93050.1 AB040502 *Allium tuberosum*
DESCRIPTION: serine acetyltransferase. ASAT5.

BAA08479.1 D49535 *Citrullus lanatus*
DESCRIPTION: serine acetyltransferase.

15 BAA12843.1 D85624 *Citrullus lanatus*
DESCRIPTION: serine acetyltransferase. Sat.

20 BAA21827.1 AB006530 *Citrullus lanatus*
DESCRIPTION: serine acetyltransferase. Sat.

25 AAF19000.1 AF212156 *Allium cepa*
DESCRIPTION: serine acetyltransferase.

422

30 BAA05079.1 D26086 *Petunia x hybrida*
DESCRIPTION: zinc-finger protein.

35 CAB77055.1 Y18788 *Medicago sativa*
DESCRIPTION: putative TFIIIA (or kruppel)-like zinc finger protein.

AAD26942.1 AF119050 *Datisca glomerata*
DESCRIPTION: zinc-finger protein 1. zfp1. DgZFP1.

40 AAB39638.1 U68763 *Glycine max*
DESCRIPTION: putative transcription factor. SCOF-1. scof-1. zinc-finger
protein.

45 AAC06243.1 AF053077 *Nicotiana tabacum*

DESCRIPTION: transcription factor. osmotic stress-induced zinc-finger protein. zfp.

5 BAA05077.1 D26084 Petunia x hybrida
DESCRIPTION: zinc-finger DNA binding protein.

10 BAA05076.1 D26083 Petunia x hybrida
DESCRIPTION: zinc-finger DNA binding protein.

15 BAA05078.1 D26085 Petunia x hybrida
DESCRIPTION: zinc-finger DNA binding protein.

AAK01713.1 AF332876 Oryza sativa
DESCRIPTION: zinc finger transcription factor ZF1.

20 AAB53260.1 U76554 Brassica rapa
DESCRIPTION: transcription factor. zinc-finger protein-1. BR42.

25 AAB53261.1 U76555 Brassica rapa
DESCRIPTION: zinc-finger protein BcZFP1. BcZFP1(3-2z).

30 BAA96070.1 AB035132 Petunia x hybrida
DESCRIPTION: C2H2 zinc-finger protein ZPT2-10. PEThy;ZPT2-10.

35 BAA21919.1 AB006597 Petunia x hybrida
DESCRIPTION: ZPT2-10. C2H2 zinc finger protein, 2 finger.

BAA96071.1 AB035133 Petunia x hybrida
DESCRIPTION: C2H2 zinc-finger protein ZPT3-3. ZPT3-3.

40 BAA21927.1 AB006605 Petunia x hybrida
DESCRIPTION: ZPT3-3. C2H2 zinc finger protein, 3 finger.

45 BAA19112.1 AB000453 Petunia x hybrida
DESCRIPTION: PEThy;ZPT3-1. Cys(2) His(2) zinc finger protein, 3 fingers.

- 5 BAA21928.1 AB006606 *Petunia x hybrida*
DESCRIPTION: ZPT4-4. C2H2 zinc finger protein, 4 finger.
- 10 BAA21922.1 AB006600 *Petunia x hybrida*
DESCRIPTION: ZPT2-13. C2H2 zinc finger protein, 2finger.
- 15 BAA19114.1 AB000455 *Petunia x hybrida*
DESCRIPTION: PETHy;ZPT4-1. Cys(2) His(2) zinc finger protein, 4 fingers.
- 20 BAA21920.1 AB006598 *Petunia x hybrida*
DESCRIPTION: ZPT2-11. C2H2 zinc finger protein, 2finger.
- 25 BAA21921.1 AB006599 *Petunia x hybrida*
DESCRIPTION: ZPT2-12. C2H2 zinc finger protein, 2 finger.
- 30 BAA19110.1 AB000451 *Petunia x hybrida*
DESCRIPTION: PETHy;ZPT2-5. Cys(2) His(2) zinc finger protein, 2 fingers.
- 35 BAA21926.1 AB006604 *Petunia x hybrida*
DESCRIPTION: ZPT2-9. C2H2 zinc finger protein, 2 finger.
- 40 BAA21925.1 AB006603 *Petunia x hybrida*
DESCRIPTION: ZPT2-8. C2H2 zinc finger protein, 2 finger.
- 45 CAA60828.1 X87374 *Pisum sativum*
DESCRIPTION: putative zinc finger protein.
- 40 BAA19111.1 AB000452 *Petunia x hybrida*
DESCRIPTION: PETHy;ZPT2-6. Cys(2) His(2) zinc finger protein, 2 fingers.
- 45 BAA21923.1 AB006601 *Petunia x hybrida*
DESCRIPTION: ZPT2-14. C2H2 zinc finger protein, 2 finger.

- BAA21924.1 AB006602 *Petunia x hybrida*
DESCRIPTION: ZPT2-7. C2H2 zinc finger protein, 2finger.
- 5 BAA19113.1 AB000454 *Petunia x hybrida*
DESCRIPTION: PETHy;ZPT3-2. Cys(2) His(2) zinc finger protein, 3 fingers.
- 10 BAA19926.1 AB000456 *Petunia x hybrida*
DESCRIPTION: PETHy; ZPT4-2. C2H2 zinc finger protein, 4 finger.
- 423

- 15 AAC49815.1 U87257 *Daucus carota*
DESCRIPTION: 4-hydroxyphenylpyruvate dioxygenase.
- 20 CAA04245.1 AJ000693 *Hordeum vulgare*
DESCRIPTION: 4-hydroxyphenylpyruvate dioxygenase.
- 424

- 25 AAC72193.1 AF069909 *Zea mays*
DESCRIPTION: pyruvate dehydrogenase E1 beta subunit isoform 2.
- 30 AAC72192.1 AF069908 *Zea mays*
DESCRIPTION: pyruvate dehydrogenase E1 beta subunit isoform 1.
- AAC72194.1 AF069910 *Zea mays*
DESCRIPTION: pyruvate dehydrogenase E1 beta subunit isoform 3.
- 35 AAB01223.1 U56697 *Pisum sativum*
DESCRIPTION: pyruvate dehydrogenase E1beta.
- 40 AAC32149.1 AF051249 *Picea mariana*
DESCRIPTION: pyruvate dehydrogenase E1 beta subunit. Sb68.
- 45 AAF43837.1 AF166114 *Chloroplast Mesostigma viride*
DESCRIPTION: beta subunit of pyruvate dehydrogenase E1 component. odpB.

AAD22077.1 AF124755 *Pinus banksiana*
DESCRIPTION: pyruvate dehydrogenase E1 beta subunit. Sb68.

5 CAA75778.1 Y15782 *Capsicum annuum*
DESCRIPTION: transketolase 2.

AAB88295.1 AF024512 *Oryza sativa*
10 DESCRIPTION: CLA1 transketolase-like protein. CLA1. similar to
Arabidopsis CLA1 product; required for chloroplast development.

426

15 AAB53764.1 U96713 *Brassica rapa*
DESCRIPTION: aminoalcoholphosphotransferase. AAPT1.

AAD56040.1 AF183933 *Brassica rapa*
20 DESCRIPTION: aminoalcoholphosphotransferase. AAPT3.

AAC79507.1 U96439 *Pimpinella brachycarpa*
25 DESCRIPTION: aminoalcoholphosphotransferase. AAPTase.

AAA67719.1 U12735 *Glycine max*
DESCRIPTION: CDP-choline:diacylglycerol cholinephosphotransferase
activity and possibly CDP-ethanolamine: diacylglycerol
30 ethanolaminephosphotransferase activity. aminoalcoholphosphotransferase.
AAPT1.

427

35 CAA56313.1 X79992 *Avena sativa*
DESCRIPTION: putative pp70 ribosomal protein S6 kinase. Aspk11.

CAB89082.1 AJ277534 *Asparagus officinalis*
40 DESCRIPTION: S6 ribosomal protein kinase. pk1. putative.

AAK18843.1 AC082645 *Oryza sativa*
45 DESCRIPTION: putative protein kinase. OSJNBb0033N16.3.

- AAC05084.1 AF033097 *Avena sativa*
DESCRIPTION: NPH1-2. NPH1-2. putative serine/threonine protein kinase.
- 5 AAC05083.1 AF033096 *Avena sativa*
DESCRIPTION: NPH1-1. NPH1-1. putative serine/threonine protein kinase.
- 10 AAK13156.1 AC078829 *Oryza sativa*
DESCRIPTION: putative protein kinase. OSJNBa0026O12.14.
- 15 AAB88817.1 AF033263 *Zea mays*
DESCRIPTION: signal transduction for phototropism. nonphototropic hypocotyl 1. nph1. NPH1; putative serine/threonine kinase; similar to oat NPH1 proteins.
- 20 CAB82852.1 Z30329 *Mesembryanthemum crystallinum*
DESCRIPTION: protein kinase MK6.
- 25 BAB18104.1 AB042714 *Chlamydomonas reinhardtii*
DESCRIPTION: cyclic nucleotide dependent protein kinase. CL-PK1.
- 30 BAB18105.1 AB042715 *Chlamydomonas reinhardtii*
DESCRIPTION: cyclic nucleotide dependent protein kinase II. CL-PK2.
- BAA83689.1 AB011968 *Oryza sativa*
DESCRIPTION: OsPK7. OsPK7. protein kinase.
- 35 AAD31900.1 AF145482 *Mesembryanthemum crystallinum*
DESCRIPTION: putative serine/threonine protein kinase.
- 40 BAA92970.1 AP001551 *Oryza sativa*
DESCRIPTION: Similar to *Arabidopsis thaliana* chromosome 4 BAC clone F28A21 ; putative protein kinase. (AL035526).
- 45 BAA92972.1 AP001551 *Oryza sativa*
DESCRIPTION: ESTs AU056183(S20356),AU056881(S20950) correspond to a region of the predicted gene. Similar to *Arabidopsis thaliana* chromosome 4

BAC clone F6I18 ; putative protein kinase. (AL022198).

5 BAA83688.1 AB011967 Oryza sativa
DESCRIPTION: OsPK4. OsPK4. protein kinase.

10 AAF22219.1 AF141378 Zea mays
DESCRIPTION: protein kinase PK4. ZmPK4.

15 CAA73067.1 Y12464 Sorghum bicolor
DESCRIPTION: serine/threonine kinase. SNFL1.

20 BAA96628.1 AP002482 Oryza sativa
DESCRIPTION: ESTs D41739(S4522),AU055999(S20214),
AU057588(S21592
correspond to a region of the predicted gene. Similar to Sorghum bicolor
serine/threonine kinase (Y12465).

25 CAA89202.1 Z49233 Chlamydomonas eugametos
DESCRIPTION: calcium-stimulated protein kinase.

30 CAA73068.1 Y12465 Sorghum bicolor
DESCRIPTION: serine/threonine kinase. SNFL2.

35 BAA34675.1 AB011670 Triticum aestivum
DESCRIPTION: wpk4 protein kinase. wpk4.

40 CAA74646.1 Y14274 Sorghum bicolor
DESCRIPTION: putative serine/threonine protein kinase. SNFL3.

45 AAF06970.1 AF162662 Kalanchoe fedtschenkoi
DESCRIPTION: phosphoenolpyruvate carboxylase kinase. calcium-independent
protein kinase.

45 AAF06969.1 AF162661 Kalanchoe fedtschenkoi
DESCRIPTION: phosphoenolpyruvate carboxylase kinase. calcium-independent
protein kinase.

- CAA39936.1 X56599 *Daucus carota*
DESCRIPTION: calcium- dependent protein kinase. DcPK431.
- 5
- BAA99439.1 AP002743 *Oryza sativa*
DESCRIPTION: putative protein kinase. P0710E05.26. contains ESTs
C22394(C30013),C22393(C30013).
- 10
- BAA90814.1 AP001168 *Oryza sativa*
DESCRIPTION: ESTs AU030197(E50746),AU030196(E50746) correspond to
a
15 region of the predicted gene.; Similar to calcium-dependent
calmodulin-independent protein kinase CDPK (U90262).
- BAB12687.1 AP002746 *Oryza sativa*
20 DESCRIPTION: putative protein kinase. P0671B11.2. contains ESTs
C22394(C30013),C22393(C30013).
- AAB62693.1 AF004947 *Oryza sativa*
25 DESCRIPTION: protein kinase.
- CAA71142.1 Y10036 *Cucumis sativus*
30 DESCRIPTION: SNF1-related protein kinase.
- BAA05649.1 D26602 *Nicotiana tabacum*
DESCRIPTION: protein kinase.
- 35
- AAC25423.1 AF072908 *Nicotiana tabacum*
DESCRIPTION: calcium-dependent protein kinase. CDPK1.
- 40
- AAF19403.1 AF203481 *Lycopersicon esculentum*
DESCRIPTION: phosphoenolpyruvate carboxylase kinase. protein kinase;
member of Ca²⁺/CaM kinase family; lacks the autoinhibitory region and EF
hands.
- 45
- AAF21062.1 AF216527 *Dunaliella tertiolecta*

DESCRIPTION: calcium-dependent protein kinase. CPK1; CDPK.

- 5 AAF19402.1 AF203480 *Lycopersicon esculentum*
DESCRIPTION: phosphoenolpyruvate carboxylase kinase. protein kinase;
member of Ca²⁺/CaM kinase family; lacks the autoinhibitory region and EF
hands.
- 10 CAA65244.1 X95997 *Solanum tuberosum*
DESCRIPTION: SNF1-related protein kinase. PKIN1.
- 15 CAA57898.1 X82548 *Hordeum vulgare*
DESCRIPTION: SNF1-related protein kinase. BKIN2.
- 20 BAA13608.1 D88399 *Oryza sativa*
DESCRIPTION: serine-threonine kinase. endosperm kinase. REK.
- 25 CAA08995.1 AJ010091 *Brassica napus*
DESCRIPTION: MAP3K alpha 1 protein kinase. MAP3K alpha 1.
- 30 AAF19401.1 AF203479 *Glycine max*
DESCRIPTION: phosphoenolpyruvate carboxylase kinase. protein kinase;
member of Ca²⁺/CaM kinase family; lacks the autoinhibitory region and EF
hands.
- 35 BAA05648.1 D26601 *Nicotiana tabacum*
DESCRIPTION: protein kinase.
- AAC69450.1 AF032465 *Nicotiana tabacum*
DESCRIPTION: putative serine/threonine protein kinase. WAPK.
- 40 AAD23582.1 AF128443 *Glycine max*
DESCRIPTION: probably involved in plant stress responses possibly
regulates gene expression. SNF-1-like serine/threonine protein kinase.
expressed in nodules, roots and leaves.
- 45 AAD00239.1 U73938 *Nicotiana tabacum*

DESCRIPTION: protein kinase. PK11-C1. PK11-C1. induced at the transcriptional level by the abscisic acid plant hormone; similar to serine/threonine protein kinase.

5

AAG60195.1 AC084763 Oryza sativa
DESCRIPTION: protein kinase REK. OSJNBa0027P10.6.

428

10

CAC17753.1 AJ294543 Dendrobium 'Sonia'
DESCRIPTION: metabolic enzyme of cytokinins. cytokinin oxidase. cko1.

15

CAC17752.1 AJ294542 Dendrobium 'Sonia'
DESCRIPTION: metabolic enzyme of cytokinins. cytokinin oxidase. cko1.

20

CAA77151.1 Y18377 Zea mays
DESCRIPTION: cytokinin oxidase. cko.

25

AAC27500.1 AF044603 Zea mays
DESCRIPTION: cytokinin oxidase. cko1.

30

BAB07927.1 AP002836 Oryza sativa
DESCRIPTION: putative cytokinin oxidase. P0512G09.9.

BAB03420.1 AP002816 Oryza sativa
DESCRIPTION: Similar to Zea mays mRNA for cytokinin oxidase. (Y18377).

429

35

BAA21922.1 AB006600 Petunia x hybrida
DESCRIPTION: ZPT2-13. C2H2 zinc finger protein, 2finger.

40

BAA21923.1 AB006601 Petunia x hybrida
DESCRIPTION: ZPT2-14. C2H2 zinc finger protein, 2 finger.

45

BAA21921.1 AB006599 Petunia x hybrida
DESCRIPTION: ZPT2-12. C2H2 zinc finger protein, 2 finger.

- BAA19110.1 AB000451 Petunia x hybrida
DESCRIPTION: PETHy;ZPT2-5. Cys(2) His(2) zinc finger protein, 2 fingers.
- 5 BAA21925.1 AB006603 Petunia x hybrida
DESCRIPTION: ZPT2-8. C2H2 zinc finger protein, 2 finger.
- 10 BAA21926.1 AB006604 Petunia x hybrida
DESCRIPTION: ZPT2-9. C2H2 zinc finger protein, 2 finger.
- 15 BAA21924.1 AB006602 Petunia x hybrida
DESCRIPTION: ZPT2-7. C2H2 zinc finger protein, 2finger.
- 20 BAA19111.1 AB000452 Petunia x hybrida
DESCRIPTION: PETHy;ZPT2-6. Cys(2) His(2) zinc finger protein, 2 fingers.
- BAA05077.1 D26084 Petunia x hybrida
DESCRIPTION: zinc-finger DNA binding protein.
- 25 AAD26942.1 AF119050 Datisca glomerata
DESCRIPTION: zinc-finger protein 1. zfp1. DgZFP1.
- 30 BAA05076.1 D26083 Petunia x hybrida
DESCRIPTION: zinc-finger DNA binding protein.
- 35 CAB77055.1 Y18788 Medicago sativa
DESCRIPTION: putative TFIIIA (or kruppel)-like zinc finger protein.
- 40 AAC06243.1 AF053077 Nicotiana tabacum
DESCRIPTION: transcription factor. osmotic stress-induced zinc-finger protein. zfp.
- 45 BAA21927.1 AB006605 Petunia x hybrida
DESCRIPTION: ZPT3-3. C2H2 zinc finger protein, 3 finger.

- BAA96071.1 AB035133 Petunia x hybrida
DESCRIPTION: C2H2 zinc-finger protein ZPT3-3. ZPT3-3.
- 5 BAA21920.1 AB006598 Petunia x hybrida
DESCRIPTION: ZPT2-11. C2H2 zinc finger protein, 2finger.
- 10 AAB53261.1 U76555 Brassica rapa
DESCRIPTION: zinc-finger protein BcZFP1. BcZFP1(3-2z).
- 15 AAB53260.1 U76554 Brassica rapa
DESCRIPTION: transcription factor. zinc-finger protein-1. BR42.
- 20 CAA60828.1 X87374 Pisum sativum
DESCRIPTION: putative zinc finger protein.
- 25 AAB39638.1 U68763 Glycine max
DESCRIPTION: putative transcription factor. SCOF-1. scof-1. zinc-finger protein.
- 30 AAK01713.1 AF332876 Oryza sativa
DESCRIPTION: zinc finger transcription factor ZF1.
- 35 BAA05079.1 D26086 Petunia x hybrida
DESCRIPTION: zinc-finger protein.
- 40 BAA96070.1 AB035132 Petunia x hybrida
DESCRIPTION: C2H2 zinc-finger protein ZPT2-10. PETHy;ZPT2-10.
- 45 BAA21919.1 AB006597 Petunia x hybrida
DESCRIPTION: ZPT2-10. C2H2 zinc finger protein, 2 finger.
- BAA05078.1 D26085 Petunia x hybrida
DESCRIPTION: zinc-finger DNA binding protein.
- BAA19112.1 AB000453 Petunia x hybrida

DESCRIPTION: PETHy;ZPT3-1. Cys(2) His(2) zinc finger protein, 3 fingers.

BAA19114.1 AB000455 Petunia x hybrida

5 DESCRIPTION: PETHy;ZPT4-1. Cys(2) His(2) zinc finger protein, 4 fingers.

BAA21928.1 AB006606 Petunia x hybrida

10 DESCRIPTION: ZPT4-4. C2H2 zinc finger protein, 4 finger.

BAA19926.1 AB000456 Petunia x hybrida

DESCRIPTION: PETHy; ZPT4-2. C2H2 zinc finger protein, 4 finger.

15 432

AAC05084.1 AF033097 Avena sativa

DESCRIPTION: NPH1-2. NPH1-2. putative serine/threonine protein kinase.

20

AAC05083.1 AF033096 Avena sativa

DESCRIPTION: NPH1-1. NPH1-1. putative serine/threonine protein kinase.

25 CAA82993.1 Z30332 Spinacia oleracea

DESCRIPTION: protein kinase.

30 AAB88817.1 AF033263 Zea mays

DESCRIPTION: signal transduction for phototropism. nonphototropic hypocotyl 1. nph1. NPH1; putative serine/threonine kinase; similar to oat NPH1 proteins.

35 CAB65325.1 AJ252142 Oryza sativa

DESCRIPTION: putative blue light receptor phototropin. non-phototropic hypocotyl NPH1. nph1.

40 CAA82994.1 Z30333 Mesembryanthemum crystallinum

DESCRIPTION: protein kinase.

45 BAA36192.1 AB012082 Adiantum capillus-veneris

DESCRIPTION: PHY3. PHY3. Ser/Thr protein kinase; chimeric structure of red/far-red light photoreceptive region (phytochrome)and putative blue

light photoreceptor in phototropism of hypocotyl (NPH1).

446

-
- 5 AAB72047.1 AF006489 *Gossypium hirsutum*
DESCRIPTION: adenine nucleotide translocator 1. CANT1.
- 10 CAA05979.1 AJ003197 *Lupinus albus*
DESCRIPTION: transfer of ATP from mitochondria to cytosol. adenine nucleotide translocator. ant1.
- 15 CAA44054.1 X62123 *Solanum tuberosum*
DESCRIPTION: ADP /ATP translocator. ant. product has dimeric subunit structure.
- 20 AAB49700.1 U89839 *Lycopersicon esculentum*
DESCRIPTION: ADP/ATP translocator.
- 25 CAA40782.1 X57557 *Solanum tuberosum*
DESCRIPTION: adenine nucleotide translocator. AAC.
- 30 BAA02161.1 D12637 *Oryza sativa*
DESCRIPTION: ATP/ADP translocator.
- 35 CAA41812.1 X59086 *Zea mays*
DESCRIPTION: adenine nucleotide translocator. MANT2.
- 40 CAA40781.1 X57556 *Zea mays*
DESCRIPTION: adenine nucleotide translocator. MANT1.
- 45 CAA33743.1 X15712 *Zea mays*
DESCRIPTION: adenine nucleotide translocator.
- CAA33742.1 X15711 *Zea mays*
DESCRIPTION: adenine nucleotide translocator.

- CAA65119.1 X95863 *Triticum turgidum*
DESCRIPTION: adenine nucleotide translocator.
- 5 CAA26600.1 X02842 *Zea mays*
DESCRIPTION: put. ATP/ADP translocator.
- 10 CAA65120.1 X95864 *Triticum turgidum*
DESCRIPTION: adenine nucleotide translocator.
- 15 CAA46311.1 X65194 *Chlamydomonas reinhardtii*
DESCRIPTION: mitochondrial ADP/ATP translocator protein. CRANT.
- 20 AAA33027.1 M76669 *Chlorella kessleri*
DESCRIPTION: ATP/ADP translocator. AAT.
- AAB72048.1 AF006490 *Gossypium hirsutum*
DESCRIPTION: adenine nucleotide translocator 2. CANT2.
- 25 BAA08104.1 D45074 *Panicum miliaceum*
DESCRIPTION: 2-oxoglutarate/malate translocator. mitochondrial
2-oxoglutarate/malate translocator.
- 30 BAA08103.1 D45073 *Panicum miliaceum*
DESCRIPTION: 2-oxoglutarate/malate translocator. mitochondrial
2-oxoglutarate/malate translocator.
- 35 BAA08105.1 D45075 *Panicum miliaceum*
DESCRIPTION: 2-oxoglutarate/malate translocator. mitochondrial
2-oxoglutarate/malate translocator.
- 447
40 -----
BAB16317.1 AB049589 *Avicennia marina*
DESCRIPTION: secretory peroxidase. PER.
- 45 AAC83463.1 AF039027 *Glycine max*
DESCRIPTION: H2O2 oxidoreductase. cationic peroxidase 2. Prx2. class III

plant peroxidase.

- 5 AAD37374.1 AF145348 Glycine max
DESCRIPTION: peroxidase. Prx2b.
- 10 CAB71128.2 AJ271660 Cicer arietinum
DESCRIPTION: cationic peroxidase.
- 15 AAD33072.1 AF149251 Nicotiana tabacum
DESCRIPTION: secretory peroxidase. PER.
- 20 BAA94962.1 AB042103 Asparagus officinalis
DESCRIPTION: peroxidase. AspPOX1.
- 25 AAF63027.1 AF244924 Spinacia oleracea
DESCRIPTION: hydrogen peroxide catabolism. peroxidase prx15 precursor.
type III peroxidase.
- 30 AAF63026.1 AF244923 Spinacia oleracea
DESCRIPTION: hydrogen peroxide catabolism. peroxidase prx14 precursor.
type III peroxidase.
- 35 BAA92500.1 AP001383 Oryza sativa
DESCRIPTION: ESTs D39300(R3292),AU030751(E60187) correspond to a
region
of the predicted gene. Similar to peroxidase ATP6a. (X98774).
- 40 AAF63025.1 AF244922 Spinacia oleracea
DESCRIPTION: hydrogen peroxide catabolism. peroxidase prx13 precursor.
type III peroxidase.
- 45 AAG46133.1 AC082644 Oryza sativa
DESCRIPTION: putative peroxidase. OSJNBa0013M12.15.

- BAA92422.1 AP001366 *Oryza sativa*
 DESCRIPTION: ESTs AU081576(R0541),AU032412(R4029) correspond to a
 region
 of the predicted gene. Similar to *A.thaliana* mRNA for peroxidase ATP18a.
 5 (X98804).
- BAA92497.1 AP001383 *Oryza sativa*
 DESCRIPTION: ESTs AU081576(R0541),AU032412(R4029) correspond to a
 10 region
 of the predicted gene. Similar to peroxidase ATP18a. (X98804).
- CAA59487.1 X85230 *Triticum aestivum*
 15 DESCRIPTION: peroxidase. pox4.
- AAA98491.1 L36981 *Petroselinum crispum*
 DESCRIPTION: anionic peroxidase.
 20
- CAA71492.1 Y10466 *Spinacia oleracea*
 DESCRIPTION: peroxidase. prxr5.
 25
- BAA96643.1 AP002482 *Oryza sativa*
 DESCRIPTION: Similar to *Arabidopsis thaliana* peroxidase ATP19a (X98805).
- 30 BAB12025.1 AP002820 *Oryza sativa*
 DESCRIPTION: putative peroxidase. P0702D12.1.
- AAB02554.1 L37790 *Stylosanthes humilis*
 35 DESCRIPTION: cationic peroxidase.
- AAF63024.1 AF244921 *Spinacia oleracea*
 DESCRIPTION: hydrogen peroxide catabolism. peroxidase prx12 precursor.
 40 type III peroxidase.
- AAC84140.1 AF101427 *Cichorium intybus*
 DESCRIPTION: peroxidase.
 45

- AAA65637.1 L13654 *Lycopersicon esculentum*
DESCRIPTION: peroxidase. TPX1.
- 5 AAC98519.1 AF007211 *Glycine max*
DESCRIPTION: peroxidase precursor. GMIPER1. pathogen-induced.
- 10 BAA14143.1 D90115 *Armoracia rusticana*
DESCRIPTION: peroxidase isozyme.
- 15 CAA62226.1 X90693 *Medicago sativa*
DESCRIPTION: peroxidase1B. prx1B.
- 20 AAD37430.1 AF149280 *Phaseolus vulgaris*
DESCRIPTION: peroxidase 5 precursor. FBP5. secretory peroxidase.
- CAA62615.1 X91232 *Mercurialis annua*
DESCRIPTION: PRX. peroxidase.
- 25 AAG46130.1 AC082644 *Oryza sativa*
DESCRIPTION: putative peroxidase. OSJNBa0013M12.18.
- 30 CAC21392.1 AJ401275 *Zea mays*
DESCRIPTION: peroxidase. pox2.
- 35 BAA07241.1 D38051 *Populus kitakamiensis*
DESCRIPTION: peroxidase. prxA4a.
- 40 BAB39277.1 AP002971 *Oryza sativa*
DESCRIPTION: putative peroxidase. P0537A05.6. contains ESTs
C23550(C52903),C97179(C52903).
- CAB65334.1 AJ250121 *Picea abies*
DESCRIPTION: peroxidase. SPI2 protein. spi2.
- 45 CAA62597.1 X91172 *Raphanus sativus*

DESCRIPTION: korean-radish isoperoxidase. prxk1.

- 5 AAC49820.1 AF014469 *Oryza sativa*
DESCRIPTION: peroxidase. POX5.1. wound inducible.
- 10 CAA71496.1 Y10470 *Spinacia oleracea*
DESCRIPTION: peroxidase. prxr9.
- BAA01950.1 D11337 *Vigna angularis*
DESCRIPTION: peroxidase.
- 15 CAA71491.1 Y10465 *Spinacia oleracea*
DESCRIPTION: peroxidase. prxr4.
- 20 BAA03911.1 D16442 *Oryza sativa*
DESCRIPTION: peroxidase.
- 449

- 25 CAA56325.1 X80023 *Triticum turgidum*
DESCRIPTION: ATP/ADP carrier protein.
- 30 CAC27140.1 AJ132535 *Picea abies*
DESCRIPTION: ADP, ATP carrier protein precursor.
- 35 a BAA92520.1 AP001383 *Oryza sativa*
DESCRIPTION: ESTs AU068633(C30614),AU068634(C30614) correspond to
region of the predicted gene. Similar to *Bos taurus* mitochondrial solute
carrier protein. (AF049236).
- 40 BAB16462.1 AP002483 *Oryza sativa*
DESCRIPTION: putative peroxisomal Ca-dependent solute carrier protein.
P0019D06.21.
- 45 BAB40117.1 AP003311 *Oryza sativa*
DESCRIPTION: putative peroxisomal Ca-dependent solute carrier protein.

P0024G09.9.

- 5 AAB71744.1 U75346 *Chlamydomonas reinhardtii*
DESCRIPTION: envelope protein. LIP-36G2. low CO2 inducible carrier
protein LIP-36 with a molecular weight of 36 kDa.
- 10 AAB71743.1 U75345 *Chlamydomonas reinhardtii*
DESCRIPTION: envelope protein. LIP-36G1. low CO2 inducible carrier
protein LIP-36 with a molecular weight of 36 kDa.
- 15 AAG48999.1 AY013246 *Hordeum vulgare*
DESCRIPTION: putative mitochondrial carrier protein. 635P2.1.
- 20 CAC12820.1 AJ299250 *Nicotiana tabacum*
DESCRIPTION: mitochondrial 2-oxoglutarate/malate carrier protein. momc1.
- 25 CAA07568.1 AJ007580 *Ribes nigrum*
DESCRIPTION: Mitochondrial carrier protein. prib7.
- 30 AAG45489.1 AY013245 *Oryza sativa*
DESCRIPTION: 36I5.1. putative mitochondrial carrier protein.
451

- 35 AAB53099.1 U68217 *Brassica napus*
DESCRIPTION: iron binding protein. ferritin. LSC30.
- 40 AAA33959.1 M64337 *Glycine max*
DESCRIPTION: ferritin light chain. ferritin.
- 45 AAA34016.1 M72894 *Glycine max*
DESCRIPTION: ferritin light chain. SOF-H2.
- CAA65771.1 X97059 *Medicago sativa*
DESCRIPTION: iron storage. ferritin. FER. abscisic acid regulated.

- AAB18928.1 U31648 Glycine max
DESCRIPTION: iron storage protein. ferritin.
- 5 AAC06026.1 AF052057 Vigna unguiculata
DESCRIPTION: iron storage and mobilization in plants. ferritin subunit
cowpea3 precursor.
- 10 AAC06027.1 AF052058 Vigna unguiculata
DESCRIPTION: iron storage and mobilization in plants. ferritin subunit
cowpea2 precursor.
- 15 CAA41213.1 X58274 Phaseolus vulgaris
DESCRIPTION: ferritin. pfe.
- 20 AAD50644.1 AF133814 Solanum tuberosum
DESCRIPTION: ferritin 1. F1.
- 25 CAA51786.1 X73369 Pisum sativum
DESCRIPTION: ferritin.
- CAA45763.1 X64417 Pisum sativum
DESCRIPTION: ferritin-precursor.
- 30 CAA43663.1 X61391 Zea mays
DESCRIPTION: ferritin.
- 35 CAA58146.1 X83076 Zea mays
DESCRIPTION: ferritin. Fer1.
- 40 CAA58147.1 X83077 Zea mays
DESCRIPTION: ferritin. Fer2.
- 45 CAA43664.1 X61392 Zea mays
DESCRIPTION: ferritin.

AAA33958.1 M58336 Glycine max
DESCRIPTION: ferritin light chain. SOF-5L.

5 CAB42587.1 AJ238628 Chlorella protothecoides
DESCRIPTION: putative ferritin. dee188.

10 BAB17852.1 AB042612 Nicotiana tabacum
DESCRIPTION: ferritin 1. tob-fer-1. putative.

15 AAC15241.1 AF028072 Pinus taeda
DESCRIPTION: ferritin.

20 CAA47982.1 X67754 Vigna unguiculata
DESCRIPTION: ferritin 1. pfe1.

CAA47984.1 X67756 Vigna unguiculata
DESCRIPTION: ferritin 5. pfe5.

25 CAA47983.1 X67755 Vigna unguiculata
DESCRIPTION: ferritin 2. pfe2.

30 AAC12282.1 AF052511 Glycine max
DESCRIPTION: iron storage and mobilization. ferritin 2. soybean 2; cowpea
2 homolog.

35 AAC12281.1 AF052513 Glycine max
DESCRIPTION: iron storage and mobilization. ferritin 1. soybean 1; cowpea
1 homolog.

452

40 CAB56619.1 AJ244024 Nicotiana tabacum
DESCRIPTION: putative role in cell plate formation. phragmoplastin.
phragmoplastin. dynamin-like protein.

454

45 CAA55039.1 X78203 Hyoscyamus muticus

DESCRIPTION: glutathione transferase.

- 5 AAB65163.1 AF002692 *Solanum commersonii*
DESCRIPTION: glutathione S-transferase, class-phi. GST1. low temperature induced.
- 10 BAA01394.1 D10524 *Nicotiana tabacum*
DESCRIPTION: glutathione S-transferase. parB.
- 15 CAA96431.1 Z71749 *Nicotiana plumbaginifolia*
DESCRIPTION: glutathione S-transferase.
- 20 AAA33931.1 M84969 *Silene vulgaris*
DESCRIPTION: glutathione-S-transferase.
- 25 AAA33930.1 M84968 *Silene vulgaris*
DESCRIPTION: glutathione-S-transferase.
- 30 AAF65767.1 AF242309 *Euphorbia esula*
DESCRIPTION: glutathione S-transferase. putative auxin-binding GST.
- 35 AAF61392.1 AF133894 *Persea americana*
DESCRIPTION: glutathione S-transferase. GTH.
- 40 CAB38119.1 AJ010296 *Zea mays*
DESCRIPTION: Glutathione transferase III(b). gst3b.
- 45 CAB38118.1 AJ010295 *Zea mays*
DESCRIPTION: Glutathione transferase III(a). gst3a.
- 50 BAB39935.1 AP002914 *Oryza sativa*
DESCRIPTION: putative glutathione S-transferase. P0493G01.17.
- 55 AAG34811.1 AF243376 *Glycine max*
DESCRIPTION: glutathione S-transferase GST 21.

- 5 BAB39939.1 AP002914 *Oryza sativa*
DESCRIPTION: putative glutathione S-transferase. P0493G01.21.
- 10 AAG34812.1 AF243377 *Glycine max*
DESCRIPTION: glutathione S-transferase GST 22.
- 15 AAG34814.1 AF243379 *Glycine max*
DESCRIPTION: glutathione S-transferase GST 24.
- 20 CAA09190.1 AJ010451 *Alopecurus myosuroides*
DESCRIPTION: glutathione transferase. GST2a.
- 25 AAG32476.1 AF309383 *Oryza sativa* subsp. *japonica*
DESCRIPTION: putative glutathione S-transferase OsGSTF4.
- 30 BAB39929.1 AP002914 *Oryza sativa*
DESCRIPTION: putative glutathione transferase. P0493G01.7.
- 35 CAA09193.1 AJ010454 *Alopecurus myosuroides*
DESCRIPTION: glutathione transferase. GST2d.
- 40 BAB39941.1 AP002914 *Oryza sativa*
DESCRIPTION: putative glutathione S-transferase. P0493G01.23.
- 45 CAA09191.1 AJ010452 *Alopecurus myosuroides*
DESCRIPTION: glutathione transferase. GST2b.
- CAA09192.1 AJ010453 *Alopecurus myosuroides*
DESCRIPTION: glutathione transferase. GST2c.
- AAD56395.1 AF184059 *Triticum aestivum*
DESCRIPTION: glutathione S-transferase. GST1.

- CAA39487.1 X56012 *Triticum aestivum*
DESCRIPTION: glutathione transferase. gstA1.
- 5 AAG32477.1 AF309384 *Oryza sativa* subsp. *japonica*
DESCRIPTION: putative glutathione S-transferase OsGSTF3.
- 10 CAA68993.1 Y07721 *Petunia x hybrida*
DESCRIPTION: conjugates glutathione to anthocyanin to facilitate transport to the vacuole. glutathione S-transferase. an9 locus.
- 15 AAA33470.1 M16901 *Zea mays*
DESCRIPTION: glutathione S-transferase I.
- 20 AAA33469.1 M16902 *Zea mays*
DESCRIPTION: glutathione S-transferase I.
- 25 AAA20585.1 U12679 *Zea mays*
DESCRIPTION: glutathione S-transferase IV. GSTIV.
- CAA56047.1 X79515 *Zea mays*
DESCRIPTION: glutathione transferase. GST27.
- 30 CAB66333.1 AJ279691 *Betula pendula*
DESCRIPTION: glutathione-S-transferase. gst.
- 35 BAB39927.1 AP002914 *Oryza sativa*
DESCRIPTION: putative glutathione S-transferase. P0493G01.1. contains ESTs AU031696(R0596),C97559(C60386),C28218(C60386), D28287(R0596).
- 40 AAC64007.1 AF062403 *Oryza sativa*
DESCRIPTION: glutathione S-transferase II.
- 45 CAA39480.1 X56004 *Triticum aestivum*
DESCRIPTION: glutathione transferase. gstA2.

AAG32475.1 AF309382 *Oryza sativa* subsp. *japonica*
DESCRIPTION: putative glutathione S-transferase OsGSTF5.

5 AAG34823.1 AF244680 *Zea mays*
DESCRIPTION: glutathione S-transferase GST 15.

BAB39940.1 AP002914 *Oryza sativa*
10 DESCRIPTION: putative glutathione S-transferase. P0493G01.22.

AAG34818.1 AF244675 *Zea mays*
DESCRIPTION: glutathione S-transferase GST 10.
15

AAG34820.1 AF244677 *Zea mays*
DESCRIPTION: glutathione S-transferase GST 11.
20

AAG34817.1 AF244674 *Zea mays*
DESCRIPTION: glutathione S-transferase GST 9.

25 AAG34821.1 AF244678 *Zea mays*
DESCRIPTION: glutathione S-transferase GST 13.

CAA05354.1 AJ002380 *Oryza sativa*
30 DESCRIPTION: glutathione S-transferase. Rgst I.

AAG34816.1 AF244673 *Zea mays*
DESCRIPTION: glutathione S-transferase GST 8.
35

AAG34822.1 AF244679 *Zea mays*
DESCRIPTION: glutathione S-transferase GST 14.

40 CAA05355.1 AJ002381 *Oryza sativa*
DESCRIPTION: glutathione S-transferase. Rgst II.

458
45 -----
AAD45623.1 AF084185 *Brassica napus*

DESCRIPTION: dehydration responsive element binding protein. DNA binding protein; DRE binding protein.

5 BAA90812.1 AP001168 Oryza sativa

DESCRIPTION: Similar to mRNA for DREB1A (AB007787).

AAK01089.1 AF298231 Hordeum vulgare

10 DESCRIPTION: CBF3-like protein BCBF3. BCBF3. AP2 domain protein; DRE binding factor.

AAG59618.1 AF239616 Hordeum vulgare

15 DESCRIPTION: CRT/DRE-binding factor. CBF.

AAK01088.1 AF298230 Hordeum vulgare

20 DESCRIPTION: CBF1-like protein BCBF1. BCBF1. AP2 domain protein; putative DRE binding factor.

AAG59619.1 AF243384 Oryza sativa

25 DESCRIPTION: CRT/DRE binding factor. CBF. DREB.

AAC29516.1 U77655 Solanum tuberosum

30 DESCRIPTION: DNA binding protein homolog. STWAAEIRD.

BAA76734.1 AB024575 Nicotiana tabacum

DESCRIPTION: ethylene responsive element binding factor.

CAB93939.1 AJ238739 Catharanthus roseus

DESCRIPTION: putative transcription factor. AP2-domain DNA-binding protein. orcal.

BAB03248.1 AB037183 Oryza sativa

DESCRIPTION: ERF protein transcriptional repressor. ethylene responsive element binding factor3. osERF3.

BAA97123.1 AB016265 Nicotiana sylvestris

DESCRIPTION: ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf3.

5

BAA97124.1 AB016266 *Nicotiana sylvestris*

DESCRIPTION: ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf4.

10

AAC50047.1 U89255 *Lycopersicon esculentum*

DESCRIPTION: binds the GCC box pathogenesis-related promoter element DNA-binding protein. Pti4.

15

AAD00708.1 U91857 *Stylosanthes hamata*

DESCRIPTION: ethylene-responsive element binding protein homolog. similar to EREBP1, -2, -3 and -4 proteins encoded by GenBank Accession Numbers D38123, D38126, D38124, and D38125 respectively.

20

AAC14323.1 AF058827 *Nicotiana tabacum*

DESCRIPTION: TS11. Tsi1. contains putative AP2 DNA-binding domain; similar to Pti6.

25

AAG60182.1 AC084763 *Oryza sativa*

DESCRIPTION: putative ethylene-responsive element binding protein. OSJNBa0027P10.12.

30

AAK31279.1 AC079890 *Oryza sativa*

DESCRIPTION: putative ethylene-responsive element binding protein. OSJNBb0089A17.16.

35

AAC49741.1 U89257 *Lycopersicon esculentum*

DESCRIPTION: DNA-binding protein binds the GCC box pathogenesis-related promoter element. Pti6.

40

BAA97122.1 AB016264 *Nicotiana sylvestris*

DESCRIPTION: ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf2.

45

- 5 CAB96900.1 AJ251250 *Catharanthus roseus*
DESCRIPTION: transcription factor. AP2-domain DNA-binding protein. orca3.
- 10 CAB96899.1 AJ251249 *Catharanthus roseus*
DESCRIPTION: transcription factor. AP2-domain DNA-binding protein. orca3.
- 15 BAB21218.1 AP002913 *Oryza sativa*
DESCRIPTION: putative DNA binding protein RAV2. P0480E02.24.
- 20 CAB93940.1 AJ238740 *Catharanthus roseus*
DESCRIPTION: putative transcription factor. AP2-domain DNA-binding protein. orca2.
- 25 BAA87068.1 AB035270 *Matricaria chamomilla*
DESCRIPTION: ethylene-responsive element binding protein1 homolog. McEREBP1.
- 30 AAC49740.1 U89256 *Lycopersicon esculentum*
DESCRIPTION: binds the GCC box pathogenesis-related promoter element DNA-binding protein. Pti5.
- 35 AAB38748.1 U81157 *Nicotiana tabacum*
DESCRIPTION: S25-XP1 DNA binding protein.
- 40 BAB21211.1 AP002913 *Oryza sativa*
DESCRIPTION: putative DNA binding protein RAV2. P0480E02.17.
- 460 BAA78732.1 AB023482 *Oryza sativa*
DESCRIPTION: Similar to *Arabidopsis thaliana* mRNA for DREB1B, complete cds.(AB007788).
- 45 AAB67721.1 AF015269 *Zea mays*
DESCRIPTION: PL transcription factor. Pl. nonfunctional due to retrotransposon insertion.

461

AAD50592.1 AF093752 Triticum aestivum

5 DESCRIPTION: phytochelatase synthase. PCS1.

AAG22095.1 AF308658 Typha latifolia

10 DESCRIPTION: phytochelatase synthase.

463

AAG13629.1 AC078840 Oryza sativa

15 DESCRIPTION: putative steroid membrane binding protein.
OSJNBb0073N24.4.

AAG13623.1 AC078840 Oryza sativa

20 DESCRIPTION: putative steroid membrane binding protein.
OSJNBb0073N24.2.

464

CAA56313.1 X79992 Avena sativa

25 DESCRIPTION: putative pp70 ribosomal protein S6 kinase. Aspk11.

CAB89082.1 AJ277534 Asparagus officinalis

30 DESCRIPTION: S6 ribosomal protein kinase. pk1. putative.

AAK18843.1 AC082645 Oryza sativa

35 DESCRIPTION: putative protein kinase. OSJNBb0033N16.3.

AAC05083.1 AF033096 Avena sativa

DESCRIPTION: NPH1-1. NPH1-1. putative serine/threonine protein kinase.

40 AAC05084.1 AF033097 Avena sativa

DESCRIPTION: NPH1-2. NPH1-2. putative serine/threonine protein kinase.

AAK13156.1 AC078829 Oryza sativa

45 DESCRIPTION: putative protein kinase. OSJNBa0026O12.14.

CAB82852.1 Z30329 Mesembryanthemum crystallinum
DESCRIPTION: protein kinase MK6.

5

AAB88817.1 AF033263 Zea mays
DESCRIPTION: signal transduction for phototropism. nonphototropic
hypocotyl 1. nph1. NPH1; putative serine/threonine kinase; similar to oat
NPH1 proteins.

10

BAB18105.1 AB042715 Chlamydomonas reinhardtii
DESCRIPTION: cyclic nucleotide dependent protein kinase II. CL-PK2.

15

BAB18104.1 AB042714 Chlamydomonas reinhardtii
DESCRIPTION: cyclic nucleotide dependent protein kinase. CL-PK1.

20

BAA83689.1 AB011968 Oryza sativa
DESCRIPTION: OsPK7. OsPK7. protein kinase.

25

BAA92970.1 AP001551 Oryza sativa
DESCRIPTION: Similar to Arabidopsis thaliana chromosome 4 BAC clone
F28A21 ; putative protein kinase. (AL035526).

30

AAD31900.1 AF145482 Mesembryanthemum crystallinum
DESCRIPTION: putative serine/threonine protein kinase.

35

BAA92972.1 AP001551 Oryza sativa
DESCRIPTION: ESTs AU056183(S20356),AU056881(S20950) correspond to a
region of the predicted gene. Similar to Arabidopsis thaliana chromosome 4
BAC clone F6I18 ; putative protein kinase. (AL022198).

40

BAA83688.1 AB011967 Oryza sativa
DESCRIPTION: OsPK4. OsPK4. protein kinase.

45

CAA73067.1 Y12464 Sorghum bicolor
DESCRIPTION: serine/threonine kinase. SNFL1.

AAF22219.1 AF141378 Zea mays
DESCRIPTION: protein kinase PK4. ZmPK4.

5 BAA96628.1 AP002482 Oryza sativa
DESCRIPTION: ESTs D41739(S4522),AU055999(S20214),
AU057588(S21592
correspond to a region of the predicted gene. Similar to Sorghum bicolor
serine/threonine kinase (Y12465).

10

CAA89202.1 Z49233 Chlamydomonas eugametos
DESCRIPTION: calcium-stimulated protein kinase.

15

CAA73068.1 Y12465 Sorghum bicolor
DESCRIPTION: serine/threonine kinase. SNFL2.

20 BAA34675.1 AB011670 Triticum aestivum
DESCRIPTION: wpk4 protein kinase. wpk4.

BAA99439.1 AP002743 Oryza sativa
25 DESCRIPTION: putative protein kinase. P0710E05.26. contains ESTs
C22394(C30013),C22393(C30013).

CAA74646.1 Y14274 Sorghum bicolor
30 DESCRIPTION: putative serine/threonine protein kinase. SNFL3.

BAB12687.1 AP002746 Oryza sativa
DESCRIPTION: putative protein kinase. P0671B11.2. contains ESTs
35 C22394(C30013),C22393(C30013).

AAF06969.1 AF162661 Kalanchoe fedtschenkoi
DESCRIPTION: phosphoenolpyruvate carboxylase kinase. calcium-independent
40 protein kinase.

AAF06970.1 AF162662 Kalanchoe fedtschenkoi
DESCRIPTION: phosphoenolpyruvate carboxylase kinase. calcium-independent
45 protein kinase.

CAA65244.1 X95997 Solanum tuberosum
 DESCRIPTION: SNF1-related protein kinase. PKIN1.

CAA57898.1 X82548 Hordeum vulgare
 DESCRIPTION: SNF1-related protein kinase. BKIN2.

AAF19401.1 AF203479 Glycine max
 DESCRIPTION: phosphoenolpyruvate carboxylase kinase. protein kinase;
 member of Ca²⁺/CaM kinase family; lacks the autoinhibitory region and EF
 hands.

AAD23582.1 AF128443 Glycine max
 DESCRIPTION: probably involved in plant stress responses possibly
 regulates gene expression. SNF-1-like serine/threonine protein kinase.
 expressed in nodules, roots and leaves.

AAF34436.1 AF172282 Oryza sativa
 DESCRIPTION: similar to mitogen-activated protein kinases. DUPR11.32.

BAA05648.1 D26601 Nicotiana tabacum
 DESCRIPTION: protein kinase.

 CAB85467.1 AJ250316 Brassica juncea
 DESCRIPTION: chloroplast omega-3 fatty acid desaturase. fad7.

BAA22441.1 D63954 Zea mays
 DESCRIPTION: fatty acid desaturase. FAD7.

BAA11475.1 D79979 Nicotiana tabacum
 DESCRIPTION: omega-3 fatty acid desaturase. NtFAD7.

AAA70334.1 U25817 Sesamum indicum
 DESCRIPTION: omega-3 fatty acid desaturase. linoleic acid and
 hexadecadienoic acids desaturase.

5 AAB39387.1 U59477 *Perilla frutescens*
DESCRIPTION: omega-3 fatty acid desaturase.

CAA07638.1 AJ007739 *Solanum tuberosum*
DESCRIPTION: w-3 desaturase.

10 AAF27933.1 AF222989 *Capsicum annuum*
DESCRIPTION: omega-3 fatty acid desaturase. FAD.

15 AAB72241.1 U75745 *Petroselinum crispum*
DESCRIPTION: omega-3 fatty acid desaturase. complements the Arabidopsis
fad7/8 fatty acid double mutant.

20 AAA61776.1 L22965 *Chloroplast Glycine soja*
DESCRIPTION: omega-3 fatty acid desaturase. Fadd.

25 AAF12821.1 AF200717 *Vernicia fordii*
DESCRIPTION: TnDES2. omega-3 fatty acid desaturase.

30 AAA86690.1 U17063 *Limnanthes douglasii*
DESCRIPTION: linoleic acid desaturation. delta-15 lineoyl desaturase.
omega-3-fatty acid desaturase.

35 AAA73511.1 L25897 *Ricinus communis*
DESCRIPTION: desaturates linoleate to alpha-linolenate. linoleoyl
desaturase. fad7. putative.

40 CAC18722.1 AJ302017 *Picea abies*
DESCRIPTION: putative plastidial w-3 fatty acid desaturase. fad3.

45 AAD13527.1 AF061027 *Vernicia fordii*
DESCRIPTION: omega-3 fatty acid desaturase precursor.

BAA22442.1 D84409 *Zea mays*

DESCRIPTION: fatty acid desaturase. FAD8.

5 BAA22440.1 D63953 Zea mays
DESCRIPTION: fatty acid desaturase. FAD8.

10 BAA07785.2 D43688 Triticum aestivum
DESCRIPTION: plastid omega-3 fatty acid desaturase. TaFAD7.

15 AAA61774.1 L22963 Chloroplast Brassica napus
DESCRIPTION: omega-3 fatty acid desaturase. Fadd.

AAC98967.1 AF047172 Vernicia fordii
DESCRIPTION: omega-3 fatty acid desaturase. Fad3.

20 CAB45155.1 AJ011004 Vernicia fordii
DESCRIPTION: omega-3 desaturase.

25 AAC16443.1 AF020204 Pelargonium x hortorum
DESCRIPTION: omega-3 desaturase. pxh-15.

30 AAA61775.1 L22962 Brassica napus
DESCRIPTION: omega-3 fatty acid desaturase. Fad3.

35 AAA61777.1 L22964 Chloroplast Glycine soja
DESCRIPTION: omega-3 fatty acid desaturase. Fad3.

AAA32994.1 L01418 Brassica napus
DESCRIPTION: desaturation of linoleic acid to linolenic acid. linoleic
acid desaturase. fad3.

40 AAD15744.1 AF047039 Perilla frutescens
DESCRIPTION: omega-3 fatty acid desaturase. FAD3.

45 BAA28358.1 D84678 Triticum aestivum
DESCRIPTION: omega-3 fatty acid desaturase. TaFAD3.

- CAA60016.1 X86021 *Solanum tuberosum*
DESCRIPTION: potassium channel. SKT1 gene. putative start codon.
- 5 CAA65254.1 X96390 *Lycopersicon esculentum*
DESCRIPTION: potassium channel. LKT1.
- 10 AAF36832.1 AF207745 *Triticum aestivum*
DESCRIPTION: AKT1-like potassium channel. TaAKT1.
- 15 CAA68912.1 Y07632 *Zea mays*
DESCRIPTION: potassium channel. ZMK1.
- 20 AAF81249.1 AF267753 *Mesembryanthemum crystallinum*
DESCRIPTION: putative potassium channel protein Mkt1p.
- CAC05489.1 AJ271447 *Populus tremula* x *Populus tremuloides*
DESCRIPTION: potassium channel. potassium channel 2. ptk2.
- 25 AAD16278.1 AF099095 *Samanea saman*
DESCRIPTION: pulvinus inward-rectifying channel for potassium SPICK1.
similar to Arabidopsis potassium channel AKT3.
- 30 CAB54856.1 AJ132686 *Zea mays*
DESCRIPTION: potassium channel protein ZMK2. ZMK2.
- 35 CAA70870.1 Y09699 *Solanum tuberosum*
DESCRIPTION: putative inward rectifying potassium channel. SKT2.
- 40 CAA71598.1 Y10579 *Vicia faba*
DESCRIPTION: potassium channel.
- BAA84085.1 AB032074 *Nicotiana paniculata*
DESCRIPTION: potassium channel. NpKT1.
- 45 CAA12645.1 AJ225805 *Egeria densa*

DESCRIPTION: inward potassium channel alpha subunit. homologous to the sequences of the family of inwardly rectifying potassium channels in plants which is structurally related to the shaker family of outwardly rectifying channels in Drosophila.

5

AAD39492.1 AF145272 Samanea saman

DESCRIPTION: pulvinus inward-rectifying channel SPICK2. potassium channel; similar to AKT2/3.

10

CAC10514.1 AJ299019 Samanea saman

DESCRIPTION: potassium release. outwardly rectifying potassium channel. spork1.

15

CAC05488.1 AJ271446 Populus tremula x Populus tremuloides

DESCRIPTION: potassium channel. outward rectifying potassium channel. ptork.

20

AAF81251.1 AF267755 Mesembryanthemum crystallinum

DESCRIPTION: potassium channel protein Mkt2p.

25

CAA70900.1 Y09753 Secale cereale

DESCRIPTION: potassium channel. encodes membrane spanning domains H5-S6.

30

CAA70899.1 Y09752 Secale cereale

DESCRIPTION: potassium channel. encodes membrane spanning domains H5-S6.

35

CAA70947.1 Y09818 Solanum tuberosum

DESCRIPTION: putative inward rectifying potassium channel. SKT3.

40

CAA70895.1 Y09748 Hordeum vulgare

DESCRIPTION: potassium channel. encodes membrane spanning domains H5-S6.

45

CAA70894.1 Y09747 Zea mays

DESCRIPTION: potassium channel. encodes membrane spanning domains H5-S6.

5 CAA70896.1 Y09749 Vicia faba

DESCRIPTION: potassium channel. encodes membrane spanning domains H5-S6.

10 CAA70897.1 Y09750 Plantago major

DESCRIPTION: potassium channel. encodes membrane spanning domains H5-S6.

15 AAF33670.1 AF079872 Nicotiana tabacum

DESCRIPTION: cyclic nucleotide-gated calmodulin-binding ion channel. CBP4.

20 AAF33669.1 AF079871 Nicotiana tabacum

DESCRIPTION: cyclic nucleotide-gated calmodulin-binding ion channel. CBP7.

25 CAA05637.1 AJ002610 Hordeum vulgare

DESCRIPTION: putative calmodulin binding transporter protein. CBT1.

30 CAA70898.1 Y09751 Plantago major

DESCRIPTION: potassium channel. encodes membrane spanning domains H5-S6.

35 AAK16188.1 AC079887 Oryza sativa

DESCRIPTION: putative cyclic nucleotide and calmodulin-regulated ion channel protein. OSJNBa0040E01.13.

468

40 AAF76226.1 AF272572 Populus x canescens

DESCRIPTION: 14-3-3 protein. 14-3-3P20-1.

45 AAC04811.1 AF037460 Fritillaria agrestis

DESCRIPTION: GF14 protein. GRF.

- AAB40395.1 U80070 *Mesembryanthemum crystallinum*
 DESCRIPTION: G-box binding factor. 14-3-3-like protein. GBF.
- 5
- AAF05737.1 AF191746 *Lilium longiflorum*
 DESCRIPTION: 14-3-3-like protein.
- 10
- AAB07457.1 U65957 *Oryza sativa*
 DESCRIPTION: GF14-c protein. rice 14-3-3 protein homolog; osGF14c.
- 15
- AAB09580.1 U70533 *Glycine max*
 DESCRIPTION: SGF14A. 14-3-3 related protein.
- 20
- AAA99431.1 L29150 *Lycopersicon esculentum*
 DESCRIPTION: 14-3-3 protein homologue.
- 25
- CAA74592.1 Y14200 *Hordeum vulgare*
 DESCRIPTION: 14-3-3 protein.
- 30
- AAB33304.1 S77133 *Zea mays*
 DESCRIPTION: GF14-6. GRF1. 14-3-3 protein homolog; This sequence comes from Fig. 5.
- 35
- CAA66309.1 X97724 *Solanum tuberosum*
 DESCRIPTION: 14-3-3 protein. leaf specific.
- 40
- AAB07456.1 U65956 *Oryza sativa*
 DESCRIPTION: GF14-b protein. rice 14-3-3 protein homolog; osGF14b.
- 45
- AAD27823.2 AF121194 *Populus x canescens*
 DESCRIPTION: 14-3-3 protein. 14-3-3P20-2.
- AAC49894.1 U91726 *Nicotiana tabacum*
 DESCRIPTION: 14-3-3 isoform e. T14-3e.

- CAA44259.1 X62388 *Hordeum vulgare*
DESCRIPTION: 14-3-3 protein homologue.
- 5 AAD27827.2 AF121198 *Picea glauca*
DESCRIPTION: 14-3-3 protein. 14-3-3EB9D.
- 10 CAA63658.1 X93170 *Hordeum vulgare*
DESCRIPTION: Hv14-3-3b.
- 15 CAB42546.2 AJ238681 *Pisum sativum*
DESCRIPTION: 14-3-3-like protein. 14-3-3.
- 20 AAA33505.1 M96856 *Zea mays*
DESCRIPTION: regulatory protein. GF14-12.
- 25 AAA85817.1 U15036 *Pisum sativum*
DESCRIPTION: 14-3-3-like protein.
- 30 AAK26634.1 AF342780 *Brassica napus*
DESCRIPTION: GF14 omega. 14-3-3 protein.
- 35 CAA72094.1 Y11211 *Nicotiana tabacum*
DESCRIPTION: 14-3-3-like protein B.
- 40 CAA72383.1 Y11687 *Solanum tuberosum*
DESCRIPTION: 14-3-3 protein. 34G.
- 45 AAC49892.1 U91724 *Nicotiana tabacum*
DESCRIPTION: 14-3-3 isoform c. T14-3c.
- CAA53700.1 X76086 *Cucurbita pepo*
DESCRIPTION: 14-3-3 protein 32kDa endonuclease. A215. single polypeptide.
- CAA72382.1 Y11686 *Solanum tuberosum*
DESCRIPTION: 14-3-3 protein. 30G.

- 5 CAB42547.1 AJ238682 *Pisum sativum*
DESCRIPTION: 14-3-3-like protein. 14-3-3.
- CAA65147.1 X95902 *Lycopersicon esculentum*
DESCRIPTION: 14-3-3 protein. tft3 gene.
- 10 AAC49891.1 U91723 *Nicotiana tabacum*
DESCRIPTION: 14-3-3 isoform b. T14-3b.
- 15 AAB07458.1 U65958 *Oryza sativa*
DESCRIPTION: GF14-d protein. rice 14-3-3 protein homolog; osGF14d.
- 20 CAA72381.1 Y11685 *Solanum tuberosum*
DESCRIPTION: 14-3-3 protein. 16R.
- 25 AAC49895.1 U91727 *Nicotiana tabacum*
DESCRIPTION: 14-3-3 isoform f. T14-3f.
- CAA72095.1 Y11212 *Nicotiana tabacum*
DESCRIPTION: 14-3-3-like protein A.
- 30 BAB11739.1 AB042193 *Triticum aestivum*
DESCRIPTION: TaWIN1. TaWIN1. TaWIN1 is a member of 14-3-3 protein family.
- 35 CAA65146.1 X95901 *Lycopersicon esculentum*
DESCRIPTION: 14-3-3 protein. tft2 gene.
- 40 CAA65148.1 X95903 *Lycopersicon esculentum*
DESCRIPTION: 14-3-3 protein. tft5 gene.
- 45 AAC17447.1 AF066076 *Helianthus annuus*
DESCRIPTION: 14-3-3-like protein.

- CAA60800.1 X87370 Solanum tuberosum
DESCRIPTION: 14-3-3 protein. RA215. root specific.
- 5 CAA55964.1 X79445 Chlamydomonas reinhardtii
DESCRIPTION: 14-3-3 protein.
- 10 CAC03467.1 Y19105 Chlamydomonas reinhardtii
DESCRIPTION: 14-3-3 protein.
- 15 CAA65149.1 X95904 Lycopersicon esculentum
DESCRIPTION: 14-3-3 protein. tft6 gene.
- 20 CAB65693.1 AJ270959 Lycopersicon esculentum
DESCRIPTION: tft3 14-3-3 protein. tft3.
- 25 BAB11740.1 AB042194 Triticum aestivum
DESCRIPTION: TaWIN2. TaWIN2. TaWIN2 is a member of 14-3-3 protein family.
- 30 AAA99430.1 L29151 Lycopersicon esculentum
DESCRIPTION: 14-3-3 protein homologue.
- CAA72384.1 Y11688 Solanum tuberosum
DESCRIPTION: 14-3-3 protein. 35G.
- 35 CAA65145.1 X95900 Lycopersicon esculentum
DESCRIPTION: 14-3-3 protein. tft1 gene.
- 40 AAC49893.1 U91725 Nicotiana tabacum
DESCRIPTION: 14-3-3 isoform d. T14-3d.
- 470
- 45 AAA19701.1 L24438 Thlaspi arvense
DESCRIPTION: cytochrome P450.

AAA32913.1 M32885 *Persea americana*
DESCRIPTION: cytochrome P-450LXXIA1 (cyp71A1).

5

AAC39318.1 AF029858 *Sorghum bicolor*
DESCRIPTION: second multifunctional cytochrome P450 in the biosynthetic
pathway of the cyanogenic glucoside dhurrin. Catalyzes the conversion of
p-hydroxyphenylacetaldoxime to p-hydroxymandelonitrile. cytochrome P450
CYP71E1. CYP71E1. No EST#s identified.

10

BAB40323.1 AB037244 *Asparagus officinalis*
DESCRIPTION: cytochrome P450. ASPI-1.

15

BAB40324.1 AB037245 *Asparagus officinalis*
DESCRIPTION: cytochrome P450. ASPI-2.

20

AAB94589.1 AF022460 *Glycine max*
DESCRIPTION: CYP83D1p. CYP83D1. cytochrome P450 monooxygenase.

25

CAA70575.1 Y09423 *Nepeta racemosa*
DESCRIPTION: cytochrome P450. CYP71A5.

30

CAA70576.1 Y09424 *Nepeta racemosa*
DESCRIPTION: cytochrome P450. CYP71A6.

35

CAA71513.1 Y10489 *Glycine max*
DESCRIPTION: putative cytochrome P450.

AAB61965.1 U48435 *Solanum chacoense*
DESCRIPTION: putative cytochrome P450.

40

AAB94588.1 AF022459 *Glycine max*
DESCRIPTION: CYP71D10p. CYP71D10. cytochrome P450 monooxygenase.

45

CAA50312.1 X70981 *Solanum melongena*
DESCRIPTION: P450 hydroxylase. CYPEG2.

- 5 CAA71514.1 Y10490 Glycine max
DESCRIPTION: putative cytochrome P450.
- 10 AAB94584.1 AF022157 Glycine max
DESCRIPTION: capable of catalyzing the metabolism of phenylurea herbicides. CYP71A10. CYP71A10. cytochrome P450 monooxygenase.
- 15 AAD47832.1 AF166332 Nicotiana tabacum
DESCRIPTION: cytochrome P450.
- 20 AAF27282.1 AF122821 Capsicum annuum
DESCRIPTION: cytochrome P450. PepCYP.
- 25 CAA71517.1 Y10493 Glycine max
DESCRIPTION: putative cytochrome P450.
- 30 CAA83941.1 Z33875 Mentha x piperita
DESCRIPTION: cytochrome P-450 oxidase.
- 35 CAB56503.1 AJ238612 Catharanthus roseus
DESCRIPTION: cytochrome P450.
- 40 AAB61964.1 U48434 Solanum chacoense
DESCRIPTION: putative cytochrome P450.
- 45 AAB69644.1 AF000403 Lotus japonicus
DESCRIPTION: putative cytochrome P450. LjNP450.
- CAA50645.1 X71654 Solanum melongena
DESCRIPTION: P450 hydroxylase.
- BAA03635.1 D14990 Solanum melongena
DESCRIPTION: Cytochrome P-450EG4.

AAD44151.1 AF124816 *Mentha x piperita*
DESCRIPTION: cytochrome p450 isoform PM17.

5

AAD44150.1 AF124815 *Mentha spicata*
DESCRIPTION: cytochrome p450.

10 AAD44152.1 AF124817 *Mentha x piperita*
DESCRIPTION: cytochrome p450 isoform PM2.

15 BAB39252.1 AP002968 *Oryza sativa*
DESCRIPTION: putative cytochrome P450. P0416G11.1.

20 AAK38084.1 AF321860 *Lolium rigidum*
DESCRIPTION: putative cytochrome P450.

AAK38083.1 AF321859 *Lolium rigidum*
DESCRIPTION: putative cytochrome P450.

25 AAK38087.1 AF321863 *Lolium rigidum*
DESCRIPTION: putative cytochrome P450.

30 AAK38082.1 AF321858 *Lolium rigidum*
DESCRIPTION: putative cytochrome P450.

35 CAC27827.1 AJ295719 *Catharanthus roseus*
DESCRIPTION: geraniol hydroxylase. cytochrome P450. cyp71.

40 AAB94587.1 AF022458 *Glycine max*
DESCRIPTION: CYP98A2p. CYP98A2. cytochrome P450 monooxygenase.

AAK38088.1 AF321864 *Lolium rigidum*
DESCRIPTION: putative cytochrome P450.

45 AAD37433.1 AF150881 *Lycopersicon esculentum x Lycopersicon peruvianum*

DESCRIPTION: catalyzes the hydroxylation of ferulic acid to 5-hydroxyferulic acid. ferulate-5-hydroxylase. CYP84. cytochrome P450-dependent monooxygenase; F5H; FAH1.

5

AAG14963.1 AF214009 Brassica napus
DESCRIPTION: cytochrome p450-dependent monooxygenase. BNF5H3.

10

CAA57425.1 X81831 Zea mays
DESCRIPTION: cytochrome P450. CYP71C4. family CYP71, subfamily CYP71C.

15

CAA72196.1 Y11368 Zea mays
DESCRIPTION: cytochrome p450. cyp71c4.

20

AAG44132.1 AF218296 Pisum sativum
DESCRIPTION: cytochrome P450. P450 isolog.

25

AAG14962.1 AF214008 Brassica napus
DESCRIPTION: cytochrome p450-dependent monooxygenase. BNF5H2.

30

AAG14961.1 AF214007 Brassica napus
DESCRIPTION: cytochrome p450-dependent monooxygenase. BNF5H1.

AAD56282.1 AF155332 Petunia x hybrida
DESCRIPTION: flavonoid 3'-hydroxylase. Ht1. cytochrome P450; CYP75B2.

471

35

AAD17855.1 AF099111 Zea mays
DESCRIPTION: sigma factor. sig2. putative sigma subunit of chloroplast Escherichia coli-like RNA polymerase; Sig2.

40

472

AAD45623.1 AF084185 Brassica napus
DESCRIPTION: dehydration responsive element binding protein. DNA binding protein; DRE binding protein.

45

- AAG43549.1 AF211531 *Nicotiana tabacum*
DESCRIPTION: Avr9/Cf-9 rapidly elicited protein 111B. ACRE111B. similar to EREBP transcription factors.
- 5 AAG43548.1 AF211530 *Nicotiana tabacum*
DESCRIPTION: Avr9/Cf-9 rapidly elicited protein 111A. ACRE111A. similar to EREBP transcription factors.
- 10 AAK01089.1 AF298231 *Hordeum vulgare*
DESCRIPTION: CBF3-like protein BCBF3. BCBF3. AP2 domain protein; DRE binding factor.
- 15 AAG59618.1 AF239616 *Hordeum vulgare*
DESCRIPTION: CRT/DRE-binding factor. CBF.
- 20 AAK01088.1 AF298230 *Hordeum vulgare*
DESCRIPTION: CBF1-like protein BCBF1. BCBF1. AP2 domain protein; putative DRE binding factor.
- 25 AAG59619.1 AF243384 *Oryza sativa*
DESCRIPTION: CRT/DRE binding factor. CBF. DREB.
- 30 AAK31271.1 AC079890 *Oryza sativa*
DESCRIPTION: putative transcriptional factor. OSJNBb0089A17.22.
- 35 CAC12822.1 AJ299252 *Nicotiana tabacum*
DESCRIPTION: AP2 domain-containing transcription factor. ap2.
- 40 BAA76734.1 AB024575 *Nicotiana tabacum*
DESCRIPTION: ethylene responsive element binding factor.
- AAC29516.1 U77655 *Solanum tuberosum*
DESCRIPTION: DNA binding protein homolog. STWAAEIRD.
- 45 AAF23899.1 AF193803 *Oryza sativa*

- 5
 AAG60182.1 AC084763 *Oryza sativa*
 DESCRIPTION: putative ethylene-responsive element binding protein.
 OSJNBa0027P10.12.
- 10
 AAK31279.1 AC079890 *Oryza sativa*
 DESCRIPTION: putative ethylene-responsive element binding protein.
 OSJNBb0089A17.16.
- 15
 AAC14323.1 AF058827 *Nicotiana tabacum*
 DESCRIPTION: TSi1. Tsi1. contains putative AP2 DNA-binding domain;
 similar to Pti6.
- 20
 AAC50047.1 U89255 *Lycopersicon esculentum*
 DESCRIPTION: binds the GCC box pathogenesis-related promoter element
 DNA-binding protein. Pti4.
- 25
 BAA97122.1 AB016264 *Nicotiana sylvestris*
 DESCRIPTION: ERF (EREBP); ethylene-responsive element binding factor for
 basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive
 element binding factor. nserf2.
- 30
 CAB96899.1 AJ251249 *Catharanthus roseus*
 DESCRIPTION: transcription factor. AP2-domain DNA-binding protein. orca3.
- 35
 CAB93940.1 AJ238740 *Catharanthus roseus*
 DESCRIPTION: putative transcription factor. AP2-domain DNA-binding
 protein. orca2.
- 40
 AAF63205.1 AF245119 *Mesembryanthemum crystallinum*
 DESCRIPTION: AP2-related transcription factor. CDBP. stress induced
 transcription factor.
- 45
 BAA87068.1 AB035270 *Matricaria chamomilla*
 DESCRIPTION: ethylene-responsive element binding protein1 homolog.
 McEREBP1.

CAB96900.1 AJ251250 Catharanthus roseus
DESCRIPTION: transcription factor. AP2-domain DNA-binding protein. orca3.

5 BAB21218.1 AP002913 Oryza sativa
DESCRIPTION: putative DNA binding protein RAV2. P0480E02.24.

10 BAA07321.1 D38123 Nicotiana tabacum
DESCRIPTION: ERF1. ethylene-responsive transcription factor.

15 AAC49740.1 U89256 Lycopersicon esculentum
DESCRIPTION: binds the GCC box pathogenesis-related promoter element
DNA-binding protein. Pti5.

20 AAB38748.1 U81157 Nicotiana tabacum
DESCRIPTION: S25-XP1 DNA binding protein.

BAB21211.1 AP002913 Oryza sativa
DESCRIPTION: putative DNA binding protein RAV2. P0480E02.17.

25 473

BAA85438.1 AP000616 Oryza sativa
DESCRIPTION: similar to RING-H2 finger protein RHA1a (AF078683).

30 AAK00436.1 AC060755 Oryza sativa
DESCRIPTION: putative zinc finger protein. OSJNBa0003O19.23.

35 AAG43550.1 AF211532 Nicotiana tabacum
DESCRIPTION: Avr9/Cf-9 rapidly elicited protein 132. ACRE132. similar to
RING finger proteins.

40 475

AAG43550.1 AF211532 Nicotiana tabacum
DESCRIPTION: Avr9/Cf-9 rapidly elicited protein 132. ACRE132. similar to
RING finger proteins.

45 BAA78746.1 AB023482 Oryza sativa

DESCRIPTION: Similar to Arabidopsis thaliana RING-H2 finger protein
RHX1a
mRNA, partial cds.(AF079184).

5

BAA96875.1 AB045121 Oryza sativa
DESCRIPTION: RING finger 1. RRF1.

10

CAA74911.1 Y14573 Hordeum vulgare
DESCRIPTION: ring finger protein. putative.

15

AAK00436.1 AC060755 Oryza sativa
DESCRIPTION: putative zinc finger protein. OSJNBa0003O19.23.

20

AAG46117.1 AC073166 Oryza sativa
DESCRIPTION: putative ring finger protein. OSJNBb0064P21.7.

25

BAA90357.1 AP001080 Oryza sativa
DESCRIPTION: EST AU070319(S10788) corresponds to a region of the
predicted gene. Similar to RING-H2 finger protein RHA2b (AC006200).

30

BAA77204.1 AB026262 Cicer arietinum
DESCRIPTION: ring finger protein.

35

BAA90806.1 AP001168 Oryza sativa
DESCRIPTION: ESTs C26000(C11448),AU082130(C11448) correspond to a
region
of the predicted gene.; Similar to mRNA for zinc-finger protein (Z36749).

476

40

BAA78764.1 AB023482 Oryza sativa
DESCRIPTION: ESTs C98382(C2985),D22444(C11129) correspond to a region
of
the predicted gene.; Similar to Arabidopsis thaliana APK1 gene for protein
tyrosine-serine-threonine kinase.(D12522).

45

AAK11674.1 AF339747 Lophopyrum elongatum
DESCRIPTION: protein kinase. ESI47.

- AA43496.1 AF131222 *Lophopyrum elongatum*
DESCRIPTION: protein serine/threonine kinase. ESI47. induced in roots by
5 salt stress, osmotic stress, and ABA treatment.
- AAG16628.1 AY007545 *Brassica napus*
DESCRIPTION: protein serine/threonine kinase BNK1.
10
- BAA94509.1 AB041503 *Populus nigra*
DESCRIPTION: protein kinase 1. PnPK1.
- 15 BAA94510.1 AB041504 *Populus nigra*
DESCRIPTION: protein kinase 2. PnPK2.
- 20 BAB07999.1 AP002525 *Oryza sativa*
DESCRIPTION: putative protein kinase. P0462H08.22. contains EST
C22619(S11214).
- 25 BAB03429.1 AP002817 *Oryza sativa*
DESCRIPTION: EST C22619(S11214) corresponds to a region of the predicted
gene. Similar to *Arabidopsis thaliana* chromosome 2, BAC clone T17D12;
putative protein kinase (AC006587).
- 30 BAA87853.1 AP000816 *Oryza sativa*
DESCRIPTION: EST AU030604(E51294) corresponds to a region of the
predicted gene. Similar to putative NAK-like Ser/Thr protein kinase.
35 (AF001308).
- BAB16871.1 AP002537 *Oryza sativa*
DESCRIPTION: putative protein kinase APK1A*Arabidopsis thaliana*.
P0001B06.24. contains ESTs C22608(R3192),D25110(R3192).
40
- BAB39409.1 AP002901 *Oryza sativa*
DESCRIPTION: putative protein kinase. P0456F08.9. contains EST
C23560(R0290).
45

AAK00425.1 AC069324 Oryza sativa
DESCRIPTION: Putative protein kinase. OSJNBa0071K19.11.

5 BAB39873.1 AP002882 Oryza sativa
DESCRIPTION: putative protein kinase. P0439B06.8. contains ESTs
AU056701(S20808),AU056702(S20808).

10 CAB51834.1 00069 Oryza sativa
DESCRIPTION: 11332.5. contains eukaryotic protein kinase domain PF.

15 BAB21240.1 AP002953 Oryza sativa
DESCRIPTION: Putative protein kinase. P0426D06.20. contains ESTs
C22359(C11461),C22360(C11461).

20 AAK21965.1 AY028699 Brassica napus
DESCRIPTION: receptor protein kinase PERK1.

25 AAG59657.1 AC084319 Oryza sativa
DESCRIPTION: putative protein kinase. OSJNBa0004B24.20.

30 AAG03090.1 AC073405 Oryza sativa
DESCRIPTION: Similar to an Arabidopsis somatic embryogenesis
receptor-like kinase (AC007504).

35 AAG25966.1 AF302082 Nicotiana tabacum
DESCRIPTION: cytokinin-regulated kinase 1. CRK1. protein kinase;
transcript abundance decreases rapidly after cytokinin treatment.

40 BAB21241.1 AP002953 Oryza sativa
DESCRIPTION: Putative Pto kinase interactor 1. P0426D06.21. contains ESTs
AU108280(E0721),D48017(S13927).

45 CAB51480.1 Y14600 Sorghum bicolor
DESCRIPTION: putative protein serine /threonine kinase. RLK1. accumulates
in mesophyll cells.

AAC61805.1 U28007 *Lycopersicon esculentum*
DESCRIPTION: serine/threonine protein kinase. Pto kinase interactor 1.
Pti1. Pti1 kinase.

5

BAA87852.1 AP000816 *Oryza sativa*
DESCRIPTION: Similar to putative Ser/Thr protein kinase. (AC004218).

10

BAA92221.1 AP001278 *Oryza sativa*
DESCRIPTION: Similar to *Arabidopsis thaliana* chromosome II BAC F12L6
genomic sequence, putative protein kinase. (AC004218).

15

AAB09771.1 U67422 *Zea mays*
DESCRIPTION: CRINKLY4 precursor. cr4. receptor kinase homolog.

20

BAA90808.1 AP001168 *Oryza sativa*
DESCRIPTION: Similar to putative receptor-like protein kinase (AL035679).

25

AAC27894.1 AF023164 *Zea mays*
DESCRIPTION: leucine-rich repeat transmembrane protein kinase 1. ltk1.

30

AAB61708.1 U93048 *Daucus carota*
DESCRIPTION: somatic embryogenesis receptor-like kinase. SERK.

35

AAF91336.1 AF249317 *Glycine max*
DESCRIPTION: Pti1 kinase-like protein. Pti1a. protein kinase.

40

AAF91337.1 AF249318 *Glycine max*
DESCRIPTION: Pti1 kinase-like protein. Pti1b. protein kinase.

45

AAG33377.1 AF290411 *Oryza meyeriana*
DESCRIPTION: serine/threonine protein kinase. R1.

AAC27895.1 AF023165 *Zea mays*
DESCRIPTION: leucine-rich repeat transmembrane protein kinase 2. ltk2.

- AAK11566.1 AF318490 *Lycopersicon hirsutum*
DESCRIPTION: Pto-like protein kinase E. LhirPtoE. confers resistance to bacterial speck disease.
- 5 CAA97692.1 Z73295 *Catharanthus roseus*
DESCRIPTION: receptor-like protein kinase. CRPK1. Autophosphorylation predominantly on Thr, less on Ser. Mechanism: autophosphorylation in cis.
- 10 AAF34428.1 AF172282 *Oryza sativa*
DESCRIPTION: receptor-like protein kinase. DUPR11.18.
- 15 AAF76306.1 AF220602 *Lycopersicon pimpinellifolium*
DESCRIPTION: Pto kinase.
- 20 AAB47423.1 U59315 *Lycopersicon pimpinellifolium*
DESCRIPTION: serine/threonine protein kinase Pto. Pto. bacterial speck disease resistance in tomato; disease resistance gene.
- 25 AAC48914.1 U02271 *Lycopersicon pimpinellifolium*
DESCRIPTION: protein kinase.
- 30 AAK11567.1 AF318491 *Lycopersicon hirsutum*
DESCRIPTION: Pto-like protein kinase F. LhirPtoF.
- 35 AAB47421.1 U59316 *Lycopersicon esculentum*
DESCRIPTION: serine/threonine protein kinase Pto. pto. allele of Pto bacterial speck disease resistance gene in tomato.
- 40 AAF76313.1 AF220603 *Lycopersicon esculentum*
DESCRIPTION: Pto kinase. LescPth5.
- 45 BAA92954.1 AP001551 *Oryza sativa*
DESCRIPTION: Similar to *Oryza sativa* protein kinase (OSPK10) mRNA.

(L27821).

BAA92953.1 AP001551 *Oryza sativa*

- 5 DESCRIPTION: Similar to *Arabidopsis thaliana* chromosome 4 BAC clone F10M6
; S-receptor kinase -like protein. (AL021811).

479

10

CAA42622.1 X60007 *Nicotiana sylvestris*

DESCRIPTION: nsGRP-2. putative glycine-rich protein of 19.7kDa.

480

15

BAA83373.1 AP000391 *Oryza sativa*

DESCRIPTION: ESTs C22657(S0014),C22656(S0014) correspond to a region
of
the predicted gene.; Similar to receptor protein kinase, ERECTA
(AC004484).

20

BAA84787.1 AP000559 *Oryza sativa*

DESCRIPTION: ESTs C22657(S0014),C22656(S0014) correspond to a region
of
the predicted gene.; Similar to receptor protein kinase, ERECTA
(AC004484).

25

AAF91324.1 AF244890 *Glycine max*

DESCRIPTION: receptor-like protein kinase 3. RLK3. GmRLK3.

30

AAF91322.1 AF244888 *Glycine max*

DESCRIPTION: receptor-like protein kinase 1. RLK1. GmRLK1.

35

AAF91323.1 AF244889 *Glycine max*

DESCRIPTION: receptor-like protein kinase 2. RLK2. GmRLK2.

40

AAB36558.1 U77888 *Ipomoea nil*

DESCRIPTION: receptor-like protein kinase INRPK1. inrpkl. leucine-rich
repeat.

45

- AAC36318.1 AF053127 *Malus x domestica*
DESCRIPTION: leucine-rich receptor-like protein kinase. LRPKml.
- 5 AAF59906.1 AF197947 *Glycine max*
DESCRIPTION: receptor protein kinase-like protein. CLV1B.
- 10 BAB40094.1 AP003210 *Oryza sativa*
DESCRIPTION: putative receptor protein kinase. OSJNBa0010K01.7.
- 15 AAF59905.1 AF197946 *Glycine max*
DESCRIPTION: receptor protein kinase-like protein. CLV1A.
- CAC20842.1 AJ250467 *Pinus sylvestris*
DESCRIPTION: receptor protein kinase. upk.
- 20 BAB03629.1 AP002522 *Oryza sativa*
DESCRIPTION: putative protein kinase Xa21. P0009G03.30.
- 25 BAB03621.1 AP002522 *Oryza sativa*
DESCRIPTION: putative protein kinase Xa21. P0009G03.21.
- 30 BAB03631.1 AP002522 *Oryza sativa*
DESCRIPTION: putative protein kinase Xa21. P0009G03.32.
- 35 AAB82755.1 U72725 *Oryza longistaminata*
DESCRIPTION: receptor kinase-like protein. Xa21 gene family member A1;
downstream of microsatellite region; disease resistance gene family
member.
- 40 AAF34426.1 AF172282 *Oryza sativa*
DESCRIPTION: leucine rich repeat containing protein kinase. DUPR11.16.
- 45 AAK27806.1 AC022457 *Oryza sativa*
DESCRIPTION: putative protein kinase. OSJNBa0006L06.21.

- CAA61510.1 X89226 *Oryza sativa*
DESCRIPTION: leucine-rich repeat/receptor protein kinase. lrk2.
- 5 AAC49123.1 U37133 *Oryza sativa*
DESCRIPTION: receptor kinase-like protein. Xa21. Xa21 disease resistance gene.
- 10 AAC80225.1 U72723 *Oryza longistaminata*
DESCRIPTION: receptor kinase-like protein. Xa21. disease resistance gene.
- 15 AAK27817.1 AC022457 *Oryza sativa*
DESCRIPTION: putative protein kinase. OSJNBa0006L06.16.
- 20 BAA82393.1 AP000367 *Oryza sativa*
DESCRIPTION: EST C96716(C10608) corresponds to a region of the predicted gene.; Similar to putative receptor protein kinase. (AC002334).
- 25 BAB03627.1 AP002522 *Oryza sativa*
DESCRIPTION: putative protein kinase Xa21. P0009G03.27.
- 30 AAB82756.1 U72724 *Oryza sativa*
DESCRIPTION: receptor kinase-like protein. Xa21 gene family member E.
- 35 AAG52992.1 U77888 *Ipomoea nil*
DESCRIPTION: receptor-like protein kinase INRPK1a. inrpk1.
- 40 BAA88636.1 AB029327 *Nicotiana tabacum*
DESCRIPTION: elicitor-inducible LRR receptor-like protein EILP. EILP.
- 45 AAB82753.1 U72726 *Oryza longistaminata*
DESCRIPTION: receptor kinase-like protein. Xa21 gene family member D.
- AAG52994.1 U77888 *Ipomoea nil*
DESCRIPTION: receptor-like protein kinase INRPK1c. inrpk1.

- CAB51480.1 Y14600 *Sorghum bicolor*
DESCRIPTION: putative protein serine /threonine kinase. RLK1. accumulates
in mesophyll cells.
- 5 AAK21965.1 AY028699 *Brassica napus*
DESCRIPTION: receptor protein kinase PERK1.
- 481
- 10 -----
CAB43505.1 AJ239051 *Cicer arietinum*
DESCRIPTION: cytochrome P450. cyp81E2.
- 15 BAA22422.1 AB001379 *Glycyrrhiza echinata*
DESCRIPTION: cytochrome P450. CYP81E1.
- 20 BAA93634.1 AB025016 *Lotus japonicus*
DESCRIPTION: cytochrome P450.
- 25 BAA74465.1 AB022732 *Glycyrrhiza echinata*
DESCRIPTION: cytochrome P450. CYP Ge-31.
- 30 CAB41490.1 AJ238439 *Cicer arietinum*
DESCRIPTION: cytochrome P450 monooxygenase. cyp81E3v2.
- CAA10067.1 AJ012581 *Cicer arietinum*
DESCRIPTION: cytochrome P450. cyp81E3.
- 35 CAA04117.1 AJ000478 *Helianthus tuberosus*
DESCRIPTION: fatty acid in-chain hydroxylase. cytochrome P450. CYP81B1l.
chimeric sequence (from 5'-race).
- 40 CAA04116.1 AJ000477 *Helianthus tuberosus*
DESCRIPTION: fatty acid in-chain hydroxylase. cytochrome P450. CYP81B1c.
- 45 AAK38080.1 AF321856 *Lolium rigidum*
DESCRIPTION: putative cytochrome P450.

- AAK38079.1 AF321855 *Lolium rigidum*
DESCRIPTION: putative cytochrome P450.
- 5
- AAK38081.1 AF321857 *Lolium rigidum*
DESCRIPTION: putative cytochrome P450.
- 10
- AAG09208.1 AF175278 *Pisum sativum*
DESCRIPTION: wound-inducible P450 hydroxylase. CYP82A1.
- 15
- CAA71876.1 Y10982 *Glycine max*
DESCRIPTION: putative cytochrome P450.
- 20
- AAC49188.2 U29333 *Pisum sativum*
DESCRIPTION: cytochrome P450 monooxygenase. CYP82. new cytochrome P450 family.
- 25
- CAA65580.1 X96784 *Nicotiana tabacum*
DESCRIPTION: cytochrome P450. hsr515.
- 30
- CAA71515.1 Y10491 *Glycine max*
DESCRIPTION: putative cytochrome P450.
- 35
- BAA92894.1 AB006790 *Petunia x hybrida*
DESCRIPTION: cytochrome P450. IMT-2.
- 40
- AAG44132.1 AF218296 *Pisum sativum*
DESCRIPTION: cytochrome P450. P450 isolog.
- 45
- CAA64635.1 X95342 *Nicotiana tabacum*
DESCRIPTION: cytochrome P450. hsr515. hypersensitivity-related gene.
- AAD56282.1 AF155332 *Petunia x hybrida*
DESCRIPTION: flavonoid 3'-hydroxylase. Ht1. cytochrome P450; CYP75B2.

AAC34853.1 AF082028 *Hemerocallis* hybrid cultivar
 DESCRIPTION: putative cyt P450-containing fatty acid hydroxylase.
 senescence-associated protein 3. SA3. mRNA accumulates in senescing
 5 petals.

BAA12159.1 D83968 *Glycine max*
 DESCRIPTION: Cytochrome P-450 (CYP93A1).
 10

AAA32913.1 M32885 *Persea americana*
 DESCRIPTION: cytochrome P-450LXXIA1 (cyp71A1).
 15

CAA70575.1 Y09423 *Nepeta racemosa*
 DESCRIPTION: cytochrome P450. CYP71A5.
 20

AAG34695.1 AF313492 *Matthiola incana*
 DESCRIPTION: putative cytochrome P450.
 25

CAA71877.1 Y10983 *Glycine max*
 DESCRIPTION: putative cytochrome P450.
 30

CAA71516.1 Y10492 *Glycine max*
 DESCRIPTION: putative cytochrome P450.
 35

AAB94587.1 AF022458 *Glycine max*
 DESCRIPTION: CYP98A2p. CYP98A2. cytochrome P450 monooxygenase.
 40

AAC39454.1 AF014802 *Eschscholzia californica*
 DESCRIPTION: (S)-N-methylcoclaurine 3'-hydroxylase. CYP82B1. cytochrome
 P-450-dependent monooxygenase; methyl jasmonate-inducible cytochrome
 P-450-dependent, homologous to wound-inducible CYP82A1 of *Pisum sativum*
 45 GenBank Accession Number U29333.

CAA70576.1 Y09424 *Nepeta racemosa*
 DESCRIPTION: cytochrome P450. CYP71A6.

- AAB94590.1 AF022461 Glycine max
DESCRIPTION: CYP82C1p. CYP82C1. cytochrome P450 monooxygenase.
- 5 BAB40323.1 AB037244 Asparagus officinalis
DESCRIPTION: cytochrome P450. ASPI-1.
- 10 BAB40324.1 AB037245 Asparagus officinalis
DESCRIPTION: cytochrome P450. ASPI-2.
- 15 AAB61965.1 U48435 Solanum chacoense
DESCRIPTION: putative cytochrome P450.
- 20 AAA19701.1 L24438 Thlaspi arvense
DESCRIPTION: cytochrome P450.
- BAA84071.1 AB028151 Antirrhinum majus
DESCRIPTION: flavone synthase II. cytochrome P450. AFNS2.
- 25 BAA13076.1 D86351 Glycine max
DESCRIPTION: cytochrome P-450 (CYP93A2).
- 30 AAD38930.1 AF135485 Glycine max
DESCRIPTION: cytochrome P450 monooxygenase CYP93D1. CYP93E1.
- 35 AAC32274.1 AF081575 Petunia x hybrida
DESCRIPTION: flavonoid 3',5'-hydroxylase. Hfl. P450 enzyme.
- 487
-
- 40 BAA96181.1 AP002093 Oryza sativa
DESCRIPTION: EST AU056651(S20760) corresponds to a region of the
predicted gene. Similar to Arabidopsis thaliana chromosome II BAC F19I3;
putative amino acid transporter (AC004238).
- 45 BAA96139.1 AP002092 Oryza sativa
DESCRIPTION: EST AU056651(S20760) corresponds to a region of the
predicted gene. Similar to Arabidopsis thaliana chromosome II BAC F19I3;

putative amino acid transporter (AC004238).

495

5 AAB71528.1 U94784 *Helianthus annuus*
DESCRIPTION: ATPase. unconventional myosin. hamy4. Hamyo4.

10 AAB71529.1 U94785 *Helianthus annuus*
DESCRIPTION: ATPase. unconventional myosin. hamy5. Hamyo5.

15 AAB71527.1 U94782 *Helianthus annuus*
DESCRIPTION: ATPase. unconventional myosin. hamy2. Hamyo2.

20 AAD17931.2 AF104924 *Zea mays*
DESCRIPTION: unconventional myosin heavy chain. MYO1. ATPase; similar
to
myosin class XI.

25 AAC27525.1 AF077352 *Chlamydomonas reinhardtii*
DESCRIPTION: myosin heavy chain. MYO1. class XI.

30 AAK21311.1 AF338254 *Petroselinum crispum*
DESCRIPTION: myosin subfamily XI heavy chain. PCM3.

BAA87057.1 AB034154 *Chara corallina*
DESCRIPTION: unconventional myosin heavy chain. ccm.

35 BAB03273.1 AB007459 *Chara corallina*
DESCRIPTION: cytoplasmic streaming. myosin. ccm1. CCM1.

40 AAF43440.1 AF233886 *Vallisneria spiralis*
DESCRIPTION: unconventional myosin XI. VMYO1.

45 AAB53062.1 U94398 *Acetabularia cliftonii*
DESCRIPTION: myosin. myo2.

AAD34597.1 AF147739 Zea mays
 DESCRIPTION: myosin XI. M2. unconventional myosin.

5 AAB53061.1 U94397 Acetabularia cliftonii
 DESCRIPTION: myosin. myo1.

10 AAD31926.1 AF147738 Zea mays
 DESCRIPTION: myosin VIII ZMM3. zmm3. unconventional myosin.

15 AAB71526.1 U94781 Helianthus annuus
 DESCRIPTION: unconventional myosin. hamy1. homologous to ATM1.

20 AAG49341.1 AF319457 Petroselinum crispum
 DESCRIPTION: myosin subfamily VIII heavy chain.

25 AAB93521.1 U94783 Helianthus annuus
 DESCRIPTION: unconventional myosin. hamy3. Hamyo3; similar to class VIII myosin.

30 CAA47476.1 X67102 Anemia phyllitidis
 DESCRIPTION: myosin heavy chain. myo15.

35 CAA47477.1 X67103 Anemia phyllitidis
 DESCRIPTION: myosin heavy chain. myo22.

40 AAF43441.1 AF233887 Vallisneria gigantea
 DESCRIPTION: unconventional myosin VIII. VMYO2.

45 AAG13633.1 AC078840 Oryza sativa
 DESCRIPTION: putative myosin. OSJNBb0073N24.16.

AAA92120.1 U48785 Vigna mungo
 DESCRIPTION: plant myosin MBM1. mbm1. head coding region.

496

AAA34138.1 M96324 *Lycopersicon esculentum*
DESCRIPTION: The calcium ATPase is a calcium ion pump. Ca²⁺-ATPase.
LCA1.

5

AAD11618.1 AF050496 *Lycopersicon esculentum*
DESCRIPTION: Ca²⁺-ATPase. LCA1B; alternative transcript.

10

AAD11617.1 AF050495 *Lycopersicon esculentum*
DESCRIPTION: Ca²⁺-ATPase. LCA1A; alternative transcript.

15

BAA90510.2 AP001111 *Oryza sativa*
DESCRIPTION: rice EST AU030811, similar to rice Ca²⁺-ATPase (U82966).

20

CAA63790.1 X93592 *Dunaliella bioculata*
DESCRIPTION: P-type ATPase. ca1. calcium pumping; CA1.

25

AAB58910.1 U82966 *Oryza sativa*
DESCRIPTION: Ca²⁺-ATPase.

30

AAF73985.1 AF096871 *Zea mays*
DESCRIPTION: calcium pump. calcium ATPase. cap1.

35

AAG28436.1 AF195029 *Glycine max*
DESCRIPTION: plasma membrane Ca²⁺-ATPase. SCA2.

40

AAG28435.1 AF195028 *Glycine max*
DESCRIPTION: plasma membrane Ca²⁺-ATPase. SCA1.

CAA68234.1 X99972 *Brassica oleracea*
DESCRIPTION: calmodulin-stimulated calcium-ATPase.

45

AAD31896.1 AF145478 *Mesembryanthemum crystallinum*
DESCRIPTION: calcium ATPase.

CAB85494.1 AJ132891 *Medicago truncatula*

DESCRIPTION: proton pump. H⁺-ATPase. ha1.

CAB85495.1 AJ132892 *Medicago truncatula*

5 DESCRIPTION: proton pump. H⁺-ATPase. ha1.

CAB69824.1 AJ271439 *Prunus persica*

10 DESCRIPTION: plasma membrane H⁺ ATPase. PPA1.

CAA52107.1 X73901 *Dunaliella bioculata*

DESCRIPTION: plasma membrane ATPase. pma1.

15 AAD46188.1 AF156691 *Nicotiana plumbaginifolia*

DESCRIPTION: plasma membrane proton ATPase. pma9.

20 BAA01058.1 D10207 *Oryza sativa*

DESCRIPTION: H-ATPase. OSA1.

AAA34094.1 M80489 *Nicotiana plumbaginifolia*

25 DESCRIPTION: plasma membrane H⁺ ATPase. pma1.

AAA34098.1 M80490 *Nicotiana plumbaginifolia*

30 DESCRIPTION: plasma membrane H⁺ ATPase. pma3.

AAA34173.1 M60166 *Lycopersicon esculentum*

DESCRIPTION: H⁺-ATPase. LHA1.

35 CAA54046.1 X76536 *Solanum tuberosum*

DESCRIPTION: H(+)-transporting ATPase. PHA1.

40 AAD55399.1 AF179442 *Lycopersicon esculentum*

DESCRIPTION: plasma membrane H⁺-ATPase isoform LHA2. LHA2.

AAB49042.1 U54690 *Dunaliella acidophila*

45 DESCRIPTION: plasma membrane proton ATPase. dha1. DaDHA1; proton pump.

- 5 AAF98344.1 AF275745 *Lycopersicon esculentum*
 DESCRIPTION: plasma membrane H⁺-ATPase. LHA2. P-type ion pump.
- 10 BAA08134.1 D45189 *Zostera marina*
 DESCRIPTION: plasma membrane H⁺-ATPase. zha1.
- 15 CAA59800.1 X85805 *Zea mays*
 DESCRIPTION: H(+) -transporting ATPase. MHA-2.
- 20 AAB17186.1 U72148 *Lycopersicon esculentum*
 DESCRIPTION: plasma membrane H⁺-ATPase. LHA4. plasma membrane
 proton
 pumping ATPase.
- 25 CAA54045.1 X76535 *Solanum tuberosum*
 DESCRIPTION: H(+) -transporting ATPase. PHA2.
- 30 CAB69823.1 AJ271438 *Prunus persica*
 DESCRIPTION: plasma membrane H⁺ ATPase. PPA2.
- 35 BAA06629.1 D31843 *Oryza sativa*
 DESCRIPTION: plasma membrane H⁺-ATPase. OSA2.
- 40 CAC29435.1 AJ310523 *Vicia faba*
 DESCRIPTION: P-type H⁺-ATPase. vha4. predominantly expressed in flowers.
- 45 CAC29436.1 AJ310524 *Vicia faba*
 DESCRIPTION: P-type H⁺-ATPase. ha5. predominantly expressed in guard
 cells and flowers.
- CAA59799.1 X85804 *Phaseolus vulgaris*

DESCRIPTION: H(+)-transporting ATPase. BHA-1.

5 AAD46186.1 AF156679 *Nicotiana plumbaginifolia*
DESCRIPTION: plasma membrane proton ATPase. pma6.

10 AAB84202.2 AF029256 *Kosteletzkya virginica*
DESCRIPTION: plasma membrane proton ATPase. ATP1.

15 AAD46187.1 AF156683 *Nicotiana plumbaginifolia*
DESCRIPTION: plasma membrane proton ATPase. pma8.

AAB60276.1 U09989 *Zea mays*
DESCRIPTION: H(+)-transporting ATPase. Mha1.

20 AAB41898.1 U84891 *Mesembryanthemum crystallinum*
DESCRIPTION: plasma membrane proton pump. H⁺-transporting ATPase.
PMA.

25 AAB35314.2 S79323 *Vicia faba*
DESCRIPTION: plasma membrane H(+)-ATPase precursor. plasma membrane
H(+)-ATPase. This sequence comes from Fig. 1; conceptual translation
presented here differs from translation in publication.

30 AAK31799.1 AY029190 *Lilium longiflorum*
DESCRIPTION: plasma membrane H⁺ ATPase. LILHA1.

35 CAA47275.1 X66737 *Nicotiana plumbaginifolia*
DESCRIPTION: plasma membrane H⁺-ATPase. pma4.

40 BAA37150.1 AB022442 *Vicia faba*
DESCRIPTION: p-type H⁺-ATPase. VHA2.

45 AAG01028.1 AF289025 *Cucumis sativus*
DESCRIPTION: plasma membrane H⁺-ATPase.

AAA81348.1 U38965 Vicia faba
DESCRIPTION: p-type H⁺-ATPase. VHA2.

5 AAK32118.1 AF308816 Hordeum vulgare
DESCRIPTION: plasmalemma H⁺-ATPase 1.

10 AAF97591.1 AF263917 Lycopersicon esculentum
DESCRIPTION: plasma membrane proton ATPase. LHA8.

15 AAK32119.1 AF308817 Hordeum vulgare
DESCRIPTION: plasmalemma H⁺-ATPase 2.

20 AAA20601.1 U08985 Zea mays
DESCRIPTION: plasma-membrane H⁺ ATPase. Zmpm1.
497

25 AAB41742.1 U82559 Lycopersicon esculentum
DESCRIPTION: aldehyde oxidase 1 homolog. TAO1. has sequence properties
of
the molybdenum cofactor containing the hydroxylase genes aldehyde oxidase
and xanthine dehydrogenase; belongs to a multigene family.

30 AAB41741.1 U82558 Lycopersicon esculentum
DESCRIPTION: aldehyde oxidase 1 homolog. TAO1. has sequence properties
of
the molybdenum cofactor containing the hydroxylase genes aldehyde oxidase
and xanthine dehydrogenase; belongs to a multigene family.

35 498

CAA73134.1 Y12531 Brassica oleracea
DESCRIPTION: serine/threonine kinase. BRLK.

40 AAB93834.1 U82481 Zea mays
DESCRIPTION: KI domain interacting kinase 1. KIK1. receptor-like protein
kinase; serine/threonine protein kinase.

45 CAA67145.1 X98520 Brassica oleracea

DESCRIPTION: receptor-like kinase. SFR2.

CAA74661.1 Y14285 Brassica oleracea

5 DESCRIPTION: SFR1. extracellular S domain: 8-1342; transmembrane domain: 1343-1411; intracellular kinase domain: 1412-2554.

CAA73133.1 Y12530 Brassica oleracea

10 DESCRIPTION: serine /threonine kinase. ARLK.

AAA62232.1 U00443 Brassica napus

15 DESCRIPTION: S-receptor kinase. protein contains an immunoglobulin-like domain.

CAB89179.1 AJ245479 Brassica napus subsp. napus

20 DESCRIPTION: ser /thr kinase. S-locus receptor kinase. srk.

AAA33008.1 M97667 Brassica napus

25 DESCRIPTION: serine/threonine kinase receptor.

BAA92836.1 AB032473 Brassica oleracea

DESCRIPTION: S18 S-locus receptor kinase. SRK18.

30 BAA23676.1 AB000970 Brassica rapa

DESCRIPTION: receptor kinase 1. BcRK1.

AAC23542.1 U20948 Ipomoea trifida

35 DESCRIPTION: receptor protein kinase. IRK1.

AAA33000.1 M76647 Brassica oleracea

40 DESCRIPTION: receptor protein kinase. SKR6.

BAA21132.1 D88193 Brassica rapa

DESCRIPTION: S-receptor kinase. SRK9 (B.c).

45

BAA06285.1 D30049 Brassica rapa

DESCRIPTION: S-receptor kinase SRK9.

CAB41879.1 Y18260 Brassica oleracea

5 DESCRIPTION: SRK15 protein. SRK15. receptor-like kinase.

BAA07577.2 D38564 Brassica rapa

10 DESCRIPTION: receptor protein kinase SRK12.

CAA74662.1 Y14286 Brassica oleracea

15 DESCRIPTION: SFR3. extracellular S domain: 123-1346; transmembrane domain: 1347-1412; intracellular kinase domain: from 1413.

BAB21001.1 AB054061 Brassica rapa

20 DESCRIPTION: S locus receptor kinase. SRK22.

BAA92837.1 AB032474 Brassica oleracea

DESCRIPTION: S60 S-locus receptor kinase. SRK60.

25 CAB41878.1 Y18259 Brassica oleracea

DESCRIPTION: SRK5 protein. SRK5. receptor-like kinase.

CAA79355.1 Z18921 Brassica oleracea

30 DESCRIPTION: S-receptor kinase-like protein.

BAA07576.1 D38563 Brassica rapa

35 DESCRIPTION: receptor protein kinase SRK8.

AAF34428.1 AF172282 Oryza sativa

DESCRIPTION: receptor-like protein kinase. DUPR11.18.

40 AAD21872.1 AF078082 Phaseolus vulgaris

DESCRIPTION: receptor-like protein kinase homolog RK20-1.

45 AAD52097.1 AF088885 Nicotiana tabacum

DESCRIPTION: receptor-like kinase CHRK1. Chrk1.

5 BAA94516.1 AP001800 *Oryza sativa*
DESCRIPTION: Similar to *Zea mays* S-domain receptor-like protein kinase
(AJ010166).

10 BAB07906.1 AP002835 *Oryza sativa*
DESCRIPTION: putative S-receptor kinase. P0417G05.14.

15 BAA94517.1 AP001800 *Oryza sativa*
DESCRIPTION: Similar to *Zea mays* S-domain receptor-like protein kinase
(AJ010166).

20 BAB07905.1 AP002835 *Oryza sativa*
DESCRIPTION: putative S-receptor kinase. P0417G05.13.

25 AAA33915.1 L27821 *Oryza sativa*
DESCRIPTION: receptor type serine/threonine kinase. protein kinase.

30 BAB18292.1 AP002860 *Oryza sativa*
DESCRIPTION: putative receptor-like protein kinase. P0409B08.19.

499 BAA94529.2 AP001800 *Oryza sativa*
DESCRIPTION: Similar to *Zea mays* S-domain receptor-like protein kinase
(AJ010166).

35 AAC36318.1 AF053127 *Malus x domestica*
DESCRIPTION: leucine-rich receptor-like protein kinase. LRPKm1.

40 AAF91324.1 AF244890 *Glycine max*
DESCRIPTION: receptor-like protein kinase 3. RLK3. GmRLK3.

45 AAF91323.1 AF244889 *Glycine max*
DESCRIPTION: receptor-like protein kinase 2. RLK2. GmRLK2.

- CAA61510.1 X89226 *Oryza sativa*
DESCRIPTION: leucine-rich repeat/receptor protein kinase. lrk2.
- 5 AAF59906.1 AF197947 *Glycine max*
DESCRIPTION: receptor protein kinase-like protein. CLV1B.
- 10 AAF59905.1 AF197946 *Glycine max*
DESCRIPTION: receptor protein kinase-like protein. CLV1A.
- 15 AAF91322.1 AF244888 *Glycine max*
DESCRIPTION: receptor-like protein kinase 1. RLK1. GmRLK1.
- 20 BAB40094.1 AP003210 *Oryza sativa*
DESCRIPTION: putative receptor protein kinase. OSJNBa0010K01.7.
- 25 CAC20842.1 AJ250467 *Pinus sylvestris*
DESCRIPTION: receptor protein kinase. upk.
- 30 AAB36558.1 U77888 *Ipomoea nil*
DESCRIPTION: receptor-like protein kinase INRPK1. inrpk1. leucine-rich repeat.
- 35 BAA83373.1 AP000391 *Oryza sativa*
DESCRIPTION: ESTs C22657(S0014),C22656(S0014) correspond to a region of the predicted gene.; Similar to receptor protein kinase, ERECTA (AC004484).
- 40 BAA84787.1 AP000559 *Oryza sativa*
DESCRIPTION: ESTs C22657(S0014),C22656(S0014) correspond to a region of the predicted gene.; Similar to receptor protein kinase, ERECTA (AC004484).
- 45 AAK27806.1 AC022457 *Oryza sativa*
DESCRIPTION: putative protein kinase. OSJNBa0006L06.21.

AAF34426.1 AF172282 Oryza sativa
DESCRIPTION: leucine rich repeat containing protein kinase. DUPR11.16.

5

BAB03627.1 AP002522 Oryza sativa
DESCRIPTION: putative protein kinase Xa21. P0009G03.27.

10

BAB03631.1 AP002522 Oryza sativa
DESCRIPTION: putative protein kinase Xa21. P0009G03.32.

15

AAK27817.1 AC022457 Oryza sativa
DESCRIPTION: putative protein kinase. OSJNBa0006L06.16.

20

BAB03621.1 AP002522 Oryza sativa
DESCRIPTION: putative protein kinase Xa21. P0009G03.21.

25

BAB03629.1 AP002522 Oryza sativa
DESCRIPTION: putative protein kinase Xa21. P0009G03.30.

30

AAC80225.1 U72723 Oryza longistaminata
DESCRIPTION: receptor kinase-like protein. Xa21. disease resistance gene.

35

AAC49123.1 U37133 Oryza sativa
DESCRIPTION: receptor kinase-like protein. Xa21. Xa21 disease resistance gene.

BAA82393.1 AP000367 Oryza sativa
DESCRIPTION: EST C96716(C10608) corresponds to a region of the predicted gene.; Similar to putative receptor protein kinase. (AC002334).

40

AAB82755.1 U72725 Oryza longistaminata
DESCRIPTION: receptor kinase-like protein. Xa21 gene family member A1; downstream of microsatellite region; disease resistance gene family member.

45

AAG52992.1 U77888 Ipomoea nil

DESCRIPTION: receptor-like protein kinase INRPK1a. inrpk1.

AAB82756.1 U72724 Oryza sativa

5 DESCRIPTION: receptor kinase-like protein. Xa21 gene family member E.

AAB82753.1 U72726 Oryza longistaminata

10 DESCRIPTION: receptor kinase-like protein. Xa21 gene family member D.

CAB51480.1 Y14600 Sorghum bicolor

15 DESCRIPTION: putative protein serine /threonine kinase. RLK1. accumulates in mesophyll cells.

BAA88636.1 AB029327 Nicotiana tabacum

20 DESCRIPTION: elicitor-inducible LRR receptor-like protein EILP. EILP.

AAG52994.1 U77888 Ipomoea nil

DESCRIPTION: receptor-like protein kinase INRPK1c. inrpk1.

25 BAA94519.1 AP001800 Oryza sativa

DESCRIPTION: ESTs AU032341(R3918),AU071016(R10613) correspond to a region of the predicted gene. Similar to Arabidopsis thaliana chromosome 4, BAC F9D16; putative receptor kinase (AL035394).

30

BAB07903.1 AP002835 Oryza sativa

35 DESCRIPTION: putative receptor kinase. P0417G05.10. contains ESTs AU032341(R3918),AU071016(R10613).

BAA87853.1 AP000816 Oryza sativa

40 DESCRIPTION: EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative NAK-like Ser/Thr protein kinase. (AF001308).

AAD38286.1 AC007789 Oryza sativa

45 DESCRIPTION: putative protein kinase. OSJNBa0049B20.13.

BAB40081.1 AP003074 *Oryza sativa*
DESCRIPTION: putative receptor protein kinase. OSJNBa0004G10.30.

5 BAB18321.1 AP002865 *Oryza sativa*
DESCRIPTION: putative receptor protein kinase. P0034C11.11.

500

10 BAB40094.1 AP003210 *Oryza sativa*
DESCRIPTION: putative receptor protein kinase. OSJNBa0010K01.7.

AAC36318.1 AF053127 *Malus x domestica*
15 DESCRIPTION: leucine-rich receptor-like protein kinase. LRPKm1.

AAF59906.1 AF197947 *Glycine max*
20 DESCRIPTION: receptor protein kinase-like protein. CLV1B.

AAF59905.1 AF197946 *Glycine max*
DESCRIPTION: receptor protein kinase-like protein. CLV1A.

25 AAF91323.1 AF244889 *Glycine max*
DESCRIPTION: receptor-like protein kinase 2. RLK2. GmRLK2.

30 AAF91322.1 AF244888 *Glycine max*
DESCRIPTION: receptor-like protein kinase 1. RLK1. GmRLK1.

35 AAF91324.1 AF244890 *Glycine max*
DESCRIPTION: receptor-like protein kinase 3. RLK3. GmRLK3.

CAA61510.1 X89226 *Oryza sativa*
40 DESCRIPTION: leucine-rich repeat/receptor protein kinase. lrk2.

CAC20842.1 AJ250467 *Pinus sylvestris*
DESCRIPTION: receptor protein kinase. upk.

45 BAA84787.1 AP000559 *Oryza sativa*

DESCRIPTION: ESTs C22657(S0014),C22656(S0014) correspond to a region
of
the predicted gene.; Similar to receptor protein kinase, ERECTA
(AC004484).

5

BAA83373.1 AP000391 Oryza sativa
DESCRIPTION: ESTs C22657(S0014),C22656(S0014) correspond to a region
of
the predicted gene.; Similar to receptor protein kinase, ERECTA
(AC004484).

10

AAK27806.1 AC022457 Oryza sativa
DESCRIPTION: putative protein kinase. OSJNBa0006L06.21.

15

AAB36558.1 U77888 Ipomoea nil
DESCRIPTION: receptor-like protein kinase INRPK1. inrpk1. leucine-rich
repeat.

20

BAB03627.1 AP002522 Oryza sativa
DESCRIPTION: putative protein kinase Xa21. P0009G03.27.

25

BAB03629.1 AP002522 Oryza sativa
DESCRIPTION: putative protein kinase Xa21. P0009G03.30.

30

BAB03631.1 AP002522 Oryza sativa
DESCRIPTION: putative protein kinase Xa21. P0009G03.32.

BAB03621.1 AP002522 Oryza sativa
DESCRIPTION: putative protein kinase Xa21. P0009G03.21.

35

AAK27817.1 AC022457 Oryza sativa
DESCRIPTION: putative protein kinase. OSJNBa0006L06.16.

40

AAF34426.1 AF172282 Oryza sativa
DESCRIPTION: leucine rich repeat containing protein kinase. DUPR11.16.

45

- 5 AAB82755.1 U72725 *Oryza longistaminata*
DESCRIPTION: receptor kinase-like protein. Xa21 gene family member A1;
downstream of microsatellite region; disease resistance gene family
member.
- 10 AAC80225.1 U72723 *Oryza longistaminata*
DESCRIPTION: receptor kinase-like protein. Xa21. disease resistance gene.
- 15 AAC49123.1 U37133 *Oryza sativa*
DESCRIPTION: receptor kinase-like protein. Xa21. Xa21 disease resistance
gene.
- 20 BAA82393.1 AP000367 *Oryza sativa*
DESCRIPTION: EST C96716(C10608) corresponds to a region of the predicted
gene.; Similar to putative receptor protein kinase. (AC002334).
- 25 AAB82756.1 U72724 *Oryza sativa*
DESCRIPTION: receptor kinase-like protein. Xa21 gene family member E.
- 30 BAA88636.1 AB029327 *Nicotiana tabacum*
DESCRIPTION: elicitor-inducible LRR receptor-like protein EILP. EILP.
- 35 AAG52992.1 U77888 *Ipomoea nil*
DESCRIPTION: receptor-like protein kinase INRPK1a. inrpkl.
- 40 AAB82753.1 U72726 *Oryza longistaminata*
DESCRIPTION: receptor kinase-like protein. Xa21 gene family member D.
- 45 CAB51480.1 Y14600 *Sorghum bicolor*
DESCRIPTION: putative protein serine /threonine kinase. RLK1. accumulates
in mesophyll cells.
- 501 AAB61708.1 U93048 *Daucus carota*
DESCRIPTION: somatic embryogenesis receptor-like kinase. SERK.
-

CAA73134.1 Y12531 Brassica oleracea
DESCRIPTION: serine/threonine kinase. BRLK.

5 AAB93834.1 U82481 Zea mays
DESCRIPTION: KI domain interacting kinase 1. KIK1. receptor-like protein
kinase; serine/threonine protein kinase.

10 CAA67145.1 X98520 Brassica oleracea
DESCRIPTION: receptor-like kinase. SFR2.

15 CAA73133.1 Y12530 Brassica oleracea
DESCRIPTION: serine /threonine kinase. ARLK.

20 CAA74661.1 Y14285 Brassica oleracea
DESCRIPTION: SFR1. extracellular S domain: 8-1342; transmembrane domain:
1343-1411; intracellular kinase domain: 1412-2554.

25 AAA62232.1 U00443 Brassica napus
DESCRIPTION: S-receptor kinase. protein contains an immunoglobulin-like
domain.

30 BAA92836.1 AB032473 Brassica oleracea
DESCRIPTION: S18 S-locus receptor kinase. SRK18.

35 CAB41878.1 Y18259 Brassica oleracea
DESCRIPTION: SRK5 protein. SRK5. receptor-like kinase.

AAC23542.1 U20948 Ipomoea trifida
DESCRIPTION: receptor protein kinase. IRK1.

40 BAA23676.1 AB000970 Brassica rapa
DESCRIPTION: receptor kinase 1. BcRK1.

45 CAB41879.1 Y18260 Brassica oleracea
DESCRIPTION: SRK15 protein. SRK15. receptor-like kinase.

- AAA33000.1 M76647 Brassica oleracea
DESCRIPTION: receptor protein kinase. SKR6.
- 5 AAA33008.1 M97667 Brassica napus
DESCRIPTION: serine/threonine kinase receptor.
- 10 CAB89179.1 AJ245479 Brassica napus subsp. napus
DESCRIPTION: ser /thr kinase. S-locus receptor kinase. srk.
- 15 CAA74662.1 Y14286 Brassica oleracea
DESCRIPTION: SFR3. extracellular S domain: 123-1346; transmembrane domain: 1347-1412; intracellular kinase domain: from 1413.
- 20 BAA06285.1 D30049 Brassica rapa
DESCRIPTION: S-receptor kinase SRK9.
- 25 BAA21132.1 D88193 Brassica rapa
DESCRIPTION: S-receptor kinase. SRK9 (B.c).
- 30 BAA07577.2 D38564 Brassica rapa
DESCRIPTION: receptor protein kinase SRK12.
- CAA79355.1 Z18921 Brassica oleracea
DESCRIPTION: S-receptor kinase-like protein.
- 35 BAA07576.1 D38563 Brassica rapa
DESCRIPTION: receptor protein kinase SRK8.
- 40 BAB21001.1 AB054061 Brassica rapa
DESCRIPTION: S locus receptor kinase. SRK22.
- 45 BAA92837.1 AB032474 Brassica oleracea
DESCRIPTION: S60 S-locus receptor kinase. SRK60.

AAD21872.1 AF078082 Phaseolus vulgaris
DESCRIPTION: receptor-like protein kinase homolog RK20-1.

5 AAF34428.1 AF172282 Oryza sativa
DESCRIPTION: receptor-like protein kinase. DUPR11.18.

AAD52097.1 AF088885 Nicotiana tabacum
10 DESCRIPTION: receptor-like kinase CHRK1. Chrk1.

BAB07906.1 AP002835 Oryza sativa
DESCRIPTION: putative S-receptor kinase. P0417G05.14.
15

BAA94516.1 AP001800 Oryza sativa
DESCRIPTION: Similar to Zea mays S-domain receptor-like protein kinase
(AJ010166).
20

BAB18292.1 AP002860 Oryza sativa
DESCRIPTION: putative receptor-like protein kinase. P0409B08.19.
25

BAB07904.1 AP002835 Oryza sativa
DESCRIPTION: putative S-receptor kinase. P0417G05.12.

30 BAA94518.1 AP001800 Oryza sativa
DESCRIPTION: Similar to Arabidopsis thaliana chromosome 2 section 111 of
255; putative receptor-like protein kinase (AC002392).

502
35 -----

AAC78596.1 AF053998 Lycopersicon esculentum
DESCRIPTION: Hcr2-5D. Hcr2-5D. similar to Lycopersicon pimpinellifolium
disease resistance protein Cf-2.2 encoded by the sequence presented in
GenBank Accession Number U42445.
40

AAC78591.1 AF053993 Lycopersicon esculentum
DESCRIPTION: disease resistance protein. Cf-5.

45 AAC78593.1 AF053995 Lycopersicon esculentum

DESCRIPTION: Hcr2-0B. Hcr2-0B. similar to *Lycopersicon pimpinellifolium* disease resistance protein Cf-2.2 encoded by the sequence presented in GenBank Accession Number U42445.

5

AAC78592.1 AF053994 *Lycopersicon esculentum*
DESCRIPTION: Hcr2-0A. Hcr2-0A. similar to *Lycopersicon pimpinellifolium* disease resistance protein Cf-2.2 encoded by the sequence presented in GenBank Accession Number U42445.

10

AAC78594.1 AF053996 *Lycopersicon pimpinellifolium*
DESCRIPTION: Hcr2-2A. Hcr2-2A. similar to *Lycopersicon pimpinellifolium* disease resistance protein Cf-2.2 encoded by the sequence presented in GenBank Accession Number U42445.

15

CAA05274.1 AJ002236 *Lycopersicon pimpinellifolium*
DESCRIPTION: resistance gene. Cf-9. Cf-9.

20

AAA65235.1 U15936 *Lycopersicon pimpinellifolium*
DESCRIPTION: Cf-9 precursor. Cf-9. this is the ninth resistance gene to disease caused by *Cladosporium fulvum* to be isolated.

25

CAA05276.1 AJ002236 *Lycopersicon pimpinellifolium*
DESCRIPTION: resistance gene. Hcr9-9E. Hcr9-9E.

30

AAC78595.1 AF053997 *Lycopersicon esculentum*
DESCRIPTION: Hcr2-5B. Hcr2-5B. similar to *Lycopersicon pimpinellifolium* disease resistance protein Cf-2.2 encoded by the sequence presented in GenBank Accession Number U42445.

35

CAA05268.1 AJ002235 *Lycopersicon hirsutum*
DESCRIPTION: Resistance gene. Cf-4. Cf-4.

40

CAA05279.1 AJ002237 *Lycopersicon esculentum*
DESCRIPTION: Hcr9-0. Hcr9-0. homologue of *Cladosporium fulvum* disease resistance gene Cf-9.

45

BAB08215.1 AP002539 *Oryza sativa*

DESCRIPTION: Similar to *Lycopersicon esculentum* disease resistance protein (AF053993).

5 BAA96776.1 AP002521 *Oryza sativa*
DESCRIPTION: Similar to *Lycopersicon esculentum* disease resistance protein (AF053993).

10 AAG21897.1 AC026815 *Oryza sativa*
DESCRIPTION: putative disease resistance protein (3' partial). OSJNBa0079L16.21.

15 AAD50430.1 AF166121 *Hordeum vulgare*
DESCRIPTION: Cf2/Cf5 disease resistance protein homolog. Big1. leucine rich repeat protein.

20 AAG21917.1 AC026815 *Oryza sativa*
DESCRIPTION: putative disease resistance protein. OSJNBa0079L16.5.

25 CAB55409.1 AL117265 *Oryza sativa*
DESCRIPTION: zhb0001.1. Incomplete at 5'end, Similar to disease resistance protein; Method: conceptual translation with partial peptide sequencing.

30 AAG21909.1 AC026815 *Oryza sativa*
DESCRIPTION: putative disease resistance protein. OSJNBa0079L16.3.

35 AAC80225.1 U72723 *Oryza longistaminata*
DESCRIPTION: receptor kinase-like protein. Xa21. disease resistance gene.

AAC49123.1 U37133 *Oryza sativa*
DESCRIPTION: receptor kinase-like protein. Xa21. Xa21 disease resistance gene.

40

503

CAA05276.1 AJ002236 *Lycopersicon pimpinellifolium*
DESCRIPTION: resistance gene. Hcr9-9E. Hcr9-9E.

45

AAC78592.1 AF053994 *Lycopersicon esculentum*
DESCRIPTION: Hcr2-0A. Hcr2-0A. similar to *Lycopersicon pimpinellifolium*
disease resistance protein Cf-2.2 encoded by the sequence presented in
GenBank Accession Number U42445.

5

CAA05274.1 AJ002236 *Lycopersicon pimpinellifolium*
DESCRIPTION: resistance gene. Cf-9. Cf-9.

10

AAA65235.1 U15936 *Lycopersicon pimpinellifolium*
DESCRIPTION: Cf-9 precursor. Cf-9. this is the ninth resistance gene to
disease caused by *Cladosporium fulvum* to be isolated.

15

AAC78594.1 AF053996 *Lycopersicon pimpinellifolium*
DESCRIPTION: Hcr2-2A. Hcr2-2A. similar to *Lycopersicon pimpinellifolium*
disease resistance protein Cf-2.2 encoded by the sequence presented in
GenBank Accession Number U42445.

20

CAA05279.1 AJ002237 *Lycopersicon esculentum*
DESCRIPTION: Hcr9-0. Hcr9-0. homologue of *Cladosporium fulvum* disease
resistance gene Cf-9.

25

AAC78595.1 AF053997 *Lycopersicon esculentum*
DESCRIPTION: Hcr2-5B. Hcr2-5B. similar to *Lycopersicon pimpinellifolium*
disease resistance protein Cf-2.2 encoded by the sequence presented in
GenBank Accession Number U42445.

30

AAC78593.1 AF053995 *Lycopersicon esculentum*
DESCRIPTION: Hcr2-0B. Hcr2-0B. similar to *Lycopersicon pimpinellifolium*
disease resistance protein Cf-2.2 encoded by the sequence presented in
GenBank Accession Number U42445.

35

CAA05268.1 AJ002235 *Lycopersicon hirsutum*
DESCRIPTION: Resistance gene. Cf-4. Cf-4.

40

AAC78596.1 AF053998 *Lycopersicon esculentum*
DESCRIPTION: Hcr2-5D. Hcr2-5D. similar to *Lycopersicon pimpinellifolium*
disease resistance protein Cf-2.2 encoded by the sequence presented in
GenBank Accession Number U42445.

45

AAC78591.1 AF053993 *Lycopersicon esculentum*
DESCRIPTION: disease resistance protein. Cf-5.

5

BAA96776.1 AP002521 *Oryza sativa*
DESCRIPTION: Similar to *Lycopersicon esculentum* disease resistance
protein (AF053993).

10

BAB08215.1 AP002539 *Oryza sativa*
DESCRIPTION: Similar to *Lycopersicon esculentum* disease resistance
protein (AF053993).

15

CAB55409.1 AL117265 *Oryza sativa*
DESCRIPTION: zhb0001.1. Incomplete at 5'end, Similar to disease resistance
protein; Method: conceptual translation with partial peptide sequencing.

20

AAD50430.1 AF166121 *Hordeum vulgare*
DESCRIPTION: Cf2/Cf5 disease resistance protein homolog. Big1. leucine
rich repeat protein.

25

AAG21897.1 AC026815 *Oryza sativa*
DESCRIPTION: putative disease resistance protein (3' partial).
OSJNBa0079L16.21.

30

AAB82755.1 U72725 *Oryza longistaminata*
DESCRIPTION: receptor kinase-like protein. Xa21 gene family member A1;
downstream of microsatellite region; disease resistance gene family
member.

35

504

AAF91324.1 AF244890 *Glycine max*
DESCRIPTION: receptor-like protein kinase 3. RLK3. GmRLK3.

40

BAA84787.1 AP000559 *Oryza sativa*
DESCRIPTION: ESTs C22657(S0014), C22656(S0014) correspond to a region
of
the predicted gene.; Similar to receptor protein kinase, ERECTA

45

(AC004484).

- 5 BAA83373.1 AP000391 *Oryza sativa*
DESCRIPTION: ESTs C22657(S0014),C22656(S0014) correspond to a region
of
the predicted gene.; Similar to receptor protein kinase, ERECTA
(AC004484).
- 10 AAF91322.1 AF244888 *Glycine max*
DESCRIPTION: receptor-like protein kinase 1. RLK1. GmRLK1.
- 15 AAF91323.1 AF244889 *Glycine max*
DESCRIPTION: receptor-like protein kinase 2. RLK2. GmRLK2.
- 20 CAC20842.1 AJ250467 *Pinus sylvestris*
DESCRIPTION: receptor protein kinase. upk.
- 25 AAK27806.1 AC022457 *Oryza sativa*
DESCRIPTION: putative protein kinase. OSJNBa0006L06.21.
- 30 AAB36558.1 U77888 *Ipomoea nil*
DESCRIPTION: receptor-like protein kinase INRPK1. inrpkl. leucine-rich
repeat.
- 35 BAA82393.1 AP000367 *Oryza sativa*
DESCRIPTION: EST C96716(C10608) corresponds to a region of the predicted
gene.; Similar to putative receptor protein kinase. (AC002334).
- 40 AAF59906.1 AF197947 *Glycine max*
DESCRIPTION: receptor protein kinase-like protein. CLV1B.
- 45 BAB03629.1 AP002522 *Oryza sativa*
DESCRIPTION: putative protein kinase Xa21. P0009G03.30.
- BAB03627.1 AP002522 *Oryza sativa*
DESCRIPTION: putative protein kinase Xa21. P0009G03.27.

- 5 AAF59905.1 AF197946 Glycine max
DESCRIPTION: receptor protein kinase-like protein. CLV1A.
- 10 AAK27817.1 AC022457 Oryza sativa
DESCRIPTION: putative protein kinase. OSJNBa0006L06.16.
- 15 BAB03631.1 AP002522 Oryza sativa
DESCRIPTION: putative protein kinase Xa21. P0009G03.32.
- 20 BAB03621.1 AP002522 Oryza sativa
DESCRIPTION: putative protein kinase Xa21. P0009G03.21.
- 25 AAF34426.1 AF172282 Oryza sativa
DESCRIPTION: leucine rich repeat containing protein kinase. DUPR11.16.
- 30 AAF66615.1 AF142596 Nicotiana tabacum
DESCRIPTION: LRR receptor-like protein kinase.
- 35 AAB82755.1 U72725 Oryza longistaminata
DESCRIPTION: receptor kinase-like protein. Xa21 gene family member A1;
downstream of microsatellite region; disease resistance gene family
member.
- 40 AAC49123.1 U37133 Oryza sativa
DESCRIPTION: receptor kinase-like protein. Xa21. Xa21 disease resistance
gene.
- 45 AAC80225.1 U72723 Oryza longistaminata
DESCRIPTION: receptor kinase-like protein. Xa21. disease resistance gene.
- 50 BAB19337.1 AP003044 Oryza sativa
DESCRIPTION: putative protein kinase. P0038C05.10. contains ESTs
AU056335(S20481),AU056336(S20481).

BAA88636.1 AB029327 *Nicotiana tabacum*

DESCRIPTION: elicitor-inducible LRR receptor-like protein EILP. EILP.

5 CAB51480.1 Y14600 *Sorghum bicolor*

DESCRIPTION: putative protein serine /threonine kinase. RLK1. accumulates in mesophyll cells.

10 AAK21965.1 AY028699 *Brassica napus*

DESCRIPTION: receptor protein kinase PERK1.

BAB39409.1 AP002901 *Oryza sativa*

15 DESCRIPTION: putative protein kinase. P0456F08.9. contains EST C23560(R0290).

BAB07903.1 AP002835 *Oryza sativa*

20 DESCRIPTION: putative receptor kinase. P0417G05.10. contains ESTs AU032341(R3918),AU071016(R10613).

BAA94519.1 AP001800 *Oryza sativa*

25 DESCRIPTION: ESTs AU032341(R3918),AU071016(R10613) correspond to a region of the predicted gene. Similar to *Arabidopsis thaliana* chromosome 4, BAC F9D16; putative receptor kinase (AL035394).

30

AAK00425.1 AC069324 *Oryza sativa*

DESCRIPTION: Putative protein kinase. OSJNBa0071K19.11.

35 AAG59657.1 AC084319 *Oryza sativa*

DESCRIPTION: putative protein kinase. OSJNBa0004B24.20.

BAA87853.1 AP000816 *Oryza sativa*

40 DESCRIPTION: EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative NAK-like Ser/Thr protein kinase. (AF001308).

45 BAB39873.1 AP002882 *Oryza sativa*

DESCRIPTION: putative protein kinase. P0439B06.8. contains ESTs

AU056701(S20808),AU056702(S20808).

- 5 AAB82756.1 U72724 *Oryza sativa*
DESCRIPTION: receptor kinase-like protein. Xa21 gene family member E.
- 10 AAB82753.1 U72726 *Oryza longistaminata*
DESCRIPTION: receptor kinase-like protein. Xa21 gene family member D.
505
-
- 15 CAA73134.1 Y12531 *Brassica oleracea*
DESCRIPTION: serine/threonine kinase. BRLK.
- 20 CAA74661.1 Y14285 *Brassica oleracea*
DESCRIPTION: SFR1. extracellular S domain: 8-1342; transmembrane domain:
1343-1411; intracellular kinase domain: 1412-2554.
- 25 AAC23542.1 U20948 *Ipomoea trifida*
DESCRIPTION: receptor protein kinase. IRK1.
- 30 BAA23676.1 AB000970 *Brassica rapa*
DESCRIPTION: receptor kinase 1. BcRK1.
- 35 AAB93834.1 U82481 *Zea mays*
DESCRIPTION: KI domain interacting kinase 1. KIK1. receptor-like protein
kinase; serine/threonine protein kinase.
- 40 CAA73133.1 Y12530 *Brassica oleracea*
DESCRIPTION: serine /threonine kinase. ARLK.
- 45 CAA67145.1 X98520 *Brassica oleracea*
DESCRIPTION: receptor-like kinase. SFR2.
- CAB89179.1 AJ245479 *Brassica napus* subsp. *napus*
DESCRIPTION: ser /thr kinase. S-locus receptor kinase. srk.

- AAA33008.1 M97667 Brassica napus
DESCRIPTION: serine/threonine kinase receptor.
- 5 BAA21132.1 D88193 Brassica rapa
DESCRIPTION: S-receptor kinase. SRK9 (B.c).
- 10 AAA62232.1 U00443 Brassica napus
DESCRIPTION: S-receptor kinase. protein contains an immunoglobulin-like domain.
- 15 BAA06285.1 D30049 Brassica rapa
DESCRIPTION: S-receptor kinase SRK9.
- 20 CAA74662.1 Y14286 Brassica oleracea
DESCRIPTION: SFR3. extracellular S domain: 123-1346; transmembrane domain: 1347-1412; intracellular kinase domain: from 1413.
- 25 AAA33000.1 M76647 Brassica oleracea
DESCRIPTION: receptor protein kinase. SKR6.
- 30 BAA07576.1 D38563 Brassica rapa
DESCRIPTION: receptor protein kinase SRK8.
- 35 BAA92836.1 AB032473 Brassica oleracea
DESCRIPTION: S18 S-locus receptor kinase. SRK18.
- 40 CAB41878.1 Y18259 Brassica oleracea
DESCRIPTION: SRK5 protein. SRK5. receptor-like kinase.
- 45 CAA79355.1 Z18921 Brassica oleracea
DESCRIPTION: S-receptor kinase-like protein.
- CAB41879.1 Y18260 Brassica oleracea
DESCRIPTION: SRK15 protein. SRK15. receptor-like kinase.

BAB21001.1 AB054061 Brassica rapa
DESCRIPTION: S locus receptor kinase. SRK22.

5 BAA92837.1 AB032474 Brassica oleracea
DESCRIPTION: S60 S-locus receptor kinase. SRK60.

10 BAA07577.2 D38564 Brassica rapa
DESCRIPTION: receptor protein kinase SRK12.

15 AAD21872.1 AF078082 Phaseolus vulgaris
DESCRIPTION: receptor-like protein kinase homolog RK20-1.

20 BAA94517.1 AP001800 Oryza sativa
DESCRIPTION: Similar to Zea mays S-domain receptor-like protein kinase (AJ010166).

BAB07905.1 AP002835 Oryza sativa
DESCRIPTION: putative S-receptor kinase. P0417G05.13.

25 BAB07906.1 AP002835 Oryza sativa
DESCRIPTION: putative S-receptor kinase. P0417G05.14.

30 BAA94516.1 AP001800 Oryza sativa
DESCRIPTION: Similar to Zea mays S-domain receptor-like protein kinase (AJ010166).

35 AAD52097.1 AF088885 Nicotiana tabacum
DESCRIPTION: receptor-like kinase CHRK1. Chrk1.

40 BAB18292.1 AP002860 Oryza sativa
DESCRIPTION: putative receptor-like protein kinase. P0409B08.19.

507

45 AAA33509.1 M62985 Zea mays
DESCRIPTION: protein kinase. putative; putative.

- CAA62476.1 X90990 Solanum tuberosum
DESCRIPTION: stpk1 protein kinase.
- 5
- AAK31277.1 AC079890 Oryza sativa
DESCRIPTION: putative protein kinase. OSJNBb0089A17.15.
- 10
- CAA66616.1 X97980 Solanum berthaultii
DESCRIPTION: protein kinase.
- AAF66637.1 AF143505 Lycopersicon esculentum
DESCRIPTION: viroid symptom modulation protein. PKv. protein kinase;
induced by viroid infection.
- 15
- BAA96593.1 AP002481 Oryza sativa
DESCRIPTION: Similar to Solanum berthaultii protein kinase. (X97980).
- 20
- AAB54117.1 U93559 Brassica rapa
DESCRIPTION: putative serine/threonine protein kinase. Bcpk1.
- 25
- AAB88817.1 AF033263 Zea mays
DESCRIPTION: signal transduction for phototropism. nonphototropic
hypocotyl 1. nph1. NPH1; putative serine/threonine kinase; similar to oat
NPH1 proteins.
- 30
- AAC05084.1 AF033097 Avena sativa
DESCRIPTION: NPH1-2. NPH1-2. putative serine/threonine protein kinase.
- 35
- CAA82994.1 Z30333 Mesembryanthemum crystallinum
DESCRIPTION: protein kinase.
- 40
- AAC05083.1 AF033096 Avena sativa
DESCRIPTION: NPH1-1. NPH1-1. putative serine/threonine protein kinase.
- 45
- CAA82992.1 Z30331 Mesembryanthemum crystallinum
DESCRIPTION: Protein Kinase.

- CAA82993.1 Z30332 *Spinacia oleracea*
DESCRIPTION: protein kinase.
- 5
- AAA50304.1 M92989 *Pisum sativum*
DESCRIPTION: protein kinase. PK5. homologue.
- 10
- AAB71418.1 U11553 *Pisum sativum*
DESCRIPTION: PsPK3. putative protein kinase.
- 15
- BAA93704.1 AB032564 *Cucumis sativus*
DESCRIPTION: cucumber protein kinase CsPK3. CsPK3. putative.
- 20
- BAA36192.1 AB012082 *Adiantum capillus-veneris*
DESCRIPTION: PHY3. PHY3. Ser/Thr protein kinase; chimeric structure of red/far-red light photoreceptive region (phytochrome) and putative blue light photoreceptor in phototropism of hypocotyl (NPH1).
- 25
- AAK18843.1 AC082645 *Oryza sativa*
DESCRIPTION: putative protein kinase. OSJNBb0033N16.3.
- 30
- CAB82852.1 Z30329 *Mesembryanthemum crystallinum*
DESCRIPTION: protein kinase MK6.
- 35
- CAA50374.1 X71057 *Nicotiana tabacum*
DESCRIPTION: protein kinase. PKTL7.
- 40
- AAK13156.1 AC078829 *Oryza sativa*
DESCRIPTION: putative protein kinase. OSJNBa0026O12.14.
- 45
- BAB03409.1 AP002816 *Oryza sativa*
DESCRIPTION: Similar to *Spinacia oleracea* protein kinase (S42867).
- CAA82991.1 Z30330 *Spinacia oleracea*
DESCRIPTION: protein kinase.

5 AAD50584.1 AF089097 *Salvia columbariae*
 DESCRIPTION: protein kinase 1. PK1.

10 AAB93860.1 U89679 *Lycopersicon esculentum*
 DESCRIPTION: protein kinase. LePK2. contains catalytic domain.

15 AAD50585.1 AF089099 *Salvia columbariae*
 DESCRIPTION: protein kinase 3. PK3.

20 AAB93859.1 U89678 *Lycopersicon esculentum*
 DESCRIPTION: protein kinase. LePK1. contains catalytic domain.

25 AAA50772.1 M69030 *Pisum sativum*
 DESCRIPTION: protein serine/threonine kinase. PsPK1. putative; putative.

30 AAB93861.1 U89680 *Lycopersicon esculentum*
 DESCRIPTION: protein kinase. LePK3. contains catalytic domain.

35 AAD50587.1 AF089101 *Salvia columbariae*
 DESCRIPTION: protein kinase 5. PK5.

40 AAD50588.1 AF089102 *Salvia columbariae*
 DESCRIPTION: protein kinase 6. PK6.

45 CAA56313.1 X79992 *Avena sativa*
 DESCRIPTION: putative pp70 ribosomal protein S6 kinase. Aspk11.

AAD50589.1 AF089103 *Salvia columbariae*
 DESCRIPTION: protein kinase 7. PK7.

CAB89082.1 AJ277534 *Asparagus officinalis*
DESCRIPTION: S6 ribosomal protein kinase. pk1. putative.

5 AAB93862.1 U89681 *Lycopersicon esculentum*
DESCRIPTION: protein kinase. LePK4. contains catalytic domain.

10 BAA92972.1 AP001551 *Oryza sativa*
DESCRIPTION: ESTs AU056183(S20356),AU056881(S20950) correspond to a region of the predicted gene. Similar to *Arabidopsis thaliana* chromosome 4 BAC clone F6I18 ; putative protein kinase. (AL022198).

15 BAB12687.1 AP002746 *Oryza sativa*
DESCRIPTION: putative protein kinase. P0671B11.2. contains ESTs C22394(C30013),C22393(C30013).

508
20 -----
BAA23676.1 AB000970 *Brassica rapa*
DESCRIPTION: receptor kinase 1. BcRK1.

25 CAA74662.1 Y14286 *Brassica oleracea*
DESCRIPTION: SFR3. extracellular S domain: 123-1346; transmembrane domain: 1347-1412; intracellular kinase domain: from 1413.

30 CAA74661.1 Y14285 *Brassica oleracea*
DESCRIPTION: SFR1. extracellular S domain: 8-1342; transmembrane domain: 1343-1411; intracellular kinase domain: 1412-2554.

35 CAA73133.1 Y12530 *Brassica oleracea*
DESCRIPTION: serine /threonine kinase. ARLK.

40 CAA67145.1 X98520 *Brassica oleracea*
DESCRIPTION: receptor-like kinase. SFR2.

45 AAA33008.1 M97667 *Brassica napus*
DESCRIPTION: serine/threonine kinase receptor.

DESCRIPTION: receptor protein kinase SRK12.

CAA73134.1 Y12531 Brassica oleracea

5 DESCRIPTION: serine/threonine kinase. BRLK.

AAB93834.1 U82481 Zea mays

10 DESCRIPTION: KI domain interacting kinase 1. KIK1. receptor-like protein kinase; serine/threonine protein kinase.

AAC23542.1 U20948 Ipomoea trifida

15 DESCRIPTION: receptor protein kinase. IRK1.

CAB41879.1 Y18260 Brassica oleracea

20 DESCRIPTION: SRK15 protein. SRK15. receptor-like kinase.

AAD52097.1 AF088885 Nicotiana tabacum

DESCRIPTION: receptor-like kinase CHRK1. Chrkl.

25 AAD21872.1 AF078082 Phaseolus vulgaris

DESCRIPTION: receptor-like protein kinase homolog RK20-1.

BAB18292.1 AP002860 Oryza sativa

30 DESCRIPTION: putative receptor-like protein kinase. P0409B08.19.

AAK02023.1 AC074283 Oryza sativa

35 DESCRIPTION: Putative protein kinase-like. OSJNBa0087H07.5.

CAA79324.1 Z18884 Brassica oleracea

DESCRIPTION: S-receptor kinase related protein.

40

BAB21240.1 AP002953 Oryza sativa

DESCRIPTION: Putative protein kinase. P0426D06.20. contains ESTs C22359(C11461),C22360(C11461).

45

CAB51836.1 AJ243961 Oryza sativa

DESCRIPTION: Putitive Ser/Thr protein kinase. 11332.7.

AAK21965.1 AY028699 Brassica napus

5 DESCRIPTION: receptor protein kinase PERK1.

BAB39873.1 AP002882 Oryza sativa

10 DESCRIPTION: putative protein kinase. P0439B06.8. contains ESTs
AU056701(S20808),AU056702(S20808).

BAA94509.1 AB041503 Populus nigra

15 DESCRIPTION: protein kinase 1. PnPK1.

AAK00425.1 AC069324 Oryza sativa

20 DESCRIPTION: Putative protein kinase. OSJNBa0071K19.11.

BAA94510.1 AB041504 Populus nigra

DESCRIPTION: protein kinase 2. PnPK2.

25 BAA92953.1 AP001551 Oryza sativa

DESCRIPTION: Similar to Arabidopsis thaliana chromosome 4 BAC clone
F10M6
; S-receptor kinase -like protein. (AL021811).

30 BAA92954.1 AP001551 Oryza sativa

DESCRIPTION: Similar to Oryza sativa protein kinase (OSPK10) mRNA.
(L27821).

35 AAG16628.1 AY007545 Brassica napus

DESCRIPTION: protein serine/threonine kinase BNK1.

40 BAB16871.1 AP002537 Oryza sativa

DESCRIPTION: putative protein kinase APK1A Arabidopsis thaliana.
P0001B06.24. contains ESTs C22608(R3192),D25110(R3192).

510

45 -----
AAG30254.1 AF307333 Hordeum vulgare

DESCRIPTION: putative nematode-resistance protein. Hs1. similar to Beta procumbens Hs1pro protein.

- 5 AAB48305.1 U79733 Beta procumbens
DESCRIPTION: nematode resistance. Hs1pro-1.

513

- 10 BAA14144.1 D90116 Armoracia rusticana
DESCRIPTION: peroxidase isozyme.

- 15 BAA14143.1 D90115 Armoracia rusticana
DESCRIPTION: peroxidase isozyme.

- 20 BAA11853.1 D83225 Populus nigra
DESCRIPTION: peroxidase.

- 25 CAA66037.1 X97351 Populus balsamifera subsp. trichocarpa
DESCRIPTION: signal for ER. peroxidase.

- CAA66034.1 X97348 Populus balsamifera subsp. trichocarpa
DESCRIPTION: signal for ER. peroxidase.

- 30 CAA66036.1 X97350 Populus balsamifera subsp. trichocarpa
DESCRIPTION: signal for ER. peroxidase.

- 35 CAA66035.1 X97349 Populus balsamifera subsp. trichocarpa
DESCRIPTION: signal for ER. peroxidase.

- 40 BAA11852.1 D83224 Populus nigra
DESCRIPTION: peroxidase.

- BAA07241.1 D38051 Populus kitakamiensis
DESCRIPTION: peroxidase. prxA4a.

- 45 BAA06335.1 D30653 Populus kitakamiensis

DESCRIPTION: peroxidase.

5 AAB47602.1 L07554 *Linum usitatissimum*
DESCRIPTION: peroxidase. FLXPER1.

10 AAC98519.1 AF007211 *Glycine max*
DESCRIPTION: peroxidase precursor. GMIPER1. pathogen-induced.

AAD37427.1 AF149277 *Phaseolus vulgaris*
DESCRIPTION: peroxidase 1 precursor. FBP1. secretory peroxidase.

15 BAA06334.1 D30652 *Populus kitakamiensis*
DESCRIPTION: peroxidase.

20 AAB97734.1 AF014502 *Glycine max*
DESCRIPTION: seed coat peroxidase precursor. Ep. H2O2 oxidoreductase;
class III plant peroxidase.

25 CAB94692.1 AJ242742 *Ipomoea batatas*
DESCRIPTION: Removal of H2O2, oxidation of toxic reductants, defence
response toward wounding. peroxidase. pod.

30 CAA62227.1 X90694 *Medicago sativa*
DESCRIPTION: peroxidase1C. prx1C.

35 CAA62226.1 X90693 *Medicago sativa*
DESCRIPTION: peroxidase1B. prx1B.

AAD37430.1 AF149280 *Phaseolus vulgaris*
DESCRIPTION: peroxidase 5 precursor. FBP5. secretory peroxidase.
40

CAA62225.1 X90692 *Medicago sativa*
DESCRIPTION: peroxidase1A. prx1A.

45 AAB41811.1 L36157 *Medicago sativa*

DESCRIPTION: peroxidase. pxdC. amino acid feature: conserved domains, aa 123 .. 129, 191 .. 198; amino acid feature: heme-binding domain, aa 68 .. 73.

5

AAB41810.1 L36156 Medicago sativa

DESCRIPTION: peroxidase. pxdA. amino acid feature: conserved motifs, aa 181 .. 188; amino acid feature: heme-binding domain, aa 60 .. 65.

10

BAA01877.1 D11102 Populus kitakamiensis

DESCRIPTION: peroxidase. prxA1.

15

CAB67121.1 Y19023 Lycopersicon esculentum

DESCRIPTION: peroxidase. cevi-1.

20

CAA50597.1 X71593 Lycopersicon esculentum

DESCRIPTION: peroxidase. CEVI-1.

25

BAA01992.1 D11396 Nicotiana tabacum

DESCRIPTION: 'peroxidase'.

AAA34108.1 J02979 Nicotiana tabacum

DESCRIPTION: lignin-forming peroxidase precursor (EC 1.11.1.7).

30

AAA33127.1 M91373 Cucumis sativus

DESCRIPTION: peroxidase. pre-peroxidase. putative.

35

BAA92500.1 AP001383 Oryza sativa

DESCRIPTION: ESTs D39300(R3292),AU030751(E60187) correspond to a region of the predicted gene. Similar to peroxidase ATP6a. (X98774).

40

CAB65334.1 AJ250121 Picea abies

DESCRIPTION: peroxidase. SPI2 protein. spi2.

45

CAA40796.1 X57564 Armoracia rusticana

DESCRIPTION: peroxidase. peroxidase precursor.

5 AAB06183.1 M37636 *Arachis hypogaea*
DESCRIPTION: cationic peroxidase. PNC1.

CAA76680.1 Y17192 *Cucurbita pepo*
DESCRIPTION: peroxidase. aprx. type III peroxidase.

10 AAA33129.1 M91372 *Cucumis sativus*
DESCRIPTION: peroxidase. pre-peroxidase.

15 CAA71492.1 Y10466 *Spinacia oleracea*
DESCRIPTION: peroxidase. prxr5.

20 AAF63027.1 AF244924 *Spinacia oleracea*
DESCRIPTION: hydrogen peroxide catabolism. peroxidase prx15 precursor.
type III peroxidase.

25 AAD43561.1 AF155124 *Gossypium hirsutum*
DESCRIPTION: bacterial-induced peroxidase precursor. Perx_Goshiko.

30 AAF63026.1 AF244923 *Spinacia oleracea*
DESCRIPTION: hydrogen peroxide catabolism. peroxidase prx14 precursor.
type III peroxidase.

35 AAA33121.1 M32742 *Cucumis sativus*
DESCRIPTION: peroxidase (CuPer2).

40 BAA92422.1 AP001366 *Oryza sativa*
DESCRIPTION: ESTs AU081576(R0541),AU032412(R4029) correspond to a
region
of the predicted gene. Similar to *A.thaliana* mRNA for peroxidase ATP18a.
(X98804).

45 BAA92497.1 AP001383 *Oryza sativa*
DESCRIPTION: ESTs AU081576(R0541),AU032412(R4029) correspond to a
region

of the predicted gene. Similar to peroxidase ATP18a. (X98804).

5 BAA77389.1 AB024439 Scutellaria baicalensis
DESCRIPTION: peroxidase 3.

10 BAA08499.1 D49551 Oryza sativa
DESCRIPTION: peroxidase. poxN.

15 AAB19129.1 U41657 Glycine max
DESCRIPTION: seed coat peroxidase isozyme. SPOD4.1. H2O2
oxidoreductase.

20 BAA03373.1 D14482 Oryza sativa
DESCRIPTION: putative peroxidase.

AAB02554.1 L37790 Stylosanthes humilis
DESCRIPTION: cationic peroxidase.
515

25 -----
AAB88134.1 AF034618 Spinacia oleracea
DESCRIPTION: cytosolic heat shock 70 protein. HSC70-1.

30 AAF34134.1 AF161180 Malus x domestica
DESCRIPTION: high molecular weight heat shock protein. Hsp2.

35 AAB99745.1 AF005993 Triticum aestivum
DESCRIPTION: HSP70. TaHSP70d. 70 kDa heat shock protein, molecular
chaperone.

40 AAA62325.1 L32165 Hordeum vulgare
DESCRIPTION: Molecular chaperone. HSP70. Heat-shock protein HSP70; The
predicted amino acid sequence is highly homologous (more than 80%
identity) to other plant heat-shock proteins (HSP70s) in the database;
however the C terminus is quite unique.; putative.

45 AAA21808.1 L23551 Spinacia oleracea

DESCRIPTION: molecular chaperone. ER-lumenal protein. HSC70.

AAA34139.1 L08830 *Lycopersicon esculentum*

5 DESCRIPTION: molecular chaperon (precursor). glucose-regulated protein 78. BiP/grp78. an endoplasmic reticulum residing heat shock protein 70 family member; precursor peptide.

10 AAB86942.1 AF031241 *Glycine max*

DESCRIPTION: endoplasmic reticulum transport protein; molecular chaperone; roles in protein folding, assembly, and transport. endoplasmic reticulum HSC70-cognate binding protein precursor. BIP. BiP; similar to HSC70 and GRP78.

15

AAK21920.1 AF338252 *Glycine max*

20 DESCRIPTION: molecular chaperone. BiP-isoform D. BiPD. ER-lumenal HSP70; binding protein GRP78.

AAB91473.1 AF035458 *Spinacia oleracea*

25 DESCRIPTION: heat shock 70 protein. HSC70-11. mitochondrial protein.

AAB96660.1 AF039084 *Spinacia oleracea*

DESCRIPTION: heat shock 70 protein. HSC70-11. molecular chaperone.

30

AAB91472.1 AF035457 *Spinacia oleracea*

DESCRIPTION: heat shock 70 protein. HSC70-10. mitochondrial protein.

516

35

CAA06927.1 AJ006233 *Nicotiana tabacum*

DESCRIPTION: putative thaumatin-like protein precursor.

40 AAF06346.1 AF195653 *Vitis vinifera*

DESCRIPTION: SCUTL1. thaumatin-like protein.

BAA28872.1 AB006009 *Pyrus pyrifolia*

45 DESCRIPTION: thaumatin-like protein precursor. PsTL1.

- CAC10270.1 AJ243427 *Malus x domestica*
DESCRIPTION: thaumatin-like protein. tl. allergen, pathogenesis-related.
- 5 AAC36740.1 AF090143 *Malus x domestica*
DESCRIPTION: thaumatin-like protein precursor Mdtl1. MDTL1.
pathogenesis-related.
- 10 CAB62167.1 AJ242828 *Castanea sativa*
DESCRIPTION: antifungal. thaumatin-like protein. tl1.
- 15 AAB38064.1 U32440 *Prunus avium*
DESCRIPTION: thaumatin-like protein precursor.
- 20 BAA74546.2 AB000834 *Nicotiana tabacum*
DESCRIPTION: thaumatin-like protein SE39b.
- 25 AAF06347.1 AF195654 *Vitis vinifera*
DESCRIPTION: SCUTL2. thaumatin-like protein.
- CAC09477.1 AL442113 *Oryza sativa*
DESCRIPTION: thaumatin-like protein. H0806H05.10.
- 30 AAB95118.1 U71244 *Brassica rapa*
DESCRIPTION: pathogenesis-related group 5 protein. BFTP. thaumatin-like
protein; PR-5.
- 35 CAA10492.1 AJ131731 *Pseudotsuga menziesii*
DESCRIPTION: Thaumatin-like protein. 5A1A.16.
- 40 BAA95017.1 AB031870 *Cestrum elegans*
DESCRIPTION: thaumatin-like protein. CETLP.
- 45 BAA95165.1 AB029918 *Nicotiana tabacum*
DESCRIPTION: pistil transmitting tissue specific thaumatin (SE39b)-like
protein. SE39b.

- 5 AAB61590.1 AF003007 *Vitis vinifera*
DESCRIPTION: VVTL1. osmotin-like protein, PR-5 protein; thaumatin-like protein.
- 10 AAD55090.1 AF178653 *Vitis riparia*
DESCRIPTION: thaumatin. osmotin; pathogenesis-related protein.
- 15 CAB85637.1 AJ237999 *Vitis vinifera*
DESCRIPTION: putative thaumatin-like protein. Tl1. alternative name grip 51.
- 20 AAF82264.1 AF227324 *Vitis vinifera*
DESCRIPTION: thaumatin-like protein.
- 25 AAB02259.1 U57787 *Avena sativa*
DESCRIPTION: permatin precursor. thaumatin-like protein.
- 30 AAB53368.1 U77657 *Oryza sativa*
DESCRIPTION: pathogenesis-related thaumatin-like protein.
- 35 CAA09228.1 AJ010501 *Cicer arietinum*
DESCRIPTION: thaumatin-like protein PR-5b.
- CAA33293.1 X15224 *Nicotiana tabacum*
DESCRIPTION: thaumatin-like protein. E22.
- 40 CAA33292.1 X15223 *Nicotiana tabacum*
DESCRIPTION: thaumatin-like protein. E2.
- 517
-
- 45 CAA71801.1 Y10848 *Brassica juncea*
DESCRIPTION: gamma-glutamylcysteine synthetase. gsh1.
- AAB71230.1 AF017983 *Lycopersicon esculentum*

DESCRIPTION: gamma-glutamylcysteine synthetase.GSH1.

AAC82334.1 AF041340 Medicago truncatula

5 DESCRIPTION: gamma-glutamylcysteine synthetase. putative plastid protein.

AAF22137.1 AF128455 Pisum sativum

10 DESCRIPTION: gamma-glutamylcysteine synthetase precursor. gsh1. putative plastid protein.

AAF22136.1 AF128454 Phaseolus vulgaris

15 DESCRIPTION: gamma-glutamylcysteine synthetase precursor. gsh1. putative plastid protein.

CAA06613.1 AJ005587 Brassica juncea

20 DESCRIPTION: gamma-glutamylcysteine synthetase.

AAG13459.1 AF128453 Glycine max

25 DESCRIPTION: gamma-glutamylcysteine synthetase precursor. gsh1.

CAA64808.1 X95563 Brassica juncea

DESCRIPTION: gamma-glutamylcysteine synthetase. gsh1.

518

30 -----

AAA75414.1 L28005 Glycine max

DESCRIPTION: TGACG-motif-binding protein. STGA1.

35 AAB31250.2 S73827 Solanum tuberosum

DESCRIPTION: mas-binding factor MBF3. transcription factor TGA1a homolog;

This sequence comes from Fig. 4.

40

AAB31249.1 S73826 Solanum tuberosum

DESCRIPTION: mas-binding factor MBF2. mas-binding factor MBF2. transcription factor TGA1a homolog; This sequence comes from Fig. 4.

45

CAA34468.1 X16449 Nicotiana sp.

DESCRIPTION: TGA1a protein (AA 1-359).

AAA34091.1 M62855 Nicotiana tabacum

5 DESCRIPTION: ASF-1/G13. leucine-zipper DNA-binding protein.

AAB31251.2 S73828 Solanum tuberosum

10 DESCRIPTION: mas-binding factor MBF1. transcription factor TGA1a
homolog;
This sequence comes from Fig. 4.

CAA48904.1 X69152 Zea mays

15 DESCRIPTION: ocs-element binding factor 3.2. OBF3.2.

CAA48905.1 X69153 Zea mays

20 DESCRIPTION: ocs-element binding factor 3.1. OBF3.1.

AAC24123.1 AF067187 Cichorium intybus

25 DESCRIPTION: cAMP responsive element binding protein. bZIP transcription
factor; CREB.

AAC24122.1 AF067186 Cichorium intybus

30 DESCRIPTION: cAMP responsive element binding protein. CREB1.

AAC49760.1 AF001454 Helianthus annuus

DESCRIPTION: Dc3 promoter-binding factor-2. DPBF-2.

521

35 -----

CAA10608.1 AJ132228 Ricinus communis

DESCRIPTION: amino acid carrier. aap3.

40 CAA07563.1 AJ007574 Ricinus communis

DESCRIPTION: amino acid carrier. aap1.

CAA70778.1 Y09591 Vicia faba

45 DESCRIPTION: amino acid transporter.

AAD16014.1 AF080543 *Nepenthes alata*
DESCRIPTION: amino acid transporter. AAP2.

5

CAA70969.1 Y09826 *Solanum tuberosum*
DESCRIPTION: amino acid transporter. AAP2. transmembrane protein.

10 AAD16015.1 AF080544 *Nepenthes alata*
DESCRIPTION: amino acid transporter. AAP3.

15 CAA70968.1 Y09825 *Solanum tuberosum*
DESCRIPTION: amino acid transporter. AAP1. transmembrane protein.

20 CAA92992.1 Z68759 *Ricinus communis*
DESCRIPTION: amino acid carrier.

AAD16013.1 AF080542 *Nepenthes alata*
DESCRIPTION: amino acid transporter. AAP1.

25

AAF15945.1 AF061435 *Vicia faba*
DESCRIPTION: amino acid transporter b. AAPB.

30 CAA72006.1 Y11121 *Ricinus communis*
DESCRIPTION: amino acid carrier.

35 AAF15944.1 AF061434 *Vicia faba*
DESCRIPTION: amino acid transporter a. AAPA.

40 AAF15946.1 AF061436 *Vicia faba*
DESCRIPTION: amino acid transporter c. AAPC.

AAB48944.1 U31932 *Nicotiana glauca*
DESCRIPTION: amino acid permease 1. NSAAP1. amino acid transporter;
Method: conceptual translation supplied by author.

45

CAA68193.1 X99937 *Spinacia oleracea*
DESCRIPTION: RNA helicase. prh75. DEAD-box protein; homologous to X99938.

5

AAG13612.1 AC078840 *Oryza sativa*
DESCRIPTION: putative RNA helicase. OSJNBb0073N24.12.

10

AAG34876.1 AF261021 *Nicotiana tabacum*
DESCRIPTION: putative chloroplast RNA helicase VDL isoform 1. VDL. alternatively spliced.

15

AAG34873.1 AF261020 *Nicotiana tabacum*
DESCRIPTION: putative chloroplast RNA helicase VDL isoform 1. VDL. essential for chloroplast development; may be involved in post-transcriptional regulation.

20

AAG34879.1 AF261024 *Nicotiana tabacum*
DESCRIPTION: putative chloroplast RNA helicase VDL' isoform 1. VDL'. alternatively spliced.

25

AAD20980.1 AF079782 *Zea mays*
DESCRIPTION: ATPase and RNA helicase. translation initiation factor 4A2. tif4A2.

30

AAG34882.1 AF261027 *Nicotiana tabacum*
DESCRIPTION: putative chloroplast RNA helicase VDL' isoform 4. VDL'. alternatively spliced.

35

BAA95705.1 AB042644 *Oryza sativa*
DESCRIPTION: DEAD box RNA helicase OsPL10b. OsPL10b.

40

BAA95704.1 AB042643 *Oryza sativa*
DESCRIPTION: DEAD box RNA helicase OsPL10a. OsPL10a.

45

AAG34883.1 AF261028 *Nicotiana tabacum*
DESCRIPTION: putative chloroplast RNA helicase VDL' isoform 5. VDL'. alternatively spliced.

AAK27688.1 AF347614 *Lycopersicon esculentum*
DESCRIPTION: sulfate transporter 2. ST2.

5 AAK27687.1 AF347613 *Lycopersicon esculentum*
DESCRIPTION: sulfate transporter 1. ST1.

10 CAA57711.1 X82256 *Stylosanthes hamata*
DESCRIPTION: high affinity sulphate transporter. SHST2.

15 AAG41419.1 AF309643 *Solanum tuberosum*
DESCRIPTION: high affinity sulfate transporter type 1. ST1.

20 CAA57710.1 X82255 *Stylosanthes hamata*
DESCRIPTION: high affinity sulphate transporter. SHST1.

AAK35215.1 AF355602 *Zea mays*
DESCRIPTION: sulfate transporter ST1.

25 CAA65291.1 X96431 *Hordeum vulgare*
DESCRIPTION: high affinity sulphate transporter. HVST1.

30 AAA97952.1 U52867 *Hordeum vulgare*
DESCRIPTION: high affinity sulfate transporter HVST1.

35 CAB42985.1 AJ238244 *Aegilops tauschii*
DESCRIPTION: putative plasma membrane sulfate transport. putative high
affinity sulfate transporter. st1.

40 CAB42986.1 AJ238245 *Aegilops tauschii*
DESCRIPTION: putative plasma membrane sulfate transport. putative high
affinity sulfate transporter. st2.

45 CAA57831.1 X82454 *Stylosanthes hamata*
DESCRIPTION: low affinity sulphate transporter. SHST3.

531

-
- AAK00436.1 AC060755 *Oryza sativa*
 DESCRIPTION: putative zinc finger protein. OSJNBa0003O19.23.
- 5 BAA85438.1 AP000616 *Oryza sativa*
 DESCRIPTION: similar to RING-H2 finger protein RHA1a (AF078683).
- 10 AAG43550.1 AF211532 *Nicotiana tabacum*
 DESCRIPTION: Avr9/Cf-9 rapidly elicited protein 132. ACRE132. similar to RING finger proteins.
- 15 BAA90357.1 AP001080 *Oryza sativa*
 DESCRIPTION: EST AU070319(S10788) corresponds to a region of the predicted gene. Similar to RING-H2 finger protein RHA2b (AC006200).
- 532
- 20 -----
 BAA81751.1 AB017517 *Marchantia polymorpha*
 DESCRIPTION: calcium-dependent protein kinase. CDPK1. CDPK-B; alternative splicing.
- 25 BAA13232.1 D87042 *Zea mays*
 DESCRIPTION: Calcium-dependent protein kinase.
- 30 BAA81749.1 AB017515 *Marchantia polymorpha*
 DESCRIPTION: calcium-dependent protein kinase. CDPK1. CDPK-B; alternative splicing.
- 35 BAA81750.1 AB017516 *Marchantia polymorpha*
 DESCRIPTION: calcium-dependent protein kinase. CDPK1. CDPK-A; alternative splicing.
- 40
- BAA85396.1 AP000615 *Oryza sativa*
 DESCRIPTION: ESTs C22369(C12239),C22370(C12239), AU057852(S21844),AU057853(S21844) correspond to a region of the predicted gene.; similar to calcium dependent protein kinase. (AF048691).
- 45

- CAA57156.1 X81393 *Oryza sativa*
DESCRIPTION: calcium-dependent protein kinase. OSCPkII.
- 5
- AAC05270.1 AF048691 *Oryza sativa*
DESCRIPTION: calcium dependent protein kinase. CDPK12.
- 10
- AAB49984.1 U90262 *Cucurbita pepo*
DESCRIPTION: calcium-dependent calmodulin-independent protein kinase
CDPK. cpCPK1. serine/threonine protein kinase that is activated by direct
binding of calcium.
- 15
- AAB70706.1 U82087 *Tortula ruralis*
DESCRIPTION: calmodulin-like domain protein kinase. TrCPK1.
- 20
- AAG46110.1 AC073166 *Oryza sativa*
DESCRIPTION: calcium-dependent protein kinase. OSJNBb0064P21.2.
- 25
- BAA02698.1 D13436 *Oryza sativa*
DESCRIPTION: calcium-dependent protein kinase. spk.
- 30
- BAA81748.1 AB017515 *Marchantia polymorpha*
DESCRIPTION: calcium-dependent protein kinase. CDPK1. CDPK-A;
alternative
splicing.
- 35
- CAA07481.1 AJ007366 *Zea mays*
DESCRIPTION: calcium-dependent protein kinase.
- 40
- AAB80692.1 U69173 *Glycine max*
DESCRIPTION: calmodulin-like domain protein kinase isoenzyme beta. CDPK
beta.
- 45
- AAC49405.1 U08140 *Vigna radiata*
DESCRIPTION: calcium dependent protein kinase. CDPK.

AAA61682.1 L27484 Zea mays
DESCRIPTION: calcium-dependent protein kinase. CDPK.

5

AAD17800.1 AF090835 Mesembryanthemum crystallinum
DESCRIPTION: Ca²⁺-dependent protein kinase. CPK1. serine/threonine
protein kinase.

10

CAA39936.1 X56599 Daucus carota
DESCRIPTION: calcium- dependent protein kinase. DcPK431.

15

AAK26164.1 AY027885 Cucumis sativus
DESCRIPTION: calcium-dependent calmodulin-independent protein kinase 5.
CDPK5. CsCDPK5.

20

AAB88537.1 AF035944 Fragaria x ananassa
DESCRIPTION: calcium-dependent protein kinase. MAX17.

25

AAF21062.1 AF216527 Dunaliella tertiolecta
DESCRIPTION: calcium-dependent protein kinase. CPK1; CDPK.

30

CAA89202.1 Z49233 Chlamydomonas eugametos
DESCRIPTION: calcium-stimulated protein kinase.

35

AAC32116.1 AF051211 Picea mariana
DESCRIPTION: probable calcium dependent protein kinase. Sb15. similar to
Vigna radiata calcium dependent protein kinase encoded by U08140.

40

AAF23900.1 AF194413 Oryza sativa
DESCRIPTION: calcium-dependent protein kinase. CDPK1. OsCDPK1.

45

AAF23901.2 AF194414 Oryza sativa
DESCRIPTION: calcium-dependent protein kinase. CDPK5. OsCDPK5.

CAB46228.1 Y18055 Arachis hypogaea
DESCRIPTION: calcium dependent protein kinase. CDPK.

- 5 AAC78558.1 AF030879 *Solanum tuberosum*
DESCRIPTION: protein kinase CPK1.
- CAA58750.1 X83869 *Daucus carota*
DESCRIPTION: CDPK-related protein kinase. CRK (or PK421).
- 10 AAB47181.1 S82324 *Zea mays*
DESCRIPTION: /gene="calcium/calmodulin-dependent
protein kinase. This sequence comes from Fig. 1.
- 15 BAA12691.1 D84507 *Zea mays*
DESCRIPTION: CDPK-related protein kinase. Does not require calcium for
its activity (by similarity).
- 20 BAA22410.1 D38452 *Zea mays*
DESCRIPTION: calcium-dependent protein kinase-related kinase.
- 25 BAA12692.1 D84508 *Zea mays*
DESCRIPTION: CDPK-related protein kinase. Does not require calcium for
its activity.
- 30 AAG01179.1 AF289237 *Zea mays*
DESCRIPTION: calcium/calmodulin dependent protein kinase MCK2. MCK2.
- 35 AAC24961.1 AF009337 *Tradescantia virginiana*
DESCRIPTION: CDPK-related protein kinase. CRK1.
- 40 a BAA90814.1 AP001168 *Oryza sativa*
DESCRIPTION: ESTs AU030197(E50746),AU030196(E50746) correspond to
region of the predicted gene.; Similar to calcium-dependent
calmodulin-independent protein kinase CDPK (U90262).
- 45 AAC49008.1 U24188 *Lilium longiflorum*
DESCRIPTION: calcium/calmodulin-dependent phosphorylation activity.

calcium/calmodulin-dependent protein kinase. CCaMK. serine/threonine kinase; binds to calcium and calmodulin.

- 5 AAF19402.1 AF203480 *Lycopersicon esculentum*
 DESCRIPTION: phosphoenolpyruvate carboxylase kinase. protein kinase;
 member of Ca²⁺/CaM kinase family; lacks the autoinhibitory region and EF
 hands.

10 535

AAK19619.1 AF336286 *Gossypium hirsutum*
 DESCRIPTION: GHMYB9. ghmyb9. similar to myb.

15

CAA64614.1 X95296 *Lycopersicon esculentum*
 DESCRIPTION: transcription factor. THM27. myb-related.

20

CAA50224.1 X70879 *Hordeum vulgare*
 DESCRIPTION: MybHv1. myb1.

25

CAA50222.1 X70877 *Hordeum vulgare*
 DESCRIPTION: MybHv1. myb1.

30

AAA33067.1 L04497 *Gossypium hirsutum*
 DESCRIPTION: MYB A; putative.

35

CAA50221.1 X70876 *Hordeum vulgare*
 DESCRIPTION: MybHv5. myb2.

BAA23337.1 D88617 *Oryza sativa*
 DESCRIPTION: transfactor. OSMYB1. Osmyb1.

40

BAA23338.1 D88618 *Oryza sativa*
 DESCRIPTION: transfactor. OSMYB2. Osmyb2.

45

AAC04720.1 AF034134 *Gossypium hirsutum*
 DESCRIPTION: putative MYB-like transcription factor. MYB-like DNA-
 binding

domain protein. Cmy-O. similar to MYB A encoded by GenBank Accession Number L04497.

5 CAA72218.1 Y11415 Oryza sativa
DESCRIPTION: myb.

10 CAA50225.1 X70880 Hordeum vulgare
DESCRIPTION: MybHv5. myb2.

15 AAA82943.1 U39448 Picea mariana
DESCRIPTION: MYB-like transcriptional factor MBF1. putative DNA binding region highly similar to the maize C1.

20 CAA78386.1 Z13996 Petunia x hybrida
DESCRIPTION: DNA binding protein; transcriptional activator. protein 1. myb.Ph3. Product related to animal myb proto-oncoproteins. Sequence from nucleotide 992 is not included in clone cPF1 and has been obtained by PCR amplification of cDNA.

25 BAA81732.1 AB029161 Glycine max
DESCRIPTION: GmMYB29A2.

30 AAK19616.1 AF336283 Gossypium hirsutum
DESCRIPTION: GHMYB25. ghmyb25. similar to myb; contains an unspliced intron.

35 AAK19611.1 AF336278 Gossypium hirsutum
DESCRIPTION: BNLGHi233. bnlghi6233. similar to myb.

40 AAK19617.1 AF336284 Gossypium hirsutum
DESCRIPTION: GHMYB36. ghmyb36. similar to myb.

45 BAA93038.1 AP001552 Oryza sativa
DESCRIPTION: EST AU082058(C12976) corresponds to a region of the predicted gene. Similar to Arabidopsis thaliana putative transcription factor (AF062916).

AAK19615.1 AF336282 *Gossypium hirsutum*
DESCRIPTION: GHMYB10. ghmyb10. similar to myb.

5

BAB39987.1 AP003020 *Oryza sativa*
DESCRIPTION: putative transcription factor (myb). P0498A12.16. contains
ESTs AU097474(S5087),D40175(S1959).

10

BAB39972.1 AP003018 *Oryza sativa*
DESCRIPTION: putative transcription factor (myb). OSJNBa0004B13.27.
contains ESTs AU097474(S5087),D40175(S1959).

15

CAB43399.1 AJ006292 *Antirrhinum majus*
DESCRIPTION: Myb-related transcription factor mixta-like 1. mybml1.

20

CAA72185.1 Y11350 *Oryza sativa*
DESCRIPTION: myb factor. myb.

25

AAF22256.1 AF161711 *Pimpinella brachycarpa*
DESCRIPTION: myb-related transcription factor.

30

AAG13574.1 AC037425 *Oryza sativa*
DESCRIPTION: myb factor. OSJNBa0055P24.4.

35

BAA81731.1 AB029160 *Glycine max*
DESCRIPTION: GmMYB29A1.

BAA81730.1 AB029159 *Glycine max*
DESCRIPTION: GmMYB29A1.

40

CAA72186.1 Y11351 *Oryza sativa*
DESCRIPTION: myb factor. myb.

45

CAA67600.1 X99210 *Lycopersicon esculentum*
DESCRIPTION: myb-related transcription factor. THM16.

- CAA75509.1 Y15219 Oryza sativa subsp. indica
DESCRIPTION: transcriptional activator. C1.
- 5 AAC04718.1 AF034132 Gossypium hirsutum
DESCRIPTION: putative MYB-like transcription factor. MYB-like DNA-binding
domain protein. CmY-J. similar to MYB A encoded by GenBank Accession
10 Number L04497.
- CAA78387.1 Z13997 Petunia x hybrida
DESCRIPTION: DNA-binding protein, transcriptional activator. protein 2.
15 myb.Ph2. related to animal myb proto-oncoproteins.
- BAA81736.1 AB029165 Glycine max
DESCRIPTION: GmMYB29B2.
20
- AAK19618.1 AF336285 Gossypium hirsutum
DESCRIPTION: GHMYB38. ghmyb38. similar to myb.
25
- CAA72217.1 Y11414 Oryza sativa
DESCRIPTION: myb.
- 30 AAC49394.1 U57002 Zea mays
DESCRIPTION: P protein. P. allele P-wr; Myb-like transcriptional
regulator with a putative zinc-finger at the C-terminal.
- 35 AAA33500.1 M73028 Zea mays
DESCRIPTION: myb-like transcription factor. P.
- BAB20661.1 AP002871 Oryza sativa
40 DESCRIPTION: putative myb-related protein P. P0475H04.31.
- AAG36774.1 AF210616 Zea mays
DESCRIPTION: P2 protein. P2. myb-like transcriptional factor; similar to
45 Zea mays P gene.

BAA81733.2 AB029162 Glycine max
DESCRIPTION: GmMYB29A2.

10 BAA23339.1 D88619 Oryza sativa
DESCRIPTION: transfactor. OSMYB3. Osmyb3.

15 BAA88224.1 AB028652 Nicotiana tabacum
DESCRIPTION: myb-related transcription factor LBM4. lbm4.

BAA88221.1 AB028649 Nicotiana tabacum
DESCRIPTION: myb-related transcription factor LBM1. lbm1.

AAB41101.1 U72762 Nicotiana tabacum
DESCRIPTION: transcription factor Myb1. myb1. TMV-inducible Myb
homolog;
contains helix-turn-helix motif; contains redox-sensitive cysteine.

536

CAA70968.1 Y09825 Solanum tuberosum
30 DESCRIPTION: amino acid transporter. AAP1, transmembrane protein.

AA15946.1 AF061436 *Vicia faba*
DESCRIPTION: amino acid transporter c. AAPC.

CAA70969.1 Y09826 Solanum tuberosum
DESCRIPTION: amino acid transporter. AAP2, transmembrane protein.

40

AAB96830.1 U64823 Nicotiana sylvestris
DESCRIPTION: amino acid transporter. amino acid permease. nsaap1.

45 CAA07563.1 AJ007574 Ricinus communis
DESCRIPTION: amino acid carrier, aap1.

5 AAB48944.1 U31932 *Nicotiana sylvestris*
DESCRIPTION: amino acid permease 1. NSAAP1. amino acid transporter;
Method: conceptual translation supplied by author.

10 AAD16015.1 AF080544 *Nepenthes alata*
DESCRIPTION: amino acid transporter. AAP3.

15 CAA70778.1 Y09591 *Vicia faba*
DESCRIPTION: amino acid transporter.

20 AAF15944.1 AF061434 *Vicia faba*
DESCRIPTION: amino acid transporter a. AAPA.

25 AAF15945.1 AF061435 *Vicia faba*
DESCRIPTION: amino acid transporter b. AAPB.

30 AAF76897.1 AF274032 *Atriplex hortensis*
DESCRIPTION: proline/glycine betaine transporter.

35 AAD16014.1 AF080543 *Nepenthes alata*
DESCRIPTION: amino acid transporter. AAP2.

40 AAD25161.1 AF014809 *Lycopersicon esculentum*
DESCRIPTION: proline transporter 2. LeProT2.

537
45 CAA10608.1 AJ132228 *Ricinus communis*
DESCRIPTION: amino acid carrier. aap3.

537
40 -----
BAA89009.1 AB027455 *Petunia x hybrida*
DESCRIPTION: anthocyanin 5-O-glucosyltransferase. PH1.

45 BAA36423.1 AB013598 *Verbena x hybrida*
DESCRIPTION: UDP-glucose:anthocyanin 5-O-glucosyltransferase. HGT8.

- 5 BAA36421.1 AB013596 *Perilla frutescens*
DESCRIPTION: UDP-glucose:anthocynin 5-O-glucosyltransferase. PF3R4.
- 10 BAB07962.1 AP002524 *Oryza sativa*
DESCRIPTION: putative anthocyanin 5-O-glucosyltransferase. P0406H10.16.
contains ESTs AU067881(C10481),AU067882(C10481).
- 15 BAA36422.1 AB013597 *Perilla frutescens*
DESCRIPTION: UDP-glucose:anthocyanin 5-O-glucosyltransferase homologue.
PF3R6.
- 20 BAA93039.1 AB033758 *Citrus unshiu*
DESCRIPTION: limonoid UDP-glucosyltransferase. LGTase.
- 25 AAF61647.1 AF190634 *Nicotiana tabacum*
DESCRIPTION: UDP-glucose:salicylic acid glucosyltransferase. SA-GTase.
- 30 AAF98390.1 AF287143 *Brassica napus*
DESCRIPTION: catalyzes the transfer of glucose from UDP-glucose to
sinapate and some other hydroxycinnamates (4-coumarate, caffeate,
ferulate). UDP-glucose:sinapate glucosyltransferase. SGT1. SGT.
- 35 AAF17077.1 AF199453 *Sorghum bicolor*
DESCRIPTION: UDP-glucose glucosyltransferase.
UDP-glucose:p-hydroxymandelonitrile-o- glucosyltransferase.
- 40 AAK16172.1 AC079887 *Oryza sativa*
DESCRIPTION: putative glucosyltransferase. OSJNBa0040E01.14.
- 45 BAA83484.1 AB031274 *Scutellaria baicalensis*
DESCRIPTION: UDP-glucose: flavonoid 7-O-glucosyltransferase. ufgt.

AAK16181.1 AC079887 *Oryza sativa*
DESCRIPTION: putative glucosyltransferase. OSJNBa0040E01.16.

5

AAG25643.1 AF303396 *Phaseolus vulgaris*
DESCRIPTION: UDP-glucosyltransferase HRA25. putative; defense associated.

10 AAK16178.1 AC079887 *Oryza sativa*
DESCRIPTION: putative glucosyltransferase. OSJNBa0040E01.5.

15 AAD21086.1 AF127218 *Forsythia x intermedia*
DESCRIPTION: adds glucose residue to position 3 of flavonoid compounds.
flavonoid 3-O-glucosyltransferase. UFGT.

20 BAA12737.1 D85186 *Gentiana triflora*
DESCRIPTION: UDP-glucose:flavonoid-3-glucosyltransferase.

25 AAK28303.1 AF346431 *Nicotiana tabacum*
DESCRIPTION: phenylpropanoid:glucosyltransferase 1. togt1.
glucosyltransferase.

30 CAB56231.1 Y18871 *Dorotheanthus bellidiformis*
DESCRIPTION: betanidin-5-O-glucosyltransferase.

35 CAA54612.1 X77462 *Manihot esculenta*
DESCRIPTION: UTP-glucose glucosyltransferase. CGT5.

BAB41019.1 AB047092 *Vitis vinifera*
DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. ItUFGT1.

40 BAB41020.1 AB047093 *Vitis vinifera*
DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. ItUFGT2.

45 AAB36653.1 U32644 *Nicotiana tabacum*
DESCRIPTION: immediate-early salicylate-induced glucosyltransferase.
IS5a.

- 5 BAB41025.1 AB047098 *Vitis vinifera*
DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. FIUFGT1.
- 10 BAB41023.1 AB047096 *Vitis vinifera*
DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. AIUFGT1.
- 15 BAB41022.1 AB047095 *Vitis vinifera*
DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. RuUFGT2.
- 20 BAB41021.1 AB047094 *Vitis vinifera*
DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. RuUFGT1.
- 25 BAA19659.1 AB002818 *Perilla frutescens*
DESCRIPTION: flavonoid 3-O-glucosyltransferase. UDP glucose.
- 30 BAB41026.1 AB047099 *Vitis vinifera*
DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. FIUFGT2.
- 35 BAB41024.1 AB047097 *Vitis vinifera*
DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. AIUFGT2.
- 40 AAK16180.1 AC079887 *Oryza sativa*
DESCRIPTION: putative glucosyltransferase. OSJNBa0040E01.21.
- 45 AAK28304.1 AF346432 *Nicotiana tabacum*
DESCRIPTION: phenylpropanoid:glucosyltransferase 2. togt2.
glucosyltransferase.
- 50 AAB36652.1 U32643 *Nicotiana tabacum*
DESCRIPTION: immediate-early salicylate-induced glucosyltransferase.
IS10a.
- 55 BAB41017.1 AB047090 *Vitis labrusca* x *Vitis vinifera*

DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. KyUFGT1.
The
gene was derived from one of the parents *V. labruscana* cv. Ishiharawase.

- 5
BAA89008.1 AB027454 *Petunia x hybrida*
DESCRIPTION: anthocyanidin 3-O-glucosyltransferase. PGT8.
- 10 CAA59450.1 X85138 *Lycopersicon esculentum*
DESCRIPTION: twi1, homologous to glucosyltransferases.
- 15 CAA54614.1 X77464 *Manihot esculenta*
DESCRIPTION: UTP-glucose glucosyltransferase. CGT7.
- 20 CAA54611.1 X77461 *Manihot esculenta*
DESCRIPTION: UTP-glucose glucosyltransferase. CGT2.
- 25 CAA54613.1 X77463 *Manihot esculenta*
DESCRIPTION: UTP-glucose glucosyltransferase. CGT6.
- 540

AAK27688.1 AF347614 *Lycopersicon esculentum*
DESCRIPTION: sulfate transporter 2. ST2.
- 30 AAG41419.1 AF309643 *Solanum tuberosum*
DESCRIPTION: high affinity sulfate transporter type 1. ST1.
- 35 AAK27687.1 AF347613 *Lycopersicon esculentum*
DESCRIPTION: sulfate transporter 1. ST1.
- 40 AAA97952.1 U52867 *Hordeum vulgare*
DESCRIPTION: high affinity sulfate transporter HVST1.
- 45 CAA57711.1 X82256 *Stylosanthes hamata*
DESCRIPTION: high affinity sulphate transporter. SHST2.

- CAA65291.1 X96431 *Hordeum vulgare*
DESCRIPTION: high affinity sulphate transporter. HVST1.
- 5 CAA57710.1 X82255 *Stylosanthes hamata*
DESCRIPTION: high affinity sulphate transporter. SHST1.
- 10 CAB42985.1 AJ238244 *Aegilops tauschii*
DESCRIPTION: putative plasma membrane sulfate transport. putative high affinity sulfate transporter. st1.
- 15 AAK35215.1 AF355602 *Zea mays*
DESCRIPTION: sulfate transporter ST1.
- 20 CAB42986.1 AJ238245 *Aegilops tauschii*
DESCRIPTION: putative plasma membrane sulfate transport. putative high affinity sulfate transporter. st2.
- 25 CAA65536.1 X96761 *Sporobolus stapfianus*
DESCRIPTION: sulphate transporter protein.
- 30 CAA57831.1 X82454 *Stylosanthes hamata*
DESCRIPTION: low affinity sulphate transporter. SHST3.
- 35 CAA11413.1 AJ223495 *Brassica juncea*
DESCRIPTION: sulfate permease. sp1.
- 541
-
- 40 AAF36491.1 AF129479 *Hordeum vulgare*
DESCRIPTION: HAK2. HAK2. similar to *Hordeum vulgare* K⁺ transporter HAK1.
- 45 BAB32443.1 AB055630 *Phragmites australis*
DESCRIPTION: high-affinity potassium transporter. PcnHAK1.

BAB32444.1 AB055631 *Phragmites australis*
 DESCRIPTION: high-affinity potassium transporter. PceHAK1A.
 5

BAB32445.1 AB055632 *Phragmites australis*
 DESCRIPTION: high-affinity potassium transporter. PceHAK1B.
 10

BAB32442.1 AB055629 *Phragmites australis*
 DESCRIPTION: high-affinity potassium transporter. PcuHAK1.
 15

AAC39315.1 AF025292 *Hordeum vulgare*
 DESCRIPTION: putative high-affinity potassium transporter. HvHAK1.
 20

AAF36497.1 AF129485 *Oryza sativa*
 DESCRIPTION: HAK4. HAK4. OsHAK4; similar to *Hordeum vulgare* K+
 transporter HAK1.
 25

AAF36496.1 AF129484 *Hordeum vulgare*
 DESCRIPTION: HAK4. HAK4. HvHAK4; similar to *Hordeum vulgare* K+
 transporter HAK1.
 30

CAC14883.1 AJ297888 *Hordeum vulgare*
 DESCRIPTION: putative potassium transporter. hak1.
 35

CAC14787.1 AJ297886 *Hordeum vulgare*
 DESCRIPTION: putative potassium transporter. hak1.
 40

AAF36492.1 AF129480 *Hordeum vulgare*
 DESCRIPTION: HAK1B. HAK1B. HvHAK1B; similar to *Hordeum vulgare* K+
 transporter HAK1.
 45

CAC15061.1 AJ300161 *Hordeum vulgare*
 DESCRIPTION: potassium transporter. hak4.
 542

AAA91053.1 M88254 Hevea brasiliensis
DESCRIPTION: ethylene-inducible protein. ER1.

546

5

CAA75386.1 Y15113 Morinda citrifolia
DESCRIPTION: 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase. DS3.
2-dehydro-3-deoxyphosphoheptonate aldolase.

10

CAA79855.1 Z21792 Lycopersicon esculentum
DESCRIPTION: phospho-2-dehydro-3-deoxyheptonate aldolase.

15

CAA79856.1 Z21793 Lycopersicon esculentum
DESCRIPTION: phospho-2-dehydro-3-deoxyheptonate aldolase.

548

20

BAA96751.1 AP002521 Oryza sativa
DESCRIPTION: Similar to Arabidopsis thaliana chromosome4, BAC clone
T16H5; lectin like protein (AL024486).

551

25

BAB19096.1 AP002839 Oryza sativa
DESCRIPTION: putative DNA-binding protein homolog. P0688A04.2.

30

BAB19075.1 AP002744 Oryza sativa
DESCRIPTION: putative DNA-binding protein homolog. P0006C01.17.

35

AAK16170.1 AC079887 Oryza sativa
DESCRIPTION: putative DNA binding protein. OSJNBa0040E01.4.

40

AAD32677.1 AF140554 Avena sativa
DESCRIPTION: DNA-binding protein WRKY1. wrky1. putative transcription
factor.

45

AAD16139.1 AF096299 Nicotiana tabacum
DESCRIPTION: DNA-binding protein 2. WRKY2. transcription factor.

CAB97004.1 AJ278507 Solanum tuberosum

DESCRIPTION: putative transcription factor. WRKY DNA binding protein. WRKY1.

5

CAA88326.1 Z48429 Avena fatua

DESCRIPTION: binds conserved cis-element from cereal alpha-Amy2 promoters. DNA-binding protein.

10

AAC49527.1 U48831 Petroselinum crispum

DESCRIPTION: WRKY1. contains two WRKY domains; WRKY-type DNA-binding protein; sequence-specific DNA-binding protein.

15

AAC49529.1 U58540 Petroselinum crispum

DESCRIPTION: WRKY2. Contains two WRKY domains; WRKY-type DNA-binding protein.

20

AAK16171.1 AC079887 Oryza sativa

DESCRIPTION: putative DNA-binding protein. OSJNBa0040E01.10.

25

AAC37515.1 L44134 Cucumis sativus

DESCRIPTION: SPF1-like DNA-binding protein.

30

AAD16138.1 AF096298 Nicotiana tabacum

DESCRIPTION: DNA-binding protein 1. WRKY1. transcription factor.

35

AAD38283.1 AC007789 Oryza sativa

DESCRIPTION: putative WRKY DNA binding protein. OSJNBa0049B20.9.

40

BAB18313.1 AP002865 Oryza sativa

DESCRIPTION: putative WRKY DNA binding protein. P0034C11.1. contains EST C26525(C12525).

45

BAB40073.1 AP003074 Oryza sativa

DESCRIPTION: putative WRKY DNA binding protein. OSJNBa0004G10.20.

contains EST C26525(C12525).

- 5 AAC49528.1 U56834 Petroselinum crispum
DESCRIPTION: DNA-binding. WRKY3. WRKY-type DNA-binding protein.
- 10 BAA77358.1 AB020023 Nicotiana tabacum
DESCRIPTION: WRKY domain Zn-finger type DNA-binding protein. DNA-binding
protein NtWRKY3.
- 15 AAG46150.1 AC018727 Oryza sativa
DESCRIPTION: putative DNA-binding protein. OSJNBa0056G17.18.
- 20 CAA88331.1 Z48431 Avena fatua
DESCRIPTION: binds conserved cis-element from cereal alpha-Amy2
promoters. DNA-binding protein.
- 25 AAD32676.1 AF140553 Avena sativa
DESCRIPTION: DNA-binding protein WRKY3. wrky3. putative transcription
factor.
- 30 CAB66338.1 AJ279697 Betula pendula
DESCRIPTION: wrky-type DNA binding protein. wrky.
- 35 AAF61863.1 AF193770 Nicotiana tabacum
DESCRIPTION: DNA-binding protein 3. WRKY3. transcription factor.
- 40 AAF61864.1 AF193771 Nicotiana tabacum
DESCRIPTION: DNA-binding protein 4. WRKY4. transcription factor.
- 45 AAD27591.1 AF121354 Petroselinum crispum
DESCRIPTION: binds sequence specifically to W Boxes (TTGACC).
transcription factor. WRKY3. sequence specific DNA-binding protein.
- 45 BAA87069.1 AB035271 Matricaria chamomilla
DESCRIPTION: elicitor-induced DNA-binding protein homolog. McWRKY1.

-
- 5 AAF34428.1 AF172282 *Oryza sativa*
DESCRIPTION: receptor-like protein kinase. DUPR11.18.
- 10 BAA94518.1 AP001800 *Oryza sativa*
DESCRIPTION: Similar to *Arabidopsis thaliana* chromosome 2 section 111 of
255; putative receptor-like protein kinase (AC002392).
- 15 BAB07904.1 AP002835 *Oryza sativa*
DESCRIPTION: putative S-receptor kinase. P0417G05.12.
- 20 BAA94516.1 AP001800 *Oryza sativa*
DESCRIPTION: Similar to *Zea mays* S-domain receptor-like protein kinase
(AJ010166).
- 25 BAB07906.1 AP002835 *Oryza sativa*
DESCRIPTION: putative S-receptor kinase. P0417G05.14.
- 30 BAA94517.1 AP001800 *Oryza sativa*
DESCRIPTION: Similar to *Zea mays* S-domain receptor-like protein kinase
(AJ010166).
- 35 BAB07905.1 AP002835 *Oryza sativa*
DESCRIPTION: putative S-receptor kinase. P0417G05.13.
- 40 BAA94528.1 AP001800 *Oryza sativa*
DESCRIPTION: Similar to *Arabidopsis thaliana* chromosome 2 BAC T20K24;
putative receptor-like protein kinase (AC002392).
- 45 BAA94529.2 AP001800 *Oryza sativa*
DESCRIPTION: Similar to *Zea mays* S-domain receptor-like protein kinase
(AJ010166).
- CAA67145.1 X98520 *Brassica oleracea*
DESCRIPTION: receptor-like kinase. SFR2.

- 5 CAA73133.1 Y12530 Brassica oleracea
DESCRIPTION: serine /threonine kinase. ARLK.
- 10 CAB89179.1 AJ245479 Brassica napus subsp. napus
DESCRIPTION: ser /thr kinase. S-locus receptor kinase. srk.
- 15 AAA33008.1 M97667 Brassica napus
DESCRIPTION: serine/threonine kinase receptor.
- 20 AAC23542.1 U20948 Ipomoea trifida
DESCRIPTION: receptor protein kinase. IRK1.
- 25 BAA23676.1 AB000970 Brassica rapa
DESCRIPTION: receptor kinase 1. BcRK1.
- 30 BAA92836.1 AB032473 Brassica oleracea
DESCRIPTION: S18 S-locus receptor kinase. SRK18.
- 35 CAB41878.1 Y18259 Brassica oleracea
DESCRIPTION: SRK5 protein. SRK5. receptor-like kinase.
- 40 CAB41879.1 Y18260 Brassica oleracea
DESCRIPTION: SRK15 protein. SRK15. receptor-like kinase.
- 45 BAA21132.1 D88193 Brassica rapa
DESCRIPTION: S-receptor kinase. SRK9 (B.c).
- BAA06285.1 D30049 Brassica rapa
DESCRIPTION: S-receptor kinase SRK9.
- CAA74662.1 Y14286 Brassica oleracea
DESCRIPTION: SFR3. extracellular S domain: 123-1346; transmembrane domain: 1347-1412; intracellular kinase domain: from 1413.

CAA79355.1 Z18921 Brassica oleracea
DESCRIPTION: S-receptor kinase-like protein.

5

BAB21001.1 AB054061 Brassica rapa
DESCRIPTION: S locus receptor kinase. SRK22.

10 AAA33915.1 L27821 Oryza sativa
DESCRIPTION: receptor type serine/threonine kinase. protein kinase.

15 BAA92954.1 AP001551 Oryza sativa
DESCRIPTION: Similar to Oryza sativa protein kinase (OSPK10) mRNA.
(L27821).

554

20 CAC05658.1 AJ250919 Brassica napus
DESCRIPTION: endopolygalacturonase. pegaz.

25 CAC05657.1 AJ250918 Brassica napus
DESCRIPTION: endopolygalacturonase. pgaz.

30 CAA65072.1 X95800 Brassica napus
DESCRIPTION: polygalacturonase.

CAA90272.1 Z49971 Brassica napus
DESCRIPTION: Hydrolytic enzyme. Polygalacturonase. pga.

35 CAA54448.1 X77231 Prunus persica
DESCRIPTION: polygalacturonase. PG.

40 AAC14453.1 L12019 Actinidia deliciosa
DESCRIPTION: polygalacturonase.

45 AAF71160.1 AF152758 Actinidia chinensis
DESCRIPTION: polygalacturonase A. PGA.

- AAA34178.1 M37304 *Lycopersicon esculentum*
DESCRIPTION: polygalacturonase.
- 5 CAA32235.1 X14074 *Lycopersicon esculentum*
DESCRIPTION: polygalacturonase.
- 10 CAA29148.1 X05656 *Lycopersicon esculentum*
DESCRIPTION: polygalacturonase (AA 1-457).
- 15 AAA32914.1 L06094 *Persea americana*
DESCRIPTION: cell wall degradation. polygalacturonase.
- 20 CAA47055.1 X66426 *Persea americana*
DESCRIPTION: polygalacturonase.
- AAC26512.1 AF062467 *Cucumis melo*
DESCRIPTION: polygalacturonase precursor. MPG3.
- 25 CAA11846.1 AJ224147 *Rubus idaeus*
DESCRIPTION: polygalacturonase. RAS3.
- 30 AAF61444.1 AF138858 *Lycopersicon esculentum*
DESCRIPTION: hydrolyses polygalacturonic acid. polygalacturonase. XOPG1.
- 35 BAA88472.1 AB035890 *Cucumis sativus*
DESCRIPTION: polygalacturonase. CUPG1.
- AAD46483.1 AF128266 *Glycine max*
DESCRIPTION: polygalacturonase PG1.
- 40 AAD46484.1 AF128267 *Glycine max*
DESCRIPTION: polygalacturonase PG2.
- 45 AAC28905.1 AF001002 *Lycopersicon esculentum*

DESCRIPTION: hydrolyzes pectin in the cell wall and middle lamella of plant cells. polygalacturonase 4. TAPG4. expressed in abscission.

- 5 AAC28906.1 AF001003 *Lycopersicon esculentum*
DESCRIPTION: hydrolyzes pectin in the cell wall and middle lamella of plant cells. polygalacturonase 5. TAPG5. expressed in abscission.

- 10 AAC28903.1 AF001000 *Lycopersicon esculentum*
DESCRIPTION: hydrolyzes pectin in the cell wall and middle lamella of plant cells. polygalacturonase 1. TAPG1. expressed in abscission.

- 15 AAA80489.1 U23053 *Lycopersicon esculentum*
DESCRIPTION: polygalacturonase precursor.

- 20 AAC64184.1 AF095577 *Prunus persica*
DESCRIPTION: endopolygalacturonase.

- 25 AAC28902.2 AF000999 *Lycopersicon esculentum*
DESCRIPTION: hydrolyzes pectin in the cell wall and middle lamella of plant cells. polygalacturonase 3. TAPG3. expressed in abscission.

- 30 AAB09575.1 U70480 *Lycopersicon esculentum*
DESCRIPTION: abscission polygalacturonase. TAPG2.

- 35 AAC28904.1 AF001001 *Lycopersicon esculentum*
DESCRIPTION: hydrolyzes pectin in the cell wall and middle lamella of plant cells. polygalacturonase 2. TAPG2. expressed in abscission.

- 40 CAA54150.1 X76735 *Prunus persica*
DESCRIPTION: endopolygalacturonase.

- AAC70951.1 AF072732 *Lycopersicon esculentum*
DESCRIPTION: hydrolyzes pectin in the cell wall and middle lamella. polygalacturonase 7. specifically and abundantly expressed in pistils.

- 45 AAC26511.1 AF062466 *Cucumis melo*

DESCRIPTION: polygalacturonase precursor. MPG2.

5 AAB09576.1 U70481 Lycopersicon esculentum
DESCRIPTION: abscission polygalacturonase. TAPG4.

10 AAC28947.1 AF029230 Lycopersicon esculentum
DESCRIPTION: polygalacturonase. TPG6.

AAA82167.1 U09717 Gossypium hirsutum
DESCRIPTION: polygalacturonase.

15 AAA58322.1 U09805 Gossypium barbadense
DESCRIPTION: polygalacturonase.

20 CAA47052.1 X66422 Zea mays
DESCRIPTION: polygalacturonase. PG.

25 AAG14416.1 AF248538 Nicotiana tabacum
DESCRIPTION: NTS1 protein. similar to polygalacturonase.

30 CAB42886.1 AJ238848 Phleum pratense
DESCRIPTION: polygalacturonase. pg.

CAA40850.1 X57627 Zea mays
DESCRIPTION: polygalacturonase.

35 CAA46679.1 X65844 Zea mays
DESCRIPTION: polygalacturonase. PGg6.

40 CAA40910.1 X57743 Zea mays
DESCRIPTION: polygalacturonase.

45 CAA44249.1 X62385 Zea mays
DESCRIPTION: polygalacturonase.

CAA45751.1 X64408 Zea mays
DESCRIPTION: polygalacturonase. PG. pollen-preferentially expressed.

5

CAA40851.1 X57628 Zea mays
DESCRIPTION: polygalacturonase.

10 CAA46680.1 X65845 Zea mays
DESCRIPTION: polygalacturonase. PGg14.

15 AAC26510.1 AF062465 Cucumis melo
DESCRIPTION: polygalacturonase precursor. MPG1.

556

20 CAA51734.1 X73301 Vigna mungo
DESCRIPTION: alpha-amylase. amyVm1.

25 CAA37217.1 X53049 Vigna mungo
DESCRIPTION: alpha-amylase (AA 1-421).

BAA33879.1 AB015131 Phaseolus vulgaris
DESCRIPTION: alpha-amylase.

30 AAA16513.1 U06754 Cuscuta reflexa
DESCRIPTION: starch hydrolysis. alpha amylase precursor. CUS AMY2.

35 AAA98615.1 J04202 Hordeum vulgare
DESCRIPTION: alpha-amylase. Amy46. precursor.

40 AAA98790.1 K02637 Hordeum vulgare
DESCRIPTION: alpha-amylase type B. Amy6-4. precursor.

45 CAA33298.1 X15226 Hordeum vulgare
DESCRIPTION: alpha-amylase.

- AAA33885.1 M24286 *Oryza sativa*
DESCRIPTION: alpha-amylase (EC 3.2.1.1).
- 5 CAA34516.1 X16509 *Oryza sativa*
DESCRIPTION: alpha-amylase.
- 10 CAA72144.1 Y11277 *Hordeum vulgare*
DESCRIPTION: alpha-amylase. amy.
- 15 CAA33299.1 X15227 *Hordeum vulgare*
DESCRIPTION: alpha amylase.
- 20 AAA32925.1 M17126 *Hordeum vulgare*
DESCRIPTION: alpha-amylase 1.
- 25 AAA32927.1 M17128 *Hordeum vulgare*
DESCRIPTION: alpha-amylase 2.
- 30 AAA32929.1 J01236 *Hordeum vulgare*
DESCRIPTION: alpha-amylase type A, EC 3.2.1.1.
- 35 CAA39777.1 X56337 *Oryza sativa*
DESCRIPTION: alpha-amylase. RAmy3B.
- 40 CAA09323.1 AJ010728 *Avena fatua*
DESCRIPTION: alpha amylase. alpha-Amy2A.
- 45 AAA33897.1 M24941 *Oryza sativa*
DESCRIPTION: alpha-amylase precursor (EC 3.2.1.1).
- CAA09324.1 AJ010729 *Avena fatua*
DESCRIPTION: alpha-amylase. alpha-Amy2D.
- CAA28803.1 X05166 *Hordeum vulgare*
DESCRIPTION: alpha-amylase type A. Amy32b.

CAA90272.1 Z49971 Brassica napus
DESCRIPTION: Hydrolytic enzyme. Polygalacturonase. pga.

5 CAA65072.1 X95800 Brassica napus
DESCRIPTION: polygalacturonase.

10 CAA67020.1 X98373 Brassica napus
DESCRIPTION: endo-polygalacturonidase.

15 CAC05658.1 AJ250919 Brassica napus
DESCRIPTION: endopolygalacturonase. pegaz.

CAC05657.1 AJ250918 Brassica napus
DESCRIPTION: endopolygalacturonase. pgaz.

20 AAC14453.1 L12019 Actinidia deliciosa
DESCRIPTION: polygalacturonase.

25 AAF71160.1 AF152758 Actinidia chinensis
DESCRIPTION: polygalacturonase A. PGA.

30 CAA54448.1 X77231 Prunus persica
DESCRIPTION: polygalacturonase. PG.

35 AAA34178.1 M37304 Lycopersicon esculentum
DESCRIPTION: polygalacturonase.

CAA29148.1 X05656 Lycopersicon esculentum
DESCRIPTION: polygalacturonase (AA 1-457).

40 CAA32235.1 X14074 Lycopersicon esculentum
DESCRIPTION: polygalacturonase.

45 AAA32914.1 L06094 Persea americana
DESCRIPTION: cell wall degradation. polygalacturonase.

CAA47055.1 X66426 *Persea americana*
DESCRIPTION: polygalacturonase.

5

AAC26512.1 AF062467 *Cucumis melo*
DESCRIPTION: polygalacturonase precursor. MPG3.

10

CAA11846.1 AJ224147 *Rubus idaeus*
DESCRIPTION: polygalacturonase. RAS3.

15

BAA88472.1 AB035890 *Cucumis sativus*
DESCRIPTION: polygalacturonase. CUPG1.

20

AAF61444.1 AF138858 *Lycopersicon esculentum*
DESCRIPTION: hydrolyses polygalacturonic acid. polygalacturonase. XOPG1.

25

AAA80489.1 U23053 *Lycopersicon esculentum*
DESCRIPTION: polygalacturonase precursor.

30

AAC28903.1 AF001000 *Lycopersicon esculentum*
DESCRIPTION: hydrolyzes pectin in the cell wall and middle lamella of
plant cells. polygalacturonase 1. TAPG1. expressed in abscission.

35

AAB09575.1 U70480 *Lycopersicon esculentum*
DESCRIPTION: abscission polygalacturonase. TAPG2.

40

AAC28904.1 AF001001 *Lycopersicon esculentum*
DESCRIPTION: hydrolyzes pectin in the cell wall and middle lamella of
plant cells. polygalacturonase 2. TAPG2. expressed in abscission.

45

AAC28905.1 AF001002 *Lycopersicon esculentum*
DESCRIPTION: hydrolyzes pectin in the cell wall and middle lamella of
plant cells. polygalacturonase 4. TAPG4. expressed in abscission.

AAC64184.1 AF095577 *Prunus persica*

DESCRIPTION: endopolygalacturonase.

5 AAD46483.1 AF128266 Glycine max
DESCRIPTION: polygalacturonase PG1.

10 AAC28906.1 AF001003 Lycopersicon esculentum
DESCRIPTION: hydrolyzes pectin in the cell wall and middle lamella of
plant cells. polygalacturonase 5. TAPG5. expressed in abscission.

15 AAD46484.1 AF128267 Glycine max
DESCRIPTION: polygalacturonase PG2.

20 CAA54150.1 X76735 Prunus persica
DESCRIPTION: endopolygalacturonase.

AAC26511.1 AF062466 Cucumis melo
DESCRIPTION: polygalacturonase precursor. MPG2.

25 AAC28902.2 AF000999 Lycopersicon esculentum
DESCRIPTION: hydrolyzes pectin in the cell wall and middle lamella of
plant cells. polygalacturonase 3. TAPG3. expressed in abscission.

30 AAC70951.1 AF072732 Lycopersicon esculentum
DESCRIPTION: hydrolyzes pectin in the cell wall and middle lamella.
polygalacturonase 7. specifically and abundantly expressed in pistils.

35 CAA47052.1 X66422 Zea mays
DESCRIPTION: polygalacturonase. PG.

40 AAC28947.1 AF029230 Lycopersicon esculentum
DESCRIPTION: polygalacturonase. TPG6.

45 AAA82167.1 U09717 Gossypium hirsutum
DESCRIPTION: polygalacturonase.

AAB09576.1 U70481 *Lycopersicon esculentum*
DESCRIPTION: abscission polygalacturonase. TAPG4.

5 CAA40910.1 X57743 *Zea mays*
DESCRIPTION: polygalacturonase.

10 CAA44249.1 X62385 *Zea mays*
DESCRIPTION: polygalacturonase.

15 CAA40850.1 X57627 *Zea mays*
DESCRIPTION: polygalacturonase.

AAG14416.1 AF248538 *Nicotiana tabacum*
DESCRIPTION: NTS1 protein. similar to polygalacturonase.

20 CAA46679.1 X65844 *Zea mays*
DESCRIPTION: polygalacturonase. PGg6.

25 AAC26510.1 AF062465 *Cucumis melo*
DESCRIPTION: polygalacturonase precursor. MPG1.

30 AAA58322.1 U09805 *Gossypium barbadense*
DESCRIPTION: polygalacturonase.

35 CAA46680.1 X65845 *Zea mays*
DESCRIPTION: polygalacturonase. PGg14.

CAA40851.1 X57628 *Zea mays*
DESCRIPTION: polygalacturonase.

40 CAA45751.1 X64408 *Zea mays*
DESCRIPTION: polygalacturonase. PG. pollen-preferentially expressed.

45 CAB42886.1 AJ238848 *Phleum pratense*
DESCRIPTION: polygalacturonase. pg.

-
- 5 CAB43937.1 AJ006348 *Fragaria x ananassa*
DESCRIPTION: cell wall hydrolysis. endo-beta-1,4-glucanase. eg1.
- 10 AAC95009.1 AF074923 *Fragaria x ananassa*
DESCRIPTION: endo-1,4-beta-glucanase precursor. Cel1.
1,4-beta-glucanohydrolase.
- 15 AAC12684.1 U76725 *Pinus radiata*
DESCRIPTION: endo-beta-1,4-glucanase. PrCel1. cellulase; PRCEL1.
- 20 AAA69909.1 U13055 *Lycopersicon esculentum*
DESCRIPTION: cell wall hydrolase. endo-1,4-beta-glucanase precursor.
Cel2. cellulase.
- 25 CAA65600.1 X96856 *Prunus persica*
DESCRIPTION: endo-beta-1,4-glucanase. ppEG1.
- 30 CAA65597.1 X96853 *Prunus persica*
DESCRIPTION: endo-beta-1,4-glucanase. pcel1.
- 35 CAA65827.1 X97189 *Capsicum annuum*
DESCRIPTION: endo-beta-1,4-glucanase. ccel3. cellulase.
- 40 AAC62241.1 AF077339 *Lycopersicon esculentum*
DESCRIPTION: endo-1,4-beta-glucanase. cel5. cellulase; also expressed in
fruit and pistils.
- 45 BAA85150.1 AB032830 *Pisum sativum*
DESCRIPTION: endo-1,4-beta-glucanase. EGL2.
- AAA80495.1 U20590 *Lycopersicon esculentum*
DESCRIPTION: endo-1,4-beta-glucanase precursor. cellulase.

- BAB32662.1 AB055886 *Atriplex lentiformis*
DESCRIPTION: beta-1,4-glucanase. Al-cel1. cellulase.
- 5 CAA65828.1 X97190 *Capsicum annuum*
DESCRIPTION: endo-beta-1,4-glucanase. ccel2.
- 10 AAC12685.1 U76756 *Pinus radiata*
DESCRIPTION: endo-beta-1,4-glucanase. PrCel2. cellulase; PRCEL2.
- 15 BAA77239.1 AB025796 *Populus alba*
DESCRIPTION: endo-1,4-beta glucanase. POPCEL2. cellulase.
- CAB59900.1 AJ010950 *Capsicum annuum*
DESCRIPTION: cell wall degradation. endo-beta-1,4-glucanase. eg2.
- 20 BAB39483.1 AB049200 *Populus alba*
DESCRIPTION: endo-1,4-beta-glucanase. PopCel2.
- 25 BAB39482.1 AB049199 *Populus alba*
DESCRIPTION: endo-1,4-beta glucanase. PopCel1.
- 30 CAA72133.1 Y11268 *Lycopersicon esculentum*
DESCRIPTION: endo-1,4-beta-D-glucanase. cel7.
- 35 AAA96135.1 L41046 *Pisum sativum*
DESCRIPTION: endo-1,4-beta-glucanase. EGL1.
- AAC78504.1 U34754 *Phaseolus vulgaris*
DESCRIPTION: endo-1,4-beta-D-glucanase. cellulase.
- 40 AAA02563.1 M57400 *Phaseolus vulgaris*
DESCRIPTION: cellulase precursor. endo-1,4-beta-D-glucanase.
- 45 CAA60737.1 X87323 *Capsicum annuum*
DESCRIPTION: catalyzes hydrolysis of cell wall polysaccharides.

cellulase. cell1. Beta-1,4-endoglycanohydrolase.

CAA65826.1 X97188 Capsicum annuum
5 DESCRIPTION: endo-beta-1,4-glucanase. ccell1. cellulase.

AAA69908.1 U13054 Lycopersicon esculentum
10 DESCRIPTION: cell wall hydrolase. endo-1,4-beta-glucanase precursor.
Cell1. cellulase.

CAB43938.1 AJ006349 Fragaria x ananassa
15 DESCRIPTION: cell wall hydrolysis. endo-beta-1,4-glucanase. eg3.

BAA96209.1 AP002094 Oryza sativa
20 DESCRIPTION: EST C72268(E1328) corresponds to a region of the predicted
gene. Similar to Fragaria x ananassa endo-beta-1,4-glucanase (AJ006349).

BAA96207.1 AP002094 Oryza sativa
25 DESCRIPTION: EST C72268(E1328) corresponds to a region of the predicted
gene. Similar to Fragaria x ananassa endo-beta-1,4-glucanase (AJ006349).

AAD08699.1 AF098292 Lycopersicon esculentum
30 DESCRIPTION: endo-beta-1,4-D-glucanase. Cel8.

BAA94257.1 AB040769 Hordeum vulgare
DESCRIPTION: endo-1,4-beta-glucanase Cell1. Cell1.

35 AAC49704.1 U78526 Lycopersicon esculentum
DESCRIPTION: endo-1,4-beta-glucanase. Cel3.

40 CAB51903.1 AJ242807 Brassica napus
DESCRIPTION: endo-1,4-beta-D-glucanase. Cell16. cellulase.

AAA20082.1 U00730 Glycine max
45 DESCRIPTION: CMCase; cellulase; endo-1,4-beta-D-glucanase.

CAA11301.1 AJ225386 *Fragaria x ananassa*
DESCRIPTION: endo-beta-1,4-glucanase. faEG1. partial cDNA obtained by
RT-PCR amplification.

5

CAA11302.1 AJ223387 *Fragaria x ananassa*
DESCRIPTION: endo-beta-1,4-glucanase. partial cDNA obtained by RT-PCR
amplification.

10

BAA21111.1 D88417 *Gossypium hirsutum*
DESCRIPTION: endo-1,4-beta-glucanase.

15

AAA20083.1 U00731 *Glycine max*
DESCRIPTION: CMCase; cellulase; endo-1,4-beta-D-glucanase.

560

20

AAB97617.1 U83687 *Apium graveolens*
DESCRIPTION: NADPH-dependent mannose 6-phosphate reductase. m6pr.
aldo-keto reductase; similar to aldose 6-phosphate reductase also known as
NADP-sorbitol-6-phosphate dehydrogenase encoded by GenBank Accession
Number D11080.

25

AAC97607.1 AF057134 *Malus x domestica*
DESCRIPTION: synthesizes sorbitol, a major photosynthetic product in many
members of the Rosaceae family. NADP-dependent sorbitol 6-phosphate
dehydrogenase. S6PDH.

30

BAA01853.1 D11080 *Malus x domestica*
DESCRIPTION: NADP-dependent D-sorbitol-6-phosphate dehydrogenase.
S6PDH.

35

561

CAB43938.1 AJ006349 *Fragaria x ananassa*
DESCRIPTION: cell wall hydrolysis. endo-beta-1,4-glucanase. eg3.

40

BAA96209.1 AP002094 *Oryza sativa*
DESCRIPTION: EST C72268(E1328) corresponds to a region of the predicted
gene. Similar to *Fragaria x ananassa* endo-beta-1,4-glucanase (AJ006349).

45

- 5 BAA96207.1 AP002094 *Oryza sativa*
DESCRIPTION: EST C72268(E1328) corresponds to a region of the predicted gene. Similar to *Fragaria x ananassa* endo-beta-1,4-glucanase (AJ006349).
- AAD08699.1 AF098292 *Lycopersicon esculentum*
DESCRIPTION: endo-beta-1,4-D-glucanase. Cel8.
- 10 BAA21111.1 D88417 *Gossypium hirsutum*
DESCRIPTION: endo-1,4-beta-glucanase.
- 15 CAA65828.1 X97190 *Capsicum annuum*
DESCRIPTION: endo-beta-1,4-glucanase. ccel2.
- 20 CAB59900.1 AJ010950 *Capsicum annuum*
DESCRIPTION: cell wall degradation. endo-beta-1,4-glucanase. eg2.
- 25 AAC95009.1 AF074923 *Fragaria x ananassa*
DESCRIPTION: endo-1,4-beta-glucanase precursor. Cell1.
1,4-beta-glucanohydrolase.
- 30 CAB43937.1 AJ006348 *Fragaria x ananassa*
DESCRIPTION: cell wall hydrolysis. endo-beta-1,4-glucanase. eg1.
- 35 AAA80495.1 U20590 *Lycopersicon esculentum*
DESCRIPTION: endo-1,4-beta-glucanase precursor. cellulase.
- BAA85150.1 AB032830 *Pisum sativum*
DESCRIPTION: endo-1,4-beta-glucanase. EGL2.
- 40 AAC12684.1 U76725 *Pinus radiata*
DESCRIPTION: endo-beta-1,4-glucanase. PrCell1. cellulase; PRCEL1.
- 45 BAB32662.1 AB055886 *Atriplex lentiformis*
DESCRIPTION: beta-1,4-glucanase. Al-cell1. cellulase.

- 5 AAC62241.1 AF077339 *Lycopersicon esculentum*
DESCRIPTION: endo-1,4-beta-glucanase. cel5. cellulase; also expressed in fruit and pistils.
- 10 CAA65826.1 X97188 *Capsicum annuum*
DESCRIPTION: endo-beta-1,4-glucanase. ccel1. cellulase.
- 15 AAA69909.1 U13055 *Lycopersicon esculentum*
DESCRIPTION: cell wall hydrolase. endo-1,4-beta-glucanase precursor. Cel2. cellulase.
- 20 CAA65597.1 X96853 *Prunus persica*
DESCRIPTION: endo-beta-1,4-glucanase. pcel1.
- 25 CAA65600.1 X96856 *Prunus persica*
DESCRIPTION: endo-beta-1,4-glucanase. ppEG1.
- 30 AAC12685.1 U76756 *Pinus radiata*
DESCRIPTION: endo-beta-1,4-glucanase. PrCel2. cellulase; PRCEL2.
- 35 BAB39482.1 AB049199 *Populus alba*
DESCRIPTION: endo-1,4-beta glucanase. PopCel1.
- 40 CAA65827.1 X97189 *Capsicum annuum*
DESCRIPTION: endo-beta-1,4-glucanase. ccel3. cellulase.
- 45 BAB39483.1 AB049200 *Populus alba*
DESCRIPTION: endo-1,4-beta-glucanase. PopCel2.
- BAA77239.1 AB025796 *Populus alba*
DESCRIPTION: endo-1,4-beta glucanase. POPCEL2. cellulase.
- AAA69908.1 U13054 *Lycopersicon esculentum*
DESCRIPTION: cell wall hydrolase. endo-1,4-beta-glucanase precursor. Cel1. cellulase.

- 5 AAC78504.1 U34754 Phaseolus vulgaris
DESCRIPTION: endo-1,4-beta-D-glucanase. cellulase.
- 10 AAA02563.1 M57400 Phaseolus vulgaris
DESCRIPTION: cellulase precursor. endo-1,4-beta-D-glucanase.
- 15 CAA72133.1 Y11268 Lycopersicon esculentum
DESCRIPTION: endo-1,4-beta-D-glucanase. cel7.
- 20 CAB51903.1 AJ242807 Brassica napus
DESCRIPTION: endo-1,4-beta-D-glucanase. Cell6. cellulase.
- 25 AAC49704.1 U78526 Lycopersicon esculentum
DESCRIPTION: endo-1,4-beta-glucanase. Cel3.
- 30 BAA94257.1 AB040769 Hordeum vulgare
DESCRIPTION: endo-1,4-beta-glucanase Cell1. Cell1.
- 35 CAA11302.1 AJ223387 Fragaria x ananassa
DESCRIPTION: endo-beta-1,4-glucanase. partial cDNA obtained by RT-PCR amplification.
- 40 AAA20082.1 U00730 Glycine max
DESCRIPTION: CMCase; cellulase; endo-1,4-beta-D-glucanase.
- 45 CAA11301.1 AJ223386 Fragaria x ananassa
DESCRIPTION: endo-beta-1,4-glucanase. faEG1. partial cDNA obtained by RT-PCR amplification.
- 45 AAC64045.1 AF077340 Lycopersicon esculentum
DESCRIPTION: endo-1,4-beta-glucanase. cel5. cellulase.

-
- 5 AAD53011.1 AF089848 *Brassica napus*
DESCRIPTION: senescence-specific cysteine protease. SAG12-1. BnSAG12-1.
- 10 AAD53012.1 AF089849 *Brassica napus*
DESCRIPTION: senescence-specific cysteine protease. SAG12-2. BnSAG12-2.
- 15 AAK27968.1 AF242372 *Ipomoea batatas*
DESCRIPTION: cysteine protease. SPCP1.
- 20 AAA50755.1 U13940 *Alnus glutinosa*
DESCRIPTION: cysteine proteinase. putative preproprotein.
- 25 BAB13759.1 AB040454 *Astragalus sinicus*
DESCRIPTION: cysteine proteinase. AsNODf32. preproprotein putative.
- AAC62396.1 AF050756 *Ricinus communis*
DESCRIPTION: cysteine endopeptidase precursor. CysEP.
- 30 CAB09698.1 Z97022 *Hordeum vulgare*
DESCRIPTION: cysteine proteinase. putative.
- CAA52425.1 X74406 *Hemerocallis* sp.
DESCRIPTION: thiol-protease. SEN102.
- 35 BAA83472.1 AB004648 *Oryza sativa*
DESCRIPTION: cysteine endopeptidase. RepA.
- 40 CAA56844.1 X80876 *Oryza sativa*
DESCRIPTION: cysteine protease.
- 45 BAA88898.1 AB020961 *Zea mays*
DESCRIPTION: cysteine protease component of protease-inhibitor complex.
CPPIC.

- 5 AAC35211.1 U12637 Hemerocallis hybrid cultivar
DESCRIPTION: cysteine proteinase. SEN11.
- 10 CAB09697.1 Z97021 Hordeum vulgare
DESCRIPTION: cysteine endopeptidase EP-A. precursor.
- 15 AAB88263.1 AF019147 Zea mays
DESCRIPTION: cysteine proteinase Mir3. mir3.
- 20 AAD28477.1 AF133839 Sandersonia aurantiaca
DESCRIPTION: papain-like cysteine protease. PRT5. senescence-related.
- 25 CAB16317.1 Z99173 Nicotiana tabacum
DESCRIPTION: storage protein hydrolysis. cysteine proteinase precursor.
- AAD09699.1 Z97023 Hordeum vulgare
DESCRIPTION: cysteine endopeptidase EP-A.
- 30 AAD10337.1 U94591 Hordeum vulgare
DESCRIPTION: cysteine proteinase precursor. EPA.
- 35 CAA06243.1 AJ004958 Pisum sativum
DESCRIPTION: thiol-protease. pre-pro-TPE4A protein. tpE4A.
- 40 CAB53515.1 AJ245924 Solanum tuberosum
DESCRIPTION: proteolysis. cysteine protease. cyp.
- 45 AAD48496.1 AF172856 Lycopersicon esculentum
DESCRIPTION: cysteine protease TDI-65. tdi-65. induced by drought;
localized in the nuclei and chloroplast (Tabaeizadeh, Z. et al., 1995.
Protoplasma, 186:208-219).
- CAA05894.1 AJ003137 Lycopersicon esculentum
DESCRIPTION: cysteine protease. CYP1. C14.

AAB37233.1 U34747 Phalaenopsis sp. SM9108
DESCRIPTION: cysteine proteinase.

CAB17076.1 Z99954 Phaseolus vulgaris
DESCRIPTION: protein hydrolysis. cysteine proteinase precursor.

CAA84378.1 Z34895 *Vicia sativa*
DESCRIPTION: storage protein degradation. cysteine proteinase.

20 CAA53377.1 X75749 Vicia sativa
DESCRIPTION: storage protein hydrolysis. cysteine protease.

25 CAB17074.1 Z99952 Phaseolus vulgaris
DESCRIPTION: degradation of storage proteins. cysteine proteinase
precursor.

AAB68374.1 U52970 Phaseolus vulgaris
30 DESCRIPTION: suggested to initiate phaseolin degradation during
germination. cysteine endopeptidase 1. PvCEP-1.

CAA12118.1 AJ224766 Phaseolus vulgaris
35 DESCRIPTION: phaseolin degradation. cysteine protease.

AAC49455.1 U41902 *Pseudotsuga menziesii*
DESCRIPTION: cysteine protease. Pseudotzain. PM33cysP.

CAA46863.1 X66061 Pisum sativum
DESCRIPTION: thiolprotease. tpp. start codon ttg.

45 AAB41816.1 U44947 Pisum sativum

DESCRIPTION: NTH1. PsCyp1. cysteine protease homolog.

- 5 BAA83473.1 AB004819 Oryza sativa
DESCRIPTION: cysteine endopeptidase. Rep1.
- 10 BAA22544.1 D38532 Ananas comosus
DESCRIPTION: precursor of cysteine proteinase. FBSB precursor. stem
bromelain precursor in fruit.
- 15 BAA11170.1 D76415 Oryza sativa
DESCRIPTION: cysteine proteinase.
- 20 AAD20453.1 AF099203 Oryza sativa
DESCRIPTION: cysteine endopeptidase precursor. EP3A.
- 25 CAA08860.1 AJ009829 Ananas comosus
DESCRIPTION: cysteine proteinase precursor, AN8. an8.
- 30 AAA85036.1 U19384 Hordeum vulgare
DESCRIPTION: cysteine proteinase EPB2 precursor.
- 35 AAA85035.1 U19359 Hordeum vulgare
DESCRIPTION: cysteine proteinase EPB1 precursor.
- 565

- 40 CAA81558.1 Z26949 Solanum tuberosum
DESCRIPTION: subunit of the mitochondrial pyruvate dehydrogenase complex.
E1 alpha subunit of pyruvate dehydrogenase precursor.
- 45 AAC72195.1 AF069911 Zea mays
DESCRIPTION: pyruvate dehydrogenase E1 alpha subunit.

AAG43499.1 AF209924 *Lycopersicon esculentum*
 DESCRIPTION: pyruvate dehydrogenase.

5 CAB08111.1 Z94180 *Lycopersicon esculentum*
 DESCRIPTION: branched chain alpha-keto acid dehydrogenase E1-alpha
 subunit.

566

10 AAD55090.1 AF178653 *Vitis riparia*
 DESCRIPTION: thaumatin. osmotin; pathogenesis-related protein.

15 CAA51432.1 X72928 *Solanum commersonii*
 DESCRIPTION: osmotin-like protein.

20 CAA47601.1 X67121 *Solanum commersonii*
 DESCRIPTION: osmotin-like protein.

25 CAC34055.1 AJ297410 *Capsicum annum*
 DESCRIPTION: osmotin-like protein. pr5 p23.

30 CAA47047.1 X66416 *Lycopersicon esculentum*
 DESCRIPTION: tpm 1. Induced during viroid infection. Osmotin-like,
 antifungal protein homologue.

35 AAB23375.1 S44889 *Nicotiana tabacum*
 DESCRIPTION: osmotin. osmotin. pathogenesis-related protein homolog; This
 sequence comes from Fig. 3.

40 AAB22459.2 S40046 *Nicotiana tabacum*
 DESCRIPTION: osmotin. abscisic acid-activated. basic PR-like protein;
 This sequence comes from Fig. 1A; conceptual translation presented here
 differs from translation in publication; mismatch(181[R->G]).

45 AAG16625.1 AY007309 *Solanum dulcamara*
 DESCRIPTION: cryoprotective osmotin-like protein.

- CAA46623.1 X65701 *Nicotiana tabacum*
DESCRIPTION: osmotin. AP24.
- 5 CAA46622.1 X65700 *Nicotiana tabacum*
DESCRIPTION: osmotin. AP24.
- 10 CAA51431.1 X72927 *Solanum commersonii*
DESCRIPTION: osmotin-like protein.
- 15 CAA64620.1 X95308 *Nicotiana tabacum*
DESCRIPTION: PR protein. osmotin.
- 20 CAA51430.1 X72926 *Solanum commersonii*
DESCRIPTION: osmotin-like protein.
- AAC64171.1 AF093743 *Lycopersicon esculentum*
DESCRIPTION: pathogenesis-related protein osmotin precursor. NP24.
- 25 AAB61590.1 AF003007 *Vitis vinifera*
DESCRIPTION: VVTL1. osmotin-like protein, PR-5 protein; thaumatin-like protein.
- 30 BAA11180.1 D76437 *Nicotiana sylvestris*
DESCRIPTION: antifungal activity. neutral PR-5 (osmotin-like protein, PR-5d). neutral isoform of pathogenesis-related protein group 5.
- 35 AAA34087.1 M64081 *Nicotiana tabacum*
DESCRIPTION: osmotin-like protein. OLP1.
- 40 CAA47669.1 X67244 *Solanum commersonii*
DESCRIPTION: osmotin-like protein.
- 45 CAA71883.1 Y10992 *Vitis vinifera*
DESCRIPTION: osmotin-like protein. OSM1.

AAFI3707.1 AF199508 *Fragaria x ananassa*
DESCRIPTION: osmotin-like protein. olp.

5 AAA34089.1 M29279 *Nicotiana tabacum*
DESCRIPTION: osmotin.

10 CAA43854.1 X61679 *Nicotiana tabacum*
DESCRIPTION: osmotin.

15 CAA04642.1 AJ001268 *Hordeum vulgare*
DESCRIPTION: antifungal. basic pathogenesis-related protein PR5.
osmotin/permatin-like.

20 CAC22330.1 AJ298304 *Fagus sylvatica*
DESCRIPTION: stress protein. osmotin-like protein. olp2.

25 CAC22329.1 AJ298303 *Fagus sylvatica*
DESCRIPTION: stress protein. osmotin-like protein. olp.

AAB67852.1 L76377 *Oryza sativa*
DESCRIPTION: osmotin. 14b.

30 CAB36911.1 AJ000692 *Quercus suber*
DESCRIPTION: stress protein. osmotin-like protein. olp.

569

35 BAA95814.1 AP002069 *Oryza sativa*
DESCRIPTION: ESTs AU082579(S2069),D40238(S2069) correspond to a
region of
the predicted gene. Similar to *Arabidopsis thaliana* vesicle-associated
membrane protein 7C; synaptobrevin 7C. (AF025332).

40 572

45 AAA92677.1 U13736 *Pisum sativum*
DESCRIPTION: binds calcium. calmodulin-like protein.

AAA34015.1 L01433 Glycine max

DESCRIPTION: calcium-binding regulatory protein. calmodulin. SCaM-4.
putative.

5

AAA33948.1 L19359 Glycine max

DESCRIPTION: calcium-binding regulatory protein. calmodulin. SCaM-5.
putative.

10

CAA66159.1 X97558 Capsicum annuum

DESCRIPTION: calmodulin-1.

15

CAA09302.1 AJ010645 Capsicum annuum

DESCRIPTION: calcium binding protein. calmodulin 3 protein. calmodulin 3.

20

AAA34144.1 M67472 Lycopersicon esculentum

DESCRIPTION: calmodulin. CALM1LE.

25

CAA62150.1 X90560 Physcomitrella patens

DESCRIPTION: Calmodulin. CaM.

30

BAA87825.1 AP000815 Oryza sativa

DESCRIPTION: ESTs AU030013(E50493),AU081341(E50493) correspond to
a

35

region of the predicted gene. Similar to O.sativa gene encoding
calmodulin. (Z12828).

40

AAF65511.1 AF108889 Capsicum annuum

DESCRIPTION: calmodulin.

45

AAA85157.1 U20297 Solanum tuberosum

DESCRIPTION: calcium-binding protein. calmodulin.

AAA85156.1 U20296 Solanum tuberosum

DESCRIPTION: calcium-binding protein. calmodulin.

5 AAA62351.1 U20295 Solanum tuberosum
DESCRIPTION: calcium-binding protein. calmodulin.

10 AAA85155.1 U20294 Solanum tuberosum
DESCRIPTION: calcium-binding protein. calmodulin.

15 AAA33900.1 L18914 Oryza sativa
DESCRIPTION: calcium binding protein, signal transduction. calmodulin.

CAA78288.1 Z12828 Oryza sativa
DESCRIPTION: calcium binding protein, signal transduction. calmodulin.

20 AAC49583.1 U48692 Triticum aestivum
DESCRIPTION: calmodulin TaCaM2-3. calcium-binding protein.

25 AAC49582.1 U48691 Triticum aestivum
DESCRIPTION: calmodulin TaCaM2-2. calcium-binding protein.

30 CAA61980.1 X89890 Bidens pilosa
DESCRIPTION: Calmodulin.

CAA67054.1 X98404 Capsicum annuum
DESCRIPTION: calmodulin-2.

35 AAA33083.1 M20729 Chlamydomonas reinhardtii
DESCRIPTION: calmodulin.

40 AAG11418.1 AF292108 Prunus avium
DESCRIPTION: calmodulin.

45 AAF33852.1 AF231026 Oryza sativa
DESCRIPTION: calmodulin-like protein.

- AAA92681.1 U13882 *Pisum sativum*
DESCRIPTION: calcium-binding protein. calmodulin.
- 5 AAA33706.1 M80836 *Petunia x hybrida*
DESCRIPTION: calmodulin. CAM81.
- 10 AAA33705.1 M80831 *Petunia x hybrida*
DESCRIPTION: calmodulin-related protein. CAM53.
- 15 AAA98933.1 U37936 *Oryza sativa*
DESCRIPTION: novel calmodulin-like protein. C-terminal of this sequence contains a CAAX box which is common in signal transport protein, but not in calmodulin.
- 20 CAA43143.1 X60738 *Malus x domestica*
DESCRIPTION: Calmodulin. CaM.
- 25 CAA78301.1 Z12839 *Lilium longiflorum*
DESCRIPTION: calcium binding protein, signal transduction. calmodulin.
- 30 AAA33397.1 L18912 *Lilium longiflorum*
DESCRIPTION: calcium binding protein, signal transduction. calmodulin. putative.
- 35 CAA42423.1 X59751 *Daucus carota*
DESCRIPTION: calmodulin. Ccam-1.
- 40 AAF73157.1 AF150059 *Brassica napus*
DESCRIPTION: calmodulin. CaM1. involved in seed germination.
- 45 AAA19571.1 U10150 *Brassica napus*
DESCRIPTION: calcium binding. calmodulin. bcm1.
- AAA87347.1 M88307 *Brassica juncea*
DESCRIPTION: calmodulin.

AAG27432.1 AF295637 *Elaeis guineensis*
 DESCRIPTION: calmodulin.
 5

BAA94697.1 AB041712 *Chara corallina*
 DESCRIPTION: calmodulin. cccam2.
 10

BAA94696.1 AB041711 *Chara corallina*
 DESCRIPTION: calmodulin. cccam1.
 15

BAA96536.1 AB044286 *Chara corallina*
 DESCRIPTION: calmodulin. ccam.
 20

AAC18355.1 AF064456 *Oryza sativa* subsp. *indica*
 DESCRIPTION: calmodulin-like protein. CAM-like.
 25

AAA34237.1 L20691 *Vigna radiata*
 DESCRIPTION: calmodulin.
 30

CAA52602.1 X74490 *Zea mays*
 DESCRIPTION: Calmodulin. ZMCALM1.
 35

CAA54583.1 X77397 *Zea mays*
 DESCRIPTION: calmodulin. CaM2.
 40

AAC49585.1 U49103 *Triticum aestivum*
 DESCRIPTION: calmodulin TaCaM3-2. calcium-binding protein.
 45

AAC49586.1 U49104 *Triticum aestivum*
 DESCRIPTION: calmodulin TaCaM3-3. calcium-binding protein.
 45

AAC49587.1 U49105 *Triticum aestivum*
 DESCRIPTION: calmodulin TaCaM4-1. calcium-binding protein.
 45

AAC49580.1 U48689 *Triticum aestivum*
DESCRIPTION: calmodulin TaCaM1-3. calcium-binding protein.

5 AAC49584.1 U48693 *Triticum aestivum*
DESCRIPTION: calmodulin TaCaM3-1. calcium-binding protein.

575

10 AAK28303.1 AF346431 *Nicotiana tabacum*
DESCRIPTION: phenylpropanoid:glucosyltransferase 1. togt1.
glucosyltransferase.

15 AAB36653.1 U32644 *Nicotiana tabacum*
DESCRIPTION: immediate-early salicylate-induced glucosyltransferase.
IS5a.

20 AAB36652.1 U32643 *Nicotiana tabacum*
DESCRIPTION: immediate-early salicylate-induced glucosyltransferase.
IS10a.

25 AAK28304.1 AF346432 *Nicotiana tabacum*
DESCRIPTION: phenylpropanoid:glucosyltransferase 2. togt2.
glucosyltransferase.

30 CAA59450.1 X85138 *Lycopersicon esculentum*
DESCRIPTION: twi1. homologous to glucosyltransferases.

CAB56231.1 Y18871 *Dorotheanthus bellidiformis*
35 DESCRIPTION: betanidin-5-O-glucosyltransferase.

BAA83484.1 AB031274 *Scutellaria baicalensis*
DESCRIPTION: UDP-glucose: flavonoid 7-O-glucosyltransferase. ufgt.
40

AAB48444.1 U82367 *Solanum tuberosum*
DESCRIPTION: UDP-glucose glucosyltransferase.

45 CAA54610.1 X77460 *Manihot esculenta*

DESCRIPTION: UTP-glucose glucosyltransferase. CGT4.

- 5 AAD04166.1 AF101972 *Phaseolus lunatus*
DESCRIPTION: catalyzes formation of O-glucosylzeatin from zeatin and UDPG; catalyzes formation of O-xylosylzeatin from zeatin and UDPX. zeatin O-glucosyltransferase. ZOG1. cytokinin O-glucosyltransferase.
- 10 BAB17182.1 AP002843 *Oryza sativa*
DESCRIPTION: putative UTP-glucose glucosyltransferase. P0407B12.19.
- 15 BAA93039.1 AB033758 *Citrus unshiu*
DESCRIPTION: limonoid UDP-glucosyltransferase. LGTase.
- 20 AAF61647.1 AF190634 *Nicotiana tabacum*
DESCRIPTION: UDP-glucose:salicylic acid glucosyltransferase. SA-GTase.
- BAB17176.1 AP002843 *Oryza sativa*
DESCRIPTION: putative UTP-glucose glucosyltransferase. P0407B12.13.
- 25 CAC09351.1 AL442007 *Oryza sativa*
DESCRIPTION: putative glucosyltransferase. H0212B02.7.
- 30 CAA54611.1 X77461 *Manihot esculenta*
DESCRIPTION: UTP-glucose glucosyltransferase. CGT2.
- 35 AAF98390.1 AF287143 *Brassica napus*
DESCRIPTION: catalyzes the transfer of glucose from UDP-glucose to sinapate and some other hydroxycinnamates (4-coumarate, caffeate, ferulate). UDP-glucose:sinapate glucosyltransferase. SGT1. SGT.
- 40 AAK16181.1 AC079887 *Oryza sativa*
DESCRIPTION: putative glucosyltransferase. OSJNBa0040E01.16.
- 45 AAK16178.1 AC079887 *Oryza sativa*
DESCRIPTION: putative glucosyltransferase. OSJNBa0040E01.5.

- CAA54612.1 X77462 *Manihot esculenta*
DESCRIPTION: UTP-glucose glucosyltransferase. CGT5.
- 5 AAK16180.1 AC079887 *Oryza sativa*
DESCRIPTION: putative glucosyltransferase. OSJNBa0040E01.21.
- 10 AAF17077.1 AF199453 *Sorghum bicolor*
DESCRIPTION: UDP-glucose glucosyltransferase.
UDP-glucose:p-hydroxymandelonitrile-o- glucosyltransferase.
- 15 CAA54609.1 X77459 *Manihot esculenta*
DESCRIPTION: UTP-glucose glucosyltransferase. CGT1.
- 20 BAB41025.1 AB047098 *Vitis vinifera*
DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. FIUFGT1.
- 25 AAK16172.1 AC079887 *Oryza sativa*
DESCRIPTION: putative glucosyltransferase. OSJNBa0040E01.14.
- 30 BAB41019.1 AB047092 *Vitis vinifera*
DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. ItUFGT1.
- 35 BAB41018.1 AB047091 *Vitis labrusca* x *Vitis vinifera*
DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. KyUFGT2.
The
gene originated in one of the parents *V. vinifera* cv. Centennial.
- 40 BAB41023.1 AB047096 *Vitis vinifera*
DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. AIUFGT1.
- 45 BAB41021.1 AB047094 *Vitis vinifera*
DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. RuUFGT1.
- 45 BAA89009.1 AB027455 *Petunia x hybrida*
DESCRIPTION: anthocyanin 5-O-glucosyltransferase. PH1.

AAB81682.1 AF000371 Vitis vinifera
 DESCRIPTION: UDP glucose:flavonoid 3-o-glucosyltransferase.
 5

BAB41017.1 AB047090 Vitis labrusca x Vitis vinifera
 DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. KyUFGT1.
 The
 10 gene was derived from one of the parents V. labruscana cv. Ishiharawase.

BAB41022.1 AB047095 Vitis vinifera
 DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. RuUFGT2.
 15

BAB41020.1 AB047093 Vitis vinifera
 DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. ItUFGT2.
 20

BAB41024.1 AB047097 Vitis vinifera
 DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. AlUFGT2.
 25

AAB81683.1 AF000372 Vitis vinifera
 DESCRIPTION: UDP glucose:flavonoid 3-o-glucosyltransferase.
 30

BAB41026.1 AB047099 Vitis vinifera
 DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. FlUFGT2.
 35

CAA54613.1 X77463 Manihot esculenta
 DESCRIPTION: UTP-glucose glucosyltransferase. CGT6.
 40

BAA89008.1 AB027454 Petunia x hybrida
 DESCRIPTION: anthocyanidin 3-O-glucosyltransferase. PGT8.
 45

BAA12737.1 D85186 Gentiana triflora
 DESCRIPTION: UDP-glucose:flavonoid-3-glucosyltransferase.
 576

 CAB60277.1 AJ002586 Solanum tuberosum

DESCRIPTION: UCP.

CAA72107.1 Y11220 Solanum tuberosum
5 DESCRIPTION: mitochondrial uncoupling protein.

BAA92172.1 AB024733 Symplocarpus renifolius
10 DESCRIPTION: SfUCPa. SfUCPa.

BAB40658.1 AB049998 Oryza sativa
DESCRIPTION: uncoupling protein. OsUCP2.

15 BAA92173.1 AB024734 Symplocarpus renifolius
DESCRIPTION: SfUCPb. SfUCPb.

20 BAB16385.1 AB042429 Triticum aestivum
DESCRIPTION: uncoupling protein. WhUCP1b.

BAB16384.1 AB042428 Triticum aestivum
25 DESCRIPTION: uncoupling protein. WhUCP1a.

BAB40657.1 AB049997 Oryza sativa
DESCRIPTION: uncoupling protein. OsUCP1.

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577

AAA19571.1 U10150 Brassica napus
35 DESCRIPTION: calcium binding. calmodulin. bcm1.

AAA87347.1 M88307 Brassica juncea
DESCRIPTION: calmodulin.

40

AAA92681.1 U13882 Pisum sativum
DESCRIPTION: calcium-binding protein. calmodulin.

45 AAA33706.1 M80836 Petunia x hybrida
DESCRIPTION: calmodulin. CAM81.

- CAA43143.1 X60738 *Malus x domestica*
DESCRIPTION: Calmodulin. CaM.
- 5
- CAA78301.1 Z12839 *Lilium longiflorum*
DESCRIPTION: calcium binding protein, signal transduction. calmodulin.
- 10
- AAA33397.1 L18912 *Lilium longiflorum*
DESCRIPTION: calcium binding protein, signal transduction. calmodulin.
putative.
- 15
- CAA42423.1 X59751 *Daucus carota*
DESCRIPTION: calmodulin. Ccam-1.
- 20
- AAG27432.1 AF295637 *Elaeis guineensis*
DESCRIPTION: calmodulin.
- 25
- AAG11418.1 AF292108 *Prunus avium*
DESCRIPTION: calmodulin.
- 30
- AAA34237.1 L20691 *Vigna radiata*
DESCRIPTION: calmodulin.
- 35
- AAC49587.1 U49105 *Triticum aestivum*
DESCRIPTION: calmodulin TaCaM4-1. calcium-binding protein.
- 40
- AAC49586.1 U49104 *Triticum aestivum*
DESCRIPTION: calmodulin TaCaM3-3. calcium-binding protein.
- 45
- AAC49585.1 U49103 *Triticum aestivum*
DESCRIPTION: calmodulin TaCaM3-2. calcium-binding protein.
- AAC49584.1 U48693 *Triticum aestivum*
DESCRIPTION: calmodulin TaCaM3-1. calcium-binding protein.

AAF65511.1 AF108889 Capsicum annuum
DESCRIPTION: calmodulin.

5 AAC36059.1 AF042840 Oryza sativa
DESCRIPTION: calmodulin. CaM1.

10 AAA34238.1 L20507 Vigna radiata
DESCRIPTION: calmodulin.

15 AAA34014.1 L01432 Glycine max
DESCRIPTION: calcium-binding regulatory protein. calmodulin. SCaM-3.
putative.

20 AAA34013.1 L01430 Glycine max
DESCRIPTION: calcium-binding regulatory protein. calmodulin. SCaM-1.
putative.

25 CAA36644.1 X52398 Medicago sativa
DESCRIPTION: calmodulin (AA 1-149).

AAB68399.1 U79736 Helianthus annuus
DESCRIPTION: calmodulin. HaCaM.

30 AAD10244.1 AF030032 Phaseolus vulgaris
DESCRIPTION: calmodulin. CaM. EF-hand protein; calcium-dependent
protein;
functions in calcium signal transduction pathways.

35

AAA33705.1 M80831 Petunia x hybrida
DESCRIPTION: calmodulin-related protein. CAM53.

40

AAA16320.1 L14071 Bryonia dioica
DESCRIPTION: calmodulin. Bc329. calcium-binding sites (amino acid #): 1.
(21..33); 2. (57..68); 3. (94..106); 4. (130..141).

45

CAA61980.1 X89890 Bidens pilosa

DESCRIPTION: Calmodulin.

- 5 AAA33900.1 L18914 Oryza sativa
DESCRIPTION: calcium binding protein, signal transduction. calmodulin.
- 10 CAA78288.1 Z12828 Oryza sativa
DESCRIPTION: calcium binding protein, signal transduction. calmodulin.
- 15 CAA74307.1 Y13974 Zea mays
DESCRIPTION: calmodulin.
- 20 AAC49583.1 U48692 Triticum aestivum
DESCRIPTION: calmodulin TaCaM2-3. calcium-binding protein.
- 25 AAC49582.1 U48691 Triticum aestivum
DESCRIPTION: calmodulin TaCaM2-2. calcium-binding protein.
- 30 AAA85157.1 U20297 Solanum tuberosum
DESCRIPTION: calcium-binding protein. calmodulin.
- 35 AAA85156.1 U20296 Solanum tuberosum
DESCRIPTION: calcium-binding protein. calmodulin.
- 40 AAA62351.1 U20295 Solanum tuberosum
DESCRIPTION: calcium-binding protein. calmodulin.
- 45 AAA85155.1 U20294 Solanum tuberosum
DESCRIPTION: calcium-binding protein. calmodulin.
- 40 CAA46150.1 X65016 Oryza sativa
DESCRIPTION: calmodulin. cam.
- 45 AAD10246.1 AF030034 Phaseolus vulgaris
DESCRIPTION: calmodulin. CaM. EF-hand protein; calcium-dependent protein;

functions in calcium signal transduction pathways.

5 AAF73157.1 AF150059 Brassica napus
DESCRIPTION: calmodulin. CaM1. involved in seed germination.

10 CAA54583.1 X77397 Zea mays
DESCRIPTION: calmodulin. CaM2.
578

15 AAF01764.2 AF184277 Glycine max
DESCRIPTION: homeodomain-leucine zipper protein 56. Hdl56. transcription
factor.

20 BAA21017.1 D26578 Daucus carota
DESCRIPTION: transcriptional regulator. DNA-binding protein. homeodomain
at nt 761-940; leucine zipper at nt 941-1048.

25 AAD37697.1 AF145728 Oryza sativa
DESCRIPTION: homeodomain leucine zipper protein. Oshox4. transcription
factor.

30 CAB67118.1 Y17306 Lycopersicon esculentum
DESCRIPTION: homeodomain protein. h52.

35 AAF01765.1 AF184278 Glycine max
DESCRIPTION: homeodomain-leucine zipper protein 57. Hdl57. transcription
factor.

40 BAA05624.1 D26575 Daucus carota
DESCRIPTION: transcriptional regulator. DNA-binding protein. homeodomain
at nt 520-699; leucine zipper at nt 700-805.

45 BAA93466.1 AB028078 Physcomitrella patens
DESCRIPTION: homeobox protein PpHB7. PpHB7. homeodomain-leucine
zipper
gene.

DESCRIPTION: homeobox protein PpHB9. PpHB9. homeodomain-leucine zipper gene.

5

BAA93460.1 AB028072 *Physcomitrella patens*

DESCRIPTION: homeobox protein PpHB1. PpHB1. homeodomain-leucine zipper gene.

10

AAD37699.1 AF145730 *Oryza sativa*

DESCRIPTION: homeodomain leucine zipper protein. Oshox6. transcription factor.

15

CAA06717.1 AJ005820 *Craterostigma plantagineum*

DESCRIPTION: transcription factor. homeodomain leucine zipper protein. hb-1.

20

BAA93463.1 AB028075 *Physcomitrella patens*

DESCRIPTION: homeobox protein PpHB4. PpHB4. homeodomain-leucine zipper gene.

25

CAA65456.2 X96681 *Oryza sativa*

DESCRIPTION: transcription factor. DNA-binding protein. Oshox1. homeodomain leucine zipper gene.

30

AAF19980.1 AF211193 *Oryza sativa*

DESCRIPTION: homeodomain-leucine zipper transcription factor. Hox1. hox1.

35

AAK31270.1 AC079890 *Oryza sativa*

DESCRIPTION: homeodomain leucine zipper protein hox1.

OSJNBb0089A17.12.

40

CAA06728.1 AJ005833 *Craterostigma plantagineum*

DESCRIPTION: transcription factor. homeodomain leucine zipper protein. hb-2.

45

AAD37696.1 AF145727 *Oryza sativa*
DESCRIPTION: homeodomain leucine zipper protein. Oshox3. transcription factor.

5 580

AAD32141.1 AF123503 *Nicotiana tabacum*
DESCRIPTION: Nt-gh3 deduced protein.

10

CAA42636.1 X60033 *Glycine max*
DESCRIPTION: auxin-responsive GH3 product. GH3.

15

BAA96221.1 AP002094 *Oryza sativa*
DESCRIPTION: ESTs C19814(E10971),AU090481(E10971) correspond to a region of the predicted gene. Similar to *Arabidopsis thaliana* chromosome 2, sequence from clones T3F17, F11C10, F13A10; auxin-responsive GH3-like protein (AC006526).

20

581

AAD13632.1 AF059488 *Lycopersicon esculentum*
25 DESCRIPTION: expansin precursor. Exp4.

AAF32410.1 AF230277 *Triphysaria versicolor*
DESCRIPTION: alpha-expansin 2.

30

CAA04385.1 AJ000885 *Brassica napus*
DESCRIPTION: Cell wall extension in plants. Expansin.

35

CAB46492.1 AJ243340 *Lycopersicon esculentum*
DESCRIPTION: expansin9. exp9.

40

AAC63088.1 U82123 *Lycopersicon esculentum*
DESCRIPTION: expansin. LeEXP1. fruit ripening regulated expansin.

45

CAA06271.2 AJ004997 *Lycopersicon esculentum*
DESCRIPTION: expansin18. exp18.

- 5 AAF62182.1 AF247164 *Oryza sativa*
DESCRIPTION: alpha-expansin OsEXP7. cell wall loosening factor; expressed in internodes and leaves.
- 10 AAF35900.1 AF230331 *Zinnia elegans*
DESCRIPTION: expansin. Exp1.
- 15 AAG13982.1 AF297521 *Prunus avium*
DESCRIPTION: expansin 1. Exp1. PruavExp1.
- 20 AAC33529.1 U93167 *Prunus armeniaca*
DESCRIPTION: expansin. PA-Exp1.
- 25 AAF21101.1 AF159563 *Fragaria x ananassa*
DESCRIPTION: expansin. Exp2. ripening regulated.
- 30 AAF35901.1 AF230332 *Zinnia elegans*
DESCRIPTION: expansin 2.
- 35 AAG13983.1 AF297522 *Prunus avium*
DESCRIPTION: expansin 2. Exp2. PruavExp2.
- 40 AAC33530.1 AF038815 *Prunus armeniaca*
DESCRIPTION: expansin. Exp2.
- 45 BAB19676.1 AB029083 *Prunus persica*
DESCRIPTION: expansin. PchExp1.
- AAB40637.1 U64893 *Pinus taeda*
DESCRIPTION: expansin. similar to Arabidopsis expansin encoded by GenBank
Accession Numbers U30476, U30478, U30480 and U30481, to *Cucumis sativus* expansin encoded by GenBank Accession Numbers U30382 and U30460, and to rice expansin encoded by GenBank Accession Numbers U30477 and U30479.

- 5 AAB37746.1 U30382 *Cucumis sativus*
DESCRIPTION: expansin S1 precursor. Cs-EXP1. similar to pollen allergen Lol pI, *Lolium perenne*, Swiss-Prot Accession Number P14946; former gene name CuExS1; expansin-29 (Ex29) protein.
- 10 CAC19184.1 AJ291817 *Cicer arietinum*
DESCRIPTION: expansin.
- 15 AAD47901.1 AF085330 *Pinus taeda*
DESCRIPTION: expansin.
- 20 AAB40634.1 U64890 *Pinus taeda*
DESCRIPTION: expansin. similar to *Arabidopsis* expansin encoded by GenBank Accession Numbers U30476, U30478, U30480 and U30481, to *Cucumis sativus* expansin encoded by GenBank Accession Numbers U30382 and U30460, and to rice expansin encoded by GenBank Accession Numbers U30477 and U30479.
- 25 AAF32409.1 AF230276 *Triphysaria versicolor*
DESCRIPTION: alpha-expansin 3.
- 30 AAC39512.1 AF043284 *Gossypium hirsutum*
DESCRIPTION: expansin. GhEX1. contains N-terminal signal peptide.
- 35 AAB40635.1 U64891 *Pinus taeda*
DESCRIPTION: expansin. similar to *Arabidopsis* expansin encoded by GenBank Accession Numbers U30476, U30478, U30480 and U30481, to *Cucumis sativus* expansin encoded by GenBank Accession Numbers U30382 and U30460, and to rice expansin encoded by GenBank Accession Numbers U30477 and U30479.
- 40 AAC96081.1 AF049354 *Nicotiana tabacum*
DESCRIPTION: involved in acid-growth response. alpha-expansin precursor. Nt-EXP5. cell wall protein.
- 45 AAB38074.1 U30477 *Oryza sativa*
DESCRIPTION: induces extension (creep) in plant cell walls. expansin Os-EXP2. Os-EXP2. former gene name RiExB.

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- 1051 -

AAD13633.1 AF059489 *Lycopersicon esculentum*

DESCRIPTION: expansin precursor. Exp5.

5

AAF62181.1 AF247163 *Oryza sativa*

DESCRIPTION: alpha-expansin OsEXP6. cell wall loosening factor; expressed in internodes and leaves.

10

AAF17571.1 AF202120 *Regnellidium diphyllum*

DESCRIPTION: alpha-expansin. EXP1. Rd-EXP1.

15

AAF62180.1 AF247162 *Oryza sativa*

DESCRIPTION: alpha-expansin OsEXP5. cell wall loosening factor; expressed in internodes, leaves, coleoptiles, and roots.

20

CAC19183.1 AJ291816 *Cicer arietinum*

DESCRIPTION: expansin.

25

CAC06433.1 AJ276007 *Festuca pratensis*

DESCRIPTION: expansin. exp2.

30

BAB32732.1 AB049406 *Eustoma grandiflorum*

DESCRIPTION: expansin. Eg Expansin.

35

AAG01875.1 AF291659 *Striga asiatica*

DESCRIPTION: alpha-expansin 3. Exp3.

40

AAB37749.1 U30460 *Cucumis sativus*

DESCRIPTION: expansin S2 precursor. Cs-EXP2. similar to pollen allergen Lol pI, *Lolium perenne*, Swiss-Prot Accession Number P14946; former gene name CuExS2; expansin-30 (Ex30) protein.

45

AAC96077.1 AF049350 *Nicotiana tabacum*

DESCRIPTION: involved in acid-growth response. alpha-expansin precursor. Nt-EXP1. cell wall protein.

AAC96079.1 AF049352 *Nicotiana tabacum*
DESCRIPTION: involved in acid-growth response. alpha-expansin precursor.
Nt-EXP3. cell wall protein.

5

AAG32920.1 AF184232 *Lycopersicon esculentum*
DESCRIPTION: expansin. Exp8.

10 CAA69105.1 Y07782 *Oryza sativa*
DESCRIPTION: expansin. RiExA.

AAC96078.1 AF049351 *Nicotiana tabacum*
15 DESCRIPTION: involved in acid-growth response. alpha-expansin precursor.
Nt-EXP2. cell wall protein.

583

20 BAA85412.1 AP000615 *Oryza sativa*
DESCRIPTION: ESTs AU065232(E60855),C23624(S1554),
AU078241(E60855)
correspond to a region of the predicted gene.; similar to putative
adenylate kinase. (AC005896).

25

BAA01181.1 D10335 *Oryza sativa*
DESCRIPTION: adenylate kinase-b. Adk-b.

30

BAA01180.1 D10334 *Oryza sativa*
DESCRIPTION: adenylate kinase-a. Adk-a.

35 BAA94761.1 AB041773 *Oryza sativa*
DESCRIPTION: adenylate kinase. Adk-a.

AAB68604.1 U82330 *Prunus armeniaca*
40 DESCRIPTION: adenylate kinase homolog.

AAAF23372.1 AF187063 *Oryza sativa*
DESCRIPTION: catalyzes the transfer of phosphate from ATP to UMP or CMP
45 to form ADP and UDP or CDP. UMP/CMP kinase b. ura6.

5 AAF23371.1 AF187062 *Oryza sativa*
 DESCRIPTION: catalyzes the transfer of phosphate from ATP to UMP or CMP
 to form ADP and UDP or CDP. UMP/CMP kinase a. ura6.

10 AAD41679.1 AF086603 *Ceratopteris richardii*
 DESCRIPTION: adenylate kinase. ADK1.

15 BAA85443.1 AP000616 *Oryza sativa*
 DESCRIPTION: similar to UMP/CMP kinase (AF000147).

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 BAA87052.2 D88273 *Hordeum vulgare*
 DESCRIPTION: nicotianamine aminotransferase A. naat-A.

20 BAA87055.1 AB024006 *Hordeum vulgare*
 DESCRIPTION: nicotianamine aminotransferase. naat-A.

25 BAA87053.1 AB005788 *Hordeum vulgare*
 DESCRIPTION: nicotianamine aminotransferase B. naat-b. NAAT-B.

30 BAA87054.1 AB024006 *Hordeum vulgare*
 DESCRIPTION: nicotianamine aminotransferase. naat-B.

35 BAA77261.1 AB007405 *Oryza sativa*
 DESCRIPTION: alanine aminotransferase. AlaAT.

40 BAA77260.1 AB007404 *Oryza sativa*
 DESCRIPTION: alanine aminotransferase. AlaAT.

45 CAA49199.1 X69421 *Panicum miliaceum*
 DESCRIPTION: alanine aminotransferase. pAlaAT-2.

45 AAB01685.1 U31975 *Chlamydomonas reinhardtii*
 DESCRIPTION: catalyzes the transfer of -NH₂ from ala to 2-oxoglutarate.
 alanine aminotransferase. The translation start site has not been

experimentally tested, but a 55 kDa product can be detected in Western blot.

- 5 AAC62456.1 AF055898 Zea mays
DESCRIPTION: alanine aminotransferase. alt. AlaAT.
- 10 CAA81231.1 Z26322 Hordeum vulgare
DESCRIPTION: alanine aminotransferase.
- 586
-
- 15 AAB94589.1 AF022460 Glycine max
DESCRIPTION: CYP83D1p. CYP83D1. cytochrome P450 monooxygenase.
- 20 AAA32913.1 M32885 Persea americana
DESCRIPTION: cytochrome P-450LXXIA1 (cyp71A1).
- 25 AAA19701.1 L24438 Thlaspi arvense
DESCRIPTION: cytochrome P450.
- 30 BAB40324.1 AB037245 Asparagus officinalis
DESCRIPTION: cytochrome P450. ASPI-2.
- 35 AAC39318.1 AF029858 Sorghum bicolor
DESCRIPTION: second multifunctional cytochrome P450 in the biosynthetic pathway of the cyanogenic glucoside dhurrin. Catalyzes the conversion of p-hydroxyphenylacetaldoxime to p-hydroxymandelonitrile. cytochrome P450 CYP71E1. CYP71E1. No EST#s identified.
- 40 BAB40323.1 AB037244 Asparagus officinalis
DESCRIPTION: cytochrome P450. ASPI-1.
- 45 CAA71517.1 Y10493 Glycine max
DESCRIPTION: putative cytochrome P450.
- AAB61965.1 U48435 Solanum chacoense
DESCRIPTION: putative cytochrome P450.

CAA70575.1 Y09423 *Nepeta racemosa*
DESCRIPTION: cytochrome P450. CYP71A5.

5

CAA71513.1 Y10489 *Glycine max*
DESCRIPTION: putative cytochrome P450.

10

AAB61964.1 U48434 *Solanum chacoense*
DESCRIPTION: putative cytochrome P450.

15 AAD47832.1 AF166332 *Nicotiana tabacum*
DESCRIPTION: cytochrome P450.

20 AAB94588.1 AF022459 *Glycine max*
DESCRIPTION: CYP71D10p. CYP71D10. cytochrome P450 monooxygenase.

25 AAF27282.1 AF122821 *Capsicum annum*
DESCRIPTION: cytochrome P450. PepCYP.

CAA50312.1 X70981 *Solanum melongena*
DESCRIPTION: P450 hydroxylase. CYPEG2.

30

CAA83941.1 Z33875 *Mentha x piperita*
DESCRIPTION: cytochrome P-450 oxidase.

35 AAG44132.1 AF218296 *Pisum sativum*
DESCRIPTION: cytochrome P450. P450 isolog.

40 CAA70576.1 Y09424 *Nepeta racemosa*
DESCRIPTION: cytochrome P450. CYP71A6.

AAD44151.1 AF124816 *Mentha x piperita*
DESCRIPTION: cytochrome p450 isoform PM17.

45

- BAA03635.1 D14990 *Solanum melongena*
DESCRIPTION: Cytochrome P-450EG4.
- 5 CAA50645.1 X71654 *Solanum melongena*
DESCRIPTION: P450 hydroxylase.
- 10 AAB69644.1 AF000403 *Lotus japonicus*
DESCRIPTION: putative cytochrome P450. LjNP450.
- 15 AAD37433.1 AF150881 *Lycopersicon esculentum* x *Lycopersicon peruvianum*
DESCRIPTION: catalyzes the hydroxylation of ferulic acid to
5-hydroxyferulic acid. ferulate-5-hydroxylase. CYP84. cytochrome
P450-dependent monooxygenase; F5H; FAH1.
- 20 CAA65580.1 X96784 *Nicotiana tabacum*
DESCRIPTION: cytochrome P450. hsr515.
- 25 AAD44152.1 AF124817 *Mentha x piperita*
DESCRIPTION: cytochrome p450 isoform PM2.
- 30 CAA64635.1 X95342 *Nicotiana tabacum*
DESCRIPTION: cytochrome P450. hsr515. hypersensitivity-related gene.
- AAG14962.1 AF214008 *Brassica napus*
DESCRIPTION: cytochrome p450-dependent monooxygenase. BNF5H2.
- 35 AAG14961.1 AF214007 *Brassica napus*
DESCRIPTION: cytochrome p450-dependent monooxygenase. BNF5H1.
- 40 CAB56503.1 AJ238612 *Catharanthus roseus*
DESCRIPTION: cytochrome P450.
- 45 AAG14963.1 AF214009 *Brassica napus*
DESCRIPTION: cytochrome p450-dependent monooxygenase. BNF5H3.

- AAK38088.1 AF321864 *Lolium rigidum*
DESCRIPTION: putative cytochrome P450.
- 5 AAD44150.1 AF124815 *Mentha spicata*
DESCRIPTION: cytochrome p450.
- 10 AAK38084.1 AF321860 *Lolium rigidum*
DESCRIPTION: putative cytochrome P450.
- 15 AAD56282.1 AF155332 *Petunia x hybrida*
DESCRIPTION: flavonoid 3'-hydroxylase. Ht1. cytochrome P450; CYP75B2.
- 20 AAK38087.1 AF321863 *Lolium rigidum*
DESCRIPTION: putative cytochrome P450.
- 25 AAK38083.1 AF321859 *Lolium rigidum*
DESCRIPTION: putative cytochrome P450.
- 30 AAB94584.1 AF022157 *Glycine max*
DESCRIPTION: capable of catalyzing the metabolism of phenylurea herbicides. CYP71A10. CYP71A10. cytochrome P450 monooxygenase.
- 35 CAA71514.1 Y10490 *Glycine max*
DESCRIPTION: putative cytochrome P450.
- 40 BAA12159.1 D83968 *Glycine max*
DESCRIPTION: Cytochrome P-450 (CYP93A1).
- 45 BAB39252.1 AP002968 *Oryza sativa*
DESCRIPTION: putative cytochrome P450. P0416G11.1.
- 587 CAA50155.1 X70824 *Solanum melongena*
DESCRIPTION: flavonoid hydroxylase (P450). CYP75.
-

- CAA60120.1 X86222 Pisum sativum
DESCRIPTION: heat shock protein. hsp22.
- 5 AAF37726.1 AF237957 Euphorbia esula
DESCRIPTION: LMW heat shock protein. putative 22 kDa mitochondrial heat shock protein.
- 10 BAA32547.1 AB017134 Lycopersicon esculentum
DESCRIPTION: mitochondrial small heat shock protein. LEMTSHP.
- 15 CAA33388.1 X15333 Chenopodium rubrum
DESCRIPTION: heat shock protein (AA 1-204).
- 20 AAB03096.1 U21722 Glycine max
DESCRIPTION: Hsp23.9. Gmhsp23.9. low molecular weight heat shock protein.
- 25 AAC12279.1 AF035460 Zea mays
DESCRIPTION: low molecular weight heat shock protein precursor. hsp22.
- 30 AAD03604.1 AF104107 Triticum aestivum
DESCRIPTION: small heat shock protein Hsp23.5. mRNA not present, or only at very low levels, prior to heat stress; mRNA abundant after two hours at 40C.
- 35 AAB01557.1 L47741 Picea glauca
DESCRIPTION: mitochondria-localized low molecular weight heat shock protein 23.5. EMB22, SMW HSP23.5.
- 40 AAD03605.1 AF104108 Triticum aestivum
DESCRIPTION: small heat shock protein Hsp23.6.
- 45 CAA38037.1 X54103 Plastid Petunia x hybrida
DESCRIPTION: heat shock protein. hsp21.
- AAF19022.1 AF197942 Funaria hygrometrica

DESCRIPTION: chloroplast-localized small heat shock protein 22. CPsHSP22.

- 5 AAB49626.1 U59917 Lycopersicon esculentum
DESCRIPTION: chromoplast-associated hsp20. pTOM111. small molecular weight heat shock protein.
- 10 AAB07023.1 U66300 Chloroplast Lycopersicon esculentum
DESCRIPTION: heat shock protein. HSP21.
- 15 BAA29064.1 D88584 Nicotiana tabacum
DESCRIPTION: heat shock protein 26 (Type I). Nthsp26a. plastid-localized small heat shock protein.
- 20 AAF19021.1 AF197941 Funaria hygrometrica
DESCRIPTION: chloroplast-localized small heat shock protein. CPsHSP21. CPsHS 21.
- 25 BAA78385.1 AB020973 Oryza sativa
DESCRIPTION: heat shock protein 26. Oshsp26. chloroplast-localized small heat shock protein.
- 30 CAA41219.1 X58280 Triticum aestivum
DESCRIPTION: heat shock protein 26.6. Tahsp26.6.
- 35 AAC96315.1 AF097657 Triticum aestivum
DESCRIPTION: heat shock protein HSP26. hsp26.6. similar to the Triticum aestivum hsp26.6G2 protein encoded by the sequence presented in GenBank Accession Number L41503; 26 kDa protein.
- 40 AAC96316.1 AF097658 Triticum aestivum
DESCRIPTION: heat shock protein HSP26. hsp26.6. 26 kDa protein.
- 45 AAC96314.1 AF097656 Triticum aestivum
DESCRIPTION: heat shock protein HSP26. hsp26.6. 26 kDa protein.
- CAA47745.1 X67328 Triticum aestivum

DESCRIPTION: heat shock protein 26.6B. hsp 26.6B.

AAC96317.1 AF097659 *Triticum aestivum*

5 DESCRIPTION: heat shock protein HSP26. hsp26.6. 26 kDa protein.

AAA33477.1 L28712 *Zea mays*

10 DESCRIPTION: heat shock protein 26. HSP26. plastid-localized low molecular weight hsp.

BAA29066.1 AB006043 *Nicotiana sylvestris*

15 DESCRIPTION: heat shock protein 26. hsp26. plastid-localized small heat shock protein.

BAA29067.1 AB006044 *Nicotiana tomentosiformis*

20 DESCRIPTION: heat shock protein 26. hsp26. plastid-localized small heat shock protein.

BAA29065.1 AB006041 *Nicotiana tabacum*

25 DESCRIPTION: heat shock protein 26 (Type I). Nthsp26a. plastid-localized small heat shock protein 26.

AAC01570.1 AF019144 *Agrostis stolonifera* var. *palustris*

30 DESCRIPTION: low molecular weight heat shock protein.

AAD30452.1 AF123255 *Lycopersicon esculentum*

35 DESCRIPTION: 17.7 kD class I small heat shock protein. HSP17.7.

CAA39603.1 X56138 *Lycopersicon esculentum*

DESCRIPTION: small heat shock protein (class I).

40 AAD30453.1 AF123256 *Lycopersicon esculentum*

DESCRIPTION: 17.8 kD class I small heat shock protein. HSP17.8.

AAD30454.1 AF123257 *Lycopersicon esculentum*

45 DESCRIPTION: 17.6 kD class I small heat shock protein. HSP17.6.

AAD49336.1 AF166277 *Nicotiana tabacum*

DESCRIPTION: low molecular weight heat-shock protein. LHS-1. TLHS-1.

5

AAF34133.1 AF161179 *Malus x domestica*

DESCRIPTION: low molecular weight heat shock protein. Hsp1.

10 AAC39360.1 U63631 *Fragaria x ananassa*

DESCRIPTION: LMW heat shock protein.

AAA61632.1 U08601 *Papaver somniferum*

15 DESCRIPTION: low molecular weight heat-shock protein.

CAA08908.1 AJ009880 *Castanea sativa*

20 DESCRIPTION: molecular chaperone. cytosolic class I small heat-shock protein HSP17.5. hsp17.5.

AAA33975.1 M11395 *Glycine max*

25 DESCRIPTION: small heat shock protein.

CAA63570.1 X92983 *Pseudotsuga menziesii*

DESCRIPTION: low molecular weight heat-shock protein.

30

AAB03893.1 M11318 *Glycine max*

DESCRIPTION: 17.5 kd heat shock protein Gmhsp17.6L.

35 CAA25578.1 X01104 *Glycine max*

DESCRIPTION: heat shock protein 6871 (aa 1-153).

AAB72109.1 AF022217 *Brassica rapa*

40 DESCRIPTION: low molecular weight heat-shock protein. BcHSP17.6. 17.6 kDa; cytosolic class I.

CAA46641.1 X65725 *Zea mays*

45 DESCRIPTION: heat shock protein 17.2. Zmhsp 17.2. Class I low molecular weight heat shock protein.

- 5 CAB08441.1 Z95153 *Helianthus annuus*
DESCRIPTION: 17.6 kD class I small heat-shock protein HSP17.6. Ha
hsp17.6.
- 10 AAA33974.1 M11317 *Glycine max*
DESCRIPTION: 17.6 kd heat shock protein Gmhsp17.6L.
588
- 15 -----
AAA32913.1 M32885 *Persea americana*
DESCRIPTION: cytochrome P-450LXXIA1 (cyp71A1).
- 20 AAA19701.1 L24438 *Thlaspi arvense*
DESCRIPTION: cytochrome P450.
- 25 AAC39318.1 AF029858 *Sorghum bicolor*
DESCRIPTION: second multifunctional cytochrome P450 in the biosynthetic
pathway of the cyanogenic glucoside dhurrin. Catalyzes the conversion of
p-hydroxyphenylacetaldoxime to p-hydroxymandelonitrile. cytochrome P450
CYP71E1. CYP71E1. No EST#s identified.
- 30 BAB40323.1 AB037244 *Asparagus officinalis*
DESCRIPTION: cytochrome P450. ASPI-1.
- 35 BAB40324.1 AB037245 *Asparagus officinalis*
DESCRIPTION: cytochrome P450. ASPI-2.
- AAB94589.1 AF022460 *Glycine max*
DESCRIPTION: CYP83D1p. CYP83D1. cytochrome P450 monooxygenase.
- 40 CAA71513.1 Y10489 *Glycine max*
DESCRIPTION: putative cytochrome P450.
- 45 CAA70575.1 Y09423 *Nepeta racemosa*
DESCRIPTION: cytochrome P450. CYP71A5.

- 5 AAB94584.1 AF022157 Glycine max
DESCRIPTION: capable of catalyzing the metabolism of phenylurea herbicides. CYP71A10. CYP71A10. cytochrome P450 monooxygenase.
- 10 AAB61965.1 U48435 Solanum chacoense
DESCRIPTION: putative cytochrome P450.
- 15 AAF27282.1 AF122821 Capsicum annuum
DESCRIPTION: cytochrome P450. PepCYP.
- 20 CAB56503.1 AJ238612 Catharanthus roseus
DESCRIPTION: cytochrome P450.
- 25 AAD47832.1 AF166332 Nicotiana tabacum
DESCRIPTION: cytochrome P450.
- 30 AAB94588.1 AF022459 Glycine max
DESCRIPTION: CYP71D10p. CYP71D10. cytochrome P450 monooxygenase.
- 35 AAB61964.1 U48434 Solanum chacoense
DESCRIPTION: putative cytochrome P450.
- 40 CAA71517.1 Y10493 Glycine max
DESCRIPTION: putative cytochrome P450.
- 45 CAA50645.1 X71654 Solanum melongena
DESCRIPTION: P450 hydroxylase.
- 50 BAA03635.1 D14990 Solanum melongena
DESCRIPTION: Cytochrome P-450EG4.
- 55 CAA50312.1 X70981 Solanum melongena
DESCRIPTION: P450 hydroxylase. CYPEG2.

- CAA71514.1 Y10490 Glycine max
DESCRIPTION: putative cytochrome P450.
- 5 AAB69644.1 AF000403 Lotus japonicus
DESCRIPTION: putative cytochrome P450. LjNP450.
- 10 CAA70576.1 Y09424 Nepeta racemosa
DESCRIPTION: cytochrome P450. CYP71A6.
- 15 AAD44151.1 AF124816 Mentha x piperita
DESCRIPTION: cytochrome p450 isoform PM17.
- 20 AAK38084.1 AF321860 Lolium rigidum
DESCRIPTION: putative cytochrome P450.
- CAA83941.1 Z33875 Mentha x piperita
DESCRIPTION: cytochrome P-450 oxidase.
- 25 AAK38083.1 AF321859 Lolium rigidum
DESCRIPTION: putative cytochrome P450.
- 30 AAD44152.1 AF124817 Mentha x piperita
DESCRIPTION: cytochrome p450 isoform PM2.
- 35 BAB39252.1 AP002968 Oryza sativa
DESCRIPTION: putative cytochrome P450. P0416G11.1.
- AAD44150.1 AF124815 Mentha spicata
DESCRIPTION: cytochrome p450.
- 40 AAK38087.1 AF321863 Lolium rigidum
DESCRIPTION: putative cytochrome P450.
- 45 AAK38082.1 AF321858 Lolium rigidum
DESCRIPTION: putative cytochrome P450.

CAA57423.1 X81829 Zea mays
DESCRIPTION: cytochrome P450. CYP71C2. family CYP71, subfamily
5 CYP71C.

CAA72208.1 Y11404 Zea mays
DESCRIPTION: cytochrome p450. cyp71c2.
10

CAC27827.1 AJ295719 Catharanthus roseus
DESCRIPTION: geraniol hydroxylase. cytochrome P450. cyp71.
15

AAG44132.1 AF218296 Pisum sativum
DESCRIPTION: cytochrome P450. P450 isolog.
20

AAK38088.1 AF321864 Lolium rigidum
DESCRIPTION: putative cytochrome P450.
25

AAG14963.1 AF214009 Brassica napus
DESCRIPTION: cytochrome p450-dependent monooxygenase. BNF5H3.
30

CAA57424.2 X81830 Zea mays
DESCRIPTION: cytochrome P450. CYP71C3. family CYP71, subfamily
30 CYP71C.

CAA72207.1 Y11403 Zea mays
DESCRIPTION: cytochrome p450. cyp71c3.
35

AAG14962.1 AF214008 Brassica napus
DESCRIPTION: cytochrome p450-dependent monooxygenase. BNF5H2.
40

AAG14961.1 AF214007 Brassica napus
DESCRIPTION: cytochrome p450-dependent monooxygenase. BNF5H1.
45

BAA12159.1 D83968 Glycine max
DESCRIPTION: Cytochrome P-450 (CYP93A1).

- AAD32207.1 AF134733 *Prunus armeniaca*
DESCRIPTION: calcium-binding protein calreticulin.
- 5 CAA61939.1 X89813 *Zea mays*
DESCRIPTION: Calreticulin precursor.
- 10 AAA32948.1 L27348 *Hordeum vulgare*
DESCRIPTION: calcium binding protein. calreticulin. CRH1.
- 15 AAA32949.1 L27349 *Hordeum vulgare*
DESCRIPTION: calcium binding protein. calreticulin. CRH2.
- 20 AAF01470.1 AF190454 *Zea mays*
DESCRIPTION: calreticulin. CRT. calcium binding protien.
- CAB54526.1 AJ000765 *Chlamydomonas reinhardtii*
DESCRIPTION: calreticulin.
- 25 AAB70919.1 AF019376 *Brassica napus*
DESCRIPTION: calreticulin. Crt1. calcium binding protein; similar to A.
thaliana calreticulin encoded by GenBank Accession Number U66343.
- 30 BAA85118.1 AB018243 *Solanum melongena*
DESCRIPTION: calreticulin-like protein. EEF22.
- 35 CAA54975.1 X78057 *Zea mays*
DESCRIPTION: calreticulin. CRH.
- 40 CAA57914.1 X82578 *Parthenium argentatum*
DESCRIPTION: calreticulin. 111R.
- 45 AAK15502.1 AF325720 *Pennisetum ciliare*
DESCRIPTION: calreticulin-like protein. Pcp4.

DESCRIPTION: NADPH oxidase. RBOH1. gp91; phox homolog.

599

5 CAC21424.1 AJ278332 *Lycopersicon esculentum*
DESCRIPTION: involved in octadecanoid biosynthesis. 12-oxophytodienoate reductase 3. opr3.

10 BAB40340.1 AB044940 *Pisum sativum*
DESCRIPTION: 12-oxophytodienoic acid 10, 11-reductase. OPDAR.

15 CAB43506.1 AJ242551 *Lycopersicon esculentum*
DESCRIPTION: involved in jasmonic acid biosynthesis. 12-oxophytodienoate reductase. opr.

20 CAC21423.1 AJ278331 *Lycopersicon esculentum*
DESCRIPTION: involved in octadecanoid biosynthesis. putative 12-oxophytodienoate reductase 2. opr2.

25 CAB97122.1 AJ297421 *Daucus carota*
DESCRIPTION: oxidoreductase. putative 12-oxophytodienoate reductase. opr2.

602

30 AAB37246.1 U58971 *Nicotiana tabacum*
DESCRIPTION: calmodulin-binding protein. TCB60.

603

35 AAK15006.1 AF233433 *Brassica napus*
DESCRIPTION: arginase. similar to *Arabidopsis thaliana* and *Glycine max* arginase.

40 AAK07744.1 AF130440 *Pinus taeda*
DESCRIPTION: converts L-arginine to L-ornithine and urea. arginase. ARS20. L-arginine amidinohydrolase.

45 AAC04613.1 AF035671 *Glycine max*
DESCRIPTION: hydrolysis of L-Arg to L-Orn and urea. arginase. pAG1. L-Arg

amidinohydrolase.

605

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- 5 CAA81210.1 Z26251 *Helianthus tuberosus*
DESCRIPTION: Catalyzes the reduction of cytochrome P450 in microsomes.
NADPH-ferrihemoprotein reductase.
- 10 AAB02721.1 U58629 *Helianthus tuberosus*
DESCRIPTION: NADPH-ferrihemoprotein oxidoreductase. HTR2.
NADPH-cytochrome P450 reductase isoform.
- 15 CAC27143.1 AJ132538 *Picea abies*
DESCRIPTION: NADPH-cytochrome P450 reductase.
- 20 AAA79131.1 U10545 *Chlamydomonas reinhardtii*
DESCRIPTION: ferredoxin-NADP⁺ reductase. fnr.
- 25 CAA55406.1 X78851 *Chlamydomonas reinhardtii*
DESCRIPTION: ferredoxin NADP reductase.
- AAB40978.1 U22328 *Volvox carteri*
DESCRIPTION: ferredoxin-NADP⁺ reductase. fnr. FNR.
- 30 AAA33029.1 M25528 *Mesembryanthemum crystallinum*
DESCRIPTION: ferredoxin-NADP⁺ reductase precursor (fnrA; EC 1.6.7.1).
- 35 CAA30978.1 X12446 *Pisum sativum*
DESCRIPTION: ferredoxin-NADH⁺ reductase preprotein (AA -52 to 308).
- 40 BAA13417.1 D87547 *Oryza sativa*
DESCRIPTION: precursor ferredoxin-NADP⁺ oxidoreductase.
- 45 AAA21758.1 U14956 *Vicia faba*
DESCRIPTION: photosynthetic electron transport. ferredoxin NADP⁺
reductase precursor. fnr.

AAA34029.1 M86349 *Spinacia oleracea*
DESCRIPTION: ferredoxin-NADP oxidoreductase. precursor protein.

5

CAB71293.1 AJ250378 *Capsicum annuum*
DESCRIPTION: chloroplast ferredoxin-NADP+ oxidoreductase precursor. fnr.

10 CAA74359.1 Y14032 *Nicotiana tabacum*
DESCRIPTION: ferredoxin--NADP(+) reductase. fnr.

15 BAA88236.1 AB035644 *Zea mays*
DESCRIPTION: NADP+ oxidoreductase. ferredoxin. L-FNRI.

20 BAA88237.1 AB035645 *Zea mays*
DESCRIPTION: NADP+ oxidoreductase. ferredoxin. L-FNRIL.

BAA20365.1 AB004307 *Nicotiana tabacum*
DESCRIPTION: ferredoxin-NADP oxidoreductase.

25 BAA07479.1 D38445 *Oryza sativa*
DESCRIPTION: root ferredoxin-NADP+ reductase. root FNR. nitrate
assimilation pathway.

30 BAA02248.1 D12815 *Oryza sativa*
DESCRIPTION: ferredoxin-NADP+ reductase enzyme.

35 BAA04232.1 D17410 *Oryza sativa*
DESCRIPTION: ferredoxin-NADP+ reductase.

40 BAA90642.1 AP001129 *Oryza sativa*
DESCRIPTION: ESTs AU078647(E1557),C72400(E1557) correspond to a
region of
the predicted gene.; Similar to *Oryza sativa*, ferredoxin-NADP+ reductase.
(D17790).

45 BAA85425.1 AP000616 *Oryza sativa*

DESCRIPTION: ESTs AU078647(E1557),C72400(E1557) correspond to a region of the predicted gene.; similar to ferredoxin-NADP+ reductase (D17790).

5

BAA04616.1 D17790 Oryza sativa
DESCRIPTION: ferredoxin-NADP+ reductase.

10

AAB40034.1 U10418 Zea mays
DESCRIPTION: ferredoxin-NADP reductase precursor.

15

CAA67796.1 X99419 Pisum sativum
DESCRIPTION: ferredoxin NADP oxidoreductase.

20

AAK09367.1 AF321525 Pisum sativum
DESCRIPTION: ferredoxin-NADP+ reductase. FNR.

25

AAK09370.1 AF321528 Pisum sativum
DESCRIPTION: ferredoxin-NADP+ reductase. FNR.

AAK09369.1 AF321527 Pisum sativum
DESCRIPTION: ferredoxin-NADP+ reductase. FNR.

30

AAK09368.1 AF321526 Pisum sativum
DESCRIPTION: ferredoxin-NADP+ reductase. FNR.

606

35

BAA82107.1 AB022693 Nicotiana tabacum
DESCRIPTION: transcription factor. NtWRKY1.

40

AAC31956.1 AF080595 Pimpinella brachycarpa
DESCRIPTION: zinc finger protein. ZFP1. WRKY1.

45

AAC49527.1 U48831 Petroselinum crispum
DESCRIPTION: WRKY1. contains two WRKY domains; WRKY-type DNA-binding protein; sequence-specific DNA-binding protein.

AAD55974.1 AF121353 Petroselinum crispum
 DESCRIPTION: zinc-finger type transcription factor WRKY1. WRKY1.
 5

BAA77383.1 AB020590 Nicotiana tabacum
 DESCRIPTION: transcription factor NtWRKY2.
 10

AAD32677.1 AF140554 Avena sativa
 DESCRIPTION: DNA-binding protein WRKY1. wrky1. putative transcription
 factor.
 15

CAA88326.1 Z48429 Avena fatua
 DESCRIPTION: binds conserved cis-element from cereal alpha-Amy2
 promoters. DNA-binding protein.
 20

BAA86031.1 AB026890 Nicotiana tabacum
 DESCRIPTION: transcription factor NtWRKY4.
 25

AAD16139.1 AF096299 Nicotiana tabacum
 DESCRIPTION: DNA-binding protein 2. WRKY2. transcription factor.
 30

AAC37515.1 L44134 Cucumis sativus
 DESCRIPTION: SPF1-like DNA-binding protein.
 35

AAF23898.1 AF193802 Oryza sativa
 DESCRIPTION: zinc finger transcription factor WRKY1.
 40

AAK16171.1 AC079887 Oryza sativa
 DESCRIPTION: putative DNA-binding protein. OSJNBa0040E01.10.
 45

AAC49529.1 U58540 Petroselinum crispum
 DESCRIPTION: WRKY2. Contains two WRKY domains; WRKY-type DNA-
 binding
 protein.

- AAD16138.1 AF096298 *Nicotiana tabacum*
DESCRIPTION: DNA-binding protein 1. WRKY1. transcription factor.
- 5 BAB19096.1 AP002839 *Oryza sativa*
DESCRIPTION: putative DNA-binding protein homolog. P0688A04.2.
- 10 BAB19075.1 AP002744 *Oryza sativa*
DESCRIPTION: putative DNA-binding protein homolog. P0006C01.17.
- 15 AAK16170.1 AC079887 *Oryza sativa*
DESCRIPTION: putative DNA binding protein. OSJNBa0040E01.4.
- 20 CAB97004.1 AJ278507 *Solanum tuberosum*
DESCRIPTION: putative transcription factor. WRKY DNA binding protein.
WRKY1.
- 25 BAB18313.1 AP002865 *Oryza sativa*
DESCRIPTION: putative WRKY DNA binding protein. P0034C11.1. contains
EST
C26525(C12525).
- 30 AAD38283.1 AC007789 *Oryza sativa*
DESCRIPTION: putative WRKY DNA binding protein. OSJNBa0049B20.9.
- 35 BAB40073.1 AP003074 *Oryza sativa*
DESCRIPTION: putative WRKY DNA binding protein. OSJNBa0004G10.20.
contains EST C26525(C12525).
- 40 AAC49528.1 U56834 *Petroselinum crispum*
DESCRIPTION: DNA-binding. WRKY3. WRKY-type DNA-binding protein.
- 45 BAB16432.1 AB041520 *Nicotiana tabacum*
DESCRIPTION: WRKY transcription factor Nt-SubD48. Nt-SubD48.
- 45 BAA77358.1 AB020023 *Nicotiana tabacum*

DESCRIPTION: WRKY domain Zn-finger type DNA-binding protein. DNA-binding protein NtWRKY3.

5

AAD32676.1 AF140553 Avena sativa
DESCRIPTION: DNA-binding protein WRKY3. wrky3. putative transcription factor.

10

CAA88331.1 Z48431 Avena fatua
DESCRIPTION: binds conserved cis-element from cereal alpha-Amy2 promoters. DNA-binding protein.

15

AAG35658.1 AF204925 Petroselinum crispum
DESCRIPTION: transcription factor WRKY4. WRKY4. binds to W box (TTGACC) elements.

20

AAG46150.1 AC018727 Oryza sativa
DESCRIPTION: putative DNA-binding protein. OSJNBa0056G17.18.

25

AAD27591.1 AF121354 Petroselinum crispum
DESCRIPTION: binds sequence specifically to W Boxes (TTGACC). transcription factor. WRKY3. sequence specific DNA-binding protein.

30

AAG35659.1 AF204926 Petroselinum crispum
DESCRIPTION: transcription factor WRKY5. WRKY5. binds to W box (TTGACC) elements.

35

CAB66338.1 AJ279697 Betula pendula
DESCRIPTION: wrky-type DNA binding protein. wrky.

40

AAF61864.1 AF193771 Nicotiana tabacum
DESCRIPTION: DNA-binding protein 4. WRKY4. transcription factor.

45

AAF61863.1 AF193770 Nicotiana tabacum
DESCRIPTION: DNA-binding protein 3. WRKY3. transcription factor.

-
- 5 BAA87853.1 AP000816 *Oryza sativa*
 DESCRIPTION: EST AU030604(E51294) corresponds to a region of the
 predicted gene. Similar to putative NAK-like Ser/Thr protein kinase.
 (AF001308).
- 10 AAK21965.1 AY028699 *Brassica napus*
 DESCRIPTION: receptor protein kinase PERK1.
- 15 BAB21240.1 AP002953 *Oryza sativa*
 DESCRIPTION: Putative protein kinase. P0426D06.20. contains ESTs
 C22359(C11461),C22360(C11461).
- 20 BAB19337.1 AP003044 *Oryza sativa*
 DESCRIPTION: putative protein kinase. P0038C05.10. contains ESTs
 AU056335(S20481),AU056336(S20481).
- 25 BAA92836.1 AB032473 *Brassica oleracea*
 DESCRIPTION: S18 S-locus receptor kinase. SRK18.
- 30 AAB61708.1 U93048 *Daucus carota*
 DESCRIPTION: somatic embryogenesis receptor-like kinase. SERK.
- 35 BAA23676.1 AB000970 *Brassica rapa*
 DESCRIPTION: receptor kinase 1. BcRK1.
- 40 AAK00425.1 AC069324 *Oryza sativa*
 DESCRIPTION: Putative protein kinase. OSJNBa0071K19.11.
- 45 BAB39873.1 AP002882 *Oryza sativa*
 DESCRIPTION: putative protein kinase. P0439B06.8. contains ESTs
 AU056701(S20808),AU056702(S20808).
- 45 AAD21872.1 AF078082 *Phaseolus vulgaris*
 DESCRIPTION: receptor-like protein kinase homolog RK20-1.

- 5 CAB41878.1 Y18259 Brassica oleracea
DESCRIPTION: SRK5 protein. SRK5. receptor-like kinase.
- 10 AAA62232.1 U00443 Brassica napus
DESCRIPTION: S-receptor kinase. protein contains an immunoglobulin-like domain.
- 15 AAA33000.1 M76647 Brassica oleracea
DESCRIPTION: receptor protein kinase. SKR6.
- 20 AAG59657.1 AC084319 Oryza sativa
DESCRIPTION: putative protein kinase. OSJNBa0004B24.20.
- 25 CAB41879.1 Y18260 Brassica oleracea
DESCRIPTION: SRK15 protein. SRK15. receptor-like kinase.
- CAA73134.1 Y12531 Brassica oleracea
DESCRIPTION: serine/threonine kinase. BRLK.
- 30 BAB16871.1 AP002537 Oryza sativa
DESCRIPTION: putative protein kinase APK1AArabidopsis thaliana. P0001B06.24. contains ESTs C22608(R3192),D25110(R3192).
- 35 BAB18292.1 AP002860 Oryza sativa
DESCRIPTION: putative receptor-like protein kinase. P0409B08.19.
- 40 BAA06285.1 D30049 Brassica rapa
DESCRIPTION: S-receptor kinase SRK9.
- BAA21132.1 D88193 Brassica rapa
DESCRIPTION: S-receptor kinase. SRK9 (B.c).
- 45 CAB89179.1 AJ245479 Brassica napus subsp. napus
DESCRIPTION: ser /thr kinase. S-locus receptor kinase. srk.

- 5 AAA33008.1 M97667 Brassica napus
DESCRIPTION: serine/threonine kinase receptor.
- CAA67145.1 X98520 Brassica oleracea
DESCRIPTION: receptor-like kinase. SFR2.
- 10 CAA73133.1 Y12530 Brassica oleracea
DESCRIPTION: serine /threonine kinase. ARLK.
- 15 AAF66615.1 AF142596 Nicotiana tabacum
DESCRIPTION: LRR receptor-like protein kinase.
- 20 AAF76314.1 AF220603 Lycopersicon esculentum
DESCRIPTION: Fen kinase. Lescfen.
- 25 AAK11568.1 AF318492 Lycopersicon hirsutum
DESCRIPTION: Pto-like protein kinase B. LhirPtoB.
- 30 CAA74662.1 Y14286 Brassica oleracea
DESCRIPTION: SFR3. extracellular S domain: 123-1346; transmembrane domain: 1347-1412; intracellular kinase domain: from 1413.
- 35 AAB47424.1 U59317 Lycopersicon pimpinellifolium
DESCRIPTION: serine/threonine protein kinase Fen. Fen. fenthion sensitivity gene from tomato.
- 40 AAB47422.1 U59318 Lycopersicon esculentum
DESCRIPTION: serine/threonine protein kinase Fen. fen. allele of Fen, fenthion sensitivity gene from tomato.
- 45 AAC48932.1 U13923 Lycopersicon pimpinellifolium
DESCRIPTION: Fen. putative serine/threonine protein kinase; similar to product encoded by Lycopersicon pimpinellifolium Pto gene, GenBank Accession Number U02271; Fen is a member of the Pto gene family.

AAF76307.1 AF220602 *Lycopersicon pimpinellifolium*
DESCRIPTION: Fen kinase.

5

BAA07576.1 D38563 *Brassica rapa*
DESCRIPTION: receptor protein kinase SRK8.

10 AAG16628.1 AY007545 *Brassica napus*
DESCRIPTION: protein serine/threonine kinase BNK1.

15 CAA97692.1 Z73295 *Catharanthus roseus*
DESCRIPTION: receptor-like protein kinase. CRPK1. Autophosphorylation
predominantly on Thr, less on Ser. Mechanism: autophosphorylation in cis.

20 CAA79355.1 Z18921 *Brassica oleracea*
DESCRIPTION: S-receptor kinase-like protein.

25 AAB93834.1 U82481 *Zea mays*
DESCRIPTION: KI domain interacting kinase 1. KIK1. receptor-like protein
kinase; serine/threonine protein kinase.

30 BAA92837.1 AB032474 *Brassica oleracea*
DESCRIPTION: S60 S-locus receptor kinase. SRK60.

AAA33915.1 L27821 *Oryza sativa*
DESCRIPTION: receptor type serine/threonine kinase. protein kinase.

35 610

BAB17348.1 AP002747 *Oryza sativa*
DESCRIPTION: putative receptor kinase. P0698G03.32.

40

BAB17345.1 AP002747 *Oryza sativa*
DESCRIPTION: putative receptor kinase. P0698G03.29.

45 BAB17126.1 AP002867 *Oryza sativa*
DESCRIPTION: putative receptor kinase. P0463F06.16.

BAB39451.1 AP003338 Oryza sativa
DESCRIPTION: putative receptor kinase. OJ1212_B09.24.

5

BAB17342.1 AP002747 Oryza sativa
DESCRIPTION: putative receptor kinase. P0698G03.26.

10

AAC27489.1 AF077130 Oryza sativa
DESCRIPTION: receptor-like protein kinase.

15 AAF78018.1 AF238474 Oryza sativa
DESCRIPTION: receptor-like kinase. RLG16. protein kinase.

20 AAC02535.1 AF044260 Oryza sativa
DESCRIPTION: receptor serine/threonine kinase. protein kinase.

25 BAB39435.1 AP003338 Oryza sativa
DESCRIPTION: putative receptor kinase. OJ1212_B09.2.

AAD46917.1 AF164021 Oryza sativa
DESCRIPTION: receptor kinase.

30

BAB39438.1 AP003338 Oryza sativa
DESCRIPTION: putative receptor kinase. OJ1212_B09.7.

35 BAB17339.1 AP002747 Oryza sativa
DESCRIPTION: putative receptor kinase. P0698G03.23.

40 AAC49629.1 U51330 Triticum aestivum
DESCRIPTION: rust resistance kinase Lr10. LRK10.

BAB17321.1 AP002747 Oryza sativa
DESCRIPTION: putative receptor kinase. P0698G03.1.

45

- BAB17129.1 AP002867 *Oryza sativa*
DESCRIPTION: putative receptor kinase. P0463F06.20.
- 5 AAF68398.1 AF237568 *Oryza sativa*
DESCRIPTION: receptor-like protein kinase. RLG2.
- 10 BAB17331.1 AP002747 *Oryza sativa*
DESCRIPTION: putative receptor kinase. P0698G03.12.
- 15 BAB17139.1 AP002867 *Oryza sativa*
DESCRIPTION: putative receptor kinase. P0463F06.31.
- AAC01746.1 AF044489 *Oryza sativa*
DESCRIPTION: receptor-like protein kinase. drpk1.
- 20 AAF78016.1 AF238472 *Oryza sativa*
DESCRIPTION: receptor-like kinase. RLG15. protein kinase.
- 25 BAB39441.1 AP003338 *Oryza sativa*
DESCRIPTION: putative receptor kinase. OJ1212_B09.11.
- 30 BAB17116.1 AP002867 *Oryza sativa*
DESCRIPTION: putative receptor kinase. P0463F06.3.
- 35 AAF78044.1 AF248493 *Oryza sativa*
DESCRIPTION: receptor-like kinase. RLG18. protein kinase.
- AAD44029.1 AF085164 *Hordeum vulgare*
DESCRIPTION: receptor-like kinase LRK10.
- 40 BAB17332.1 AP002747 *Oryza sativa*
DESCRIPTION: putative receptor kinase. P0698G03.13. contains ESTs
D47575(S13157),AU032665(S13157).
- 45 BAB17347.1 AP002747 *Oryza sativa*

DESCRIPTION: putative receptor kinase. P0698G03.31. contains ESTs
D47575(S13157),AU032665(S13157).

5 BAB17344.1 AP002747 Oryza sativa
DESCRIPTION: putative receptor kinase. P0698G03.28. contains ESTs
D47575(S13157),AU032665(S13157).

10 BAB17337.1 AP002747 Oryza sativa
DESCRIPTION: putative receptor kinase. P0698G03.21. contains ESTs
D47575(S13157),AU032665(S13157).

15 BAB17335.1 AP002747 Oryza sativa
DESCRIPTION: putative receptor kinase. P0698G03.17. contains ESTs
D47575(S13157),AU032665(S13157).

20 BAB17115.1 AP002867 Oryza sativa
DESCRIPTION: putative receptor kinase. P0463F06.2.

BAB39440.1 AP003338 Oryza sativa
25 DESCRIPTION: putative receptor kinase. OJ1212_B09.10.

BAB39437.1 AP003338 Oryza sativa
DESCRIPTION: receptor-like kinase. OJ1212_B09.6.
30

AAF78019.1 AF238475 Oryza sativa
DESCRIPTION: receptor-like kinase. RLG17. protein kinase.

35 BAB17127.1 AP002867 Oryza sativa
DESCRIPTION: putative receptor kinase. P0463F06.17.

40 AAD46916.1 AF164020 Oryza sativa
DESCRIPTION: receptor kinase.

AAF78021.1 AF238477 Oryza sativa
45 DESCRIPTION: receptor-like kinase. RLG5. protein kinase.

AAD46417.1 AF100767 Oryza sativa
DESCRIPTION: receptor-like kinase. 8ARK3. similar to wheat ARK1AS.

5

AAD46415.1 AF100765 Oryza sativa
DESCRIPTION: receptor-like kinase. 8ARK1. similar to wheat ARK1AS.

10

BAB17128.1 AP002867 Oryza sativa
DESCRIPTION: putative receptor kinase. P0463F06.18.

15

AAF68400.1 AF237570 Oryza sativa
DESCRIPTION: receptor-like protein kinase. RLG3.

20

BAB17323.1 AP002747 Oryza sativa
DESCRIPTION: putative receptor kinase. P0698G03.3.

25

BAB17131.1 AP002867 Oryza sativa
DESCRIPTION: putative receptor kinase. P0463F06.22.

AAF68397.1 AF237567 Oryza sativa
DESCRIPTION: receptor-like protein kinase. RLG1.

30

AAF78015.1 AF238471 Oryza sativa
DESCRIPTION: receptor-like kinase. RLG10. protein kinase.

35

AAD43962.1 U78762 Triticum aestivum
DESCRIPTION: receptor-like kinase ARK1AS. ARK1AS.

611

40

BAA78764.1 AB023482 Oryza sativa
DESCRIPTION: ESTs C98382(C2985),D22444(C11129) correspond to a region
of
the predicted gene.; Similar to Arabidopsis thaliana APK1 gene for protein
tyrosine-serine-threonine kinase.(D12522).

45

AAK11674.1 AF339747 Lophopyrum elongatum

DESCRIPTION: protein kinase. ESI47.

AAF43496.1 AF131222 *Lophopyrum elongatum*

5 DESCRIPTION: protein serine/threonine kinase. ESI47. induced in roots by salt stress, osmotic stress, and ABA treatment.

AAG16628.1 AY007545 *Brassica napus*

10 DESCRIPTION: protein serine/threonine kinase BNK1.

BAA94509.1 AB041503 *Populus nigra*

15 DESCRIPTION: protein kinase 1. PnPK1.

BAA94510.1 AB041504 *Populus nigra*

20 DESCRIPTION: protein kinase 2. PnPK2.

BAB07999.1 AP002525 *Oryza sativa*

25 DESCRIPTION: putative protein kinase. P0462H08.22. contains EST C22619(S11214).

BAB03429.1 AP002817 *Oryza sativa*

30 DESCRIPTION: EST C22619(S11214) corresponds to a region of the predicted gene. Similar to *Arabidopsis thaliana* chromosome 2, BAC clone T17D12; putative protein kinase (AC006587).

BAA87853.1 AP000816 *Oryza sativa*

35 DESCRIPTION: EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative NAK-like Ser/Thr protein kinase. (AF001308).

BAB16871.1 AP002537 *Oryza sativa*

40 DESCRIPTION: putative protein kinase APK1A *Arabidopsis thaliana*. P0001B06.24. contains ESTs C22608(R3192), D25110(R3192).

BAB39409.1 AP002901 *Oryza sativa*

45 DESCRIPTION: putative protein kinase. P0456F08.9. contains EST C23560(R0290).

CAB51834.1 00069 *Oryza sativa*
DESCRIPTION: 11332.5. contains eukaryotic protein kinase domain PF.

5

BAB21240.1 AP002953 *Oryza sativa*
DESCRIPTION: Putative protein kinase. P0426D06.20. contains ESTs
C22359(C11461),C22360(C11461).

10

AAK00425.1 AC069324 *Oryza sativa*
DESCRIPTION: Putative protein kinase. OSJNBa0071K19.11.

15

BAB39873.1 AP002882 *Oryza sativa*
DESCRIPTION: putative protein kinase. P0439B06.8. contains ESTs
AU056701(S20808),AU056702(S20808).

20

AAK11567.1 AF318491 *Lycopersicon hirsutum*
DESCRIPTION: Pto-like protein kinase F. LhirPtoF.

25

BAA90808.1 AP001168 *Oryza sativa*
DESCRIPTION: Similar to putative receptor-like protein kinase (AL035679).

30

AAK21965.1 AY028699 *Brassica napus*
DESCRIPTION: receptor protein kinase PERK1.

35

AAC48932.1 U13923 *Lycopersicon pimpinellifolium*
DESCRIPTION: Fen. putative serine/threonine protein kinase; similar to
product encoded by *Lycopersicon pimpinellifolium* Pto gene, GenBank
Accession Number U02271; Fen is a member of the Pto gene family.

40

AAB47424.1 U59317 *Lycopersicon pimpinellifolium*
DESCRIPTION: serine/threonine protein kinase Fen. Fen. fenthion
sensitivity gene from tomato.

45

AAF76307.1 AF220602 *Lycopersicon pimpinellifolium*
DESCRIPTION: Fen kinase.

AAK11566.1 AF318490 *Lycopersicon hirsutum*
DESCRIPTION: Pto-like protein kinase E. LhirPtoE. confers resistance to bacterial speck disease.

5

AAG03090.1 AC073405 *Oryza sativa*
DESCRIPTION: Similar to an Arabidopsis somatic embryogenesis receptor-like kinase (AC007504).

10

AAF76314.1 AF220603 *Lycopersicon esculentum*
DESCRIPTION: Fen kinase. Lescfen.

15

AAB47421.1 U59316 *Lycopersicon esculentum*
DESCRIPTION: serine/threonine protein kinase Pto. pto. allele of Pto bacterial speck disease resistance gene in tomato.

20

AAF76313.1 AF220603 *Lycopersicon esculentum*
DESCRIPTION: Pto kinase. LescPth5.

25

AAB47422.1 U59318 *Lycopersicon esculentum*
DESCRIPTION: serine/threonine protein kinase Fen. fen. allele of Fen, fenthion sensitivity gene from tomato.

30

AAG59657.1 AC084319 *Oryza sativa*
DESCRIPTION: putative protein kinase. OSJNBa0004B24.20.

35

AAF76306.1 AF220602 *Lycopersicon pimpinellifolium*
DESCRIPTION: Pto kinase.

40

AAB47423.1 U59315 *Lycopersicon pimpinellifolium*
DESCRIPTION: serine/threonine protein kinase Pto. Pto. bacterial speck disease resistance in tomato; disease resistance gene.

45

AAK11568.1 AF318492 *Lycopersicon hirsutum*

DESCRIPTION: Pto-like protein kinase B. LhirPtoB.

- 5 BAB21241.1 AP002953 *Oryza sativa*
DESCRIPTION: Putative Pto kinase interactor 1. P0426D06.21. contains ESTs
AU108280(E0721),D48017(S13927).
- 10 AAC27894.1 AF023164 *Zea mays*
DESCRIPTION: leucine-rich repeat transmembrane protein kinase 1. ltk1.
- 15 AAF91337.1 AF249318 *Glycine max*
DESCRIPTION: Pti1 kinase-like protein. Pti1b. protein kinase.
- 20 AAC61805.1 U28007 *Lycopersicon esculentum*
DESCRIPTION: serine/threonine protein kinase. Pto kinase interactor 1.
Pti1. Pti1 kinase.
- 25 CAA97692.1 Z73295 *Catharanthus roseus*
DESCRIPTION: receptor-like protein kinase. CRPK1. Autophosphorylation
predominantly on Thr, less on Ser. Mechanism: autophosphorylation in cis.
- 30 AAF91336.1 AF249317 *Glycine max*
DESCRIPTION: Pti1 kinase-like protein. Pti1a. protein kinase.
- 35 AAB61708.1 U93048 *Daucus carota*
DESCRIPTION: somatic embryogenesis receptor-like kinase. SERK.
- 40 AAK11569.1 AF318493 *Lycopersicon hirsutum*
DESCRIPTION: Pto-like protein kinase D. LhirPtoD.
- 45 BAA92221.1 AP001278 *Oryza sativa*
DESCRIPTION: Similar to *Arabidopsis thaliana* chromosome II BAC F12L6
genomic sequence, putative protein kinase. (AC004218).

BAA87852.1 AP000816 *Oryza sativa*
 DESCRIPTION: Similar to putative Ser/Thr protein kinase. (AC004218).

5

AAC27895.1 AF023165 *Zea mays*
 DESCRIPTION: leucine-rich repeat transmembrane protein kinase 2. ltk2.

612

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CAA54613.1 X77463 *Manihot esculenta*
 DESCRIPTION: UTP-glucose glucosyltransferase. CGT6.

15

CAA54609.1 X77459 *Manihot esculenta*
 DESCRIPTION: UTP-glucose glucosyltransferase. CGT1.

20

CAA54611.1 X77461 *Manihot esculenta*
 DESCRIPTION: UTP-glucose glucosyltransferase. CGT2.

25

CAA54612.1 X77462 *Manihot esculenta*
 DESCRIPTION: UTP-glucose glucosyltransferase. CGT5.

30

BAB17182.1 AP002843 *Oryza sativa*
 DESCRIPTION: putative UTP-glucose glucosyltransferase. P0407B12.19.

35

BAB17176.1 AP002843 *Oryza sativa*
 DESCRIPTION: putative UTP-glucose glucosyltransferase. P0407B12.13.

40

CAB56231.1 Y18871 *Dorotheanthus bellidiformis*
 DESCRIPTION: betanidin-5-O-glucosyltransferase.

45

BAA83484.1 AB031274 *Scutellaria baicalensis*
 DESCRIPTION: UDP-glucose: flavonoid 7-O-glucosyltransferase. ufgt.

AAB36653.1 U32644 *Nicotiana tabacum*
 DESCRIPTION: immediate-early salicylate-induced glucosyltransferase.
 IS5a.

- AAK28303.1 AF346431 *Nicotiana tabacum*
DESCRIPTION: phenylpropanoid:glucosyltransferase 1. togt1.
glucosyltransferase.
- CAA59450.1 X85138 *Lycopersicon esculentum*
DESCRIPTION: twi1. homologous to glucosyltransferases.
- AAB36652.1 U32643 *Nicotiana tabacum*
DESCRIPTION: immediate-early salicylate-induced glucosyltransferase.
IS10a.
- AAK28304.1 AF346432 *Nicotiana tabacum*
DESCRIPTION: phenylpropanoid:glucosyltransferase 2. togt2.
glucosyltransferase.
- BAA89009.1 AB027455 *Petunia x hybrida*
DESCRIPTION: anthocyanin 5-O-glucosyltransferase. PH1.
- AAG25643.1 AF303396 *Phaseolus vulgaris*
DESCRIPTION: UDP-glucosyltransferase HRA25. putative; defense associated.
- AAF61647.1 AF190634 *Nicotiana tabacum*
DESCRIPTION: UDP-glucose:salicylic acid glucosyltransferase. SA-GTase.
- BAA93039.1 AB033758 *Citrus unshiu*
DESCRIPTION: limonoid UDP-glucosyltransferase. LGTase.
- AAB48444.1 U82367 *Solanum tuberosum*
DESCRIPTION: UDP-glucose glucosyltransferase.
- AAD21086.1 AF127218 *Forsythia x intermedia*
DESCRIPTION: adds glucose residue to position 3 of flavonoid compounds.
flavonoid 3-O-glucosyltransferase. UFGT.
- AAK16175.1 AC079887 *Oryza sativa*

DESCRIPTION: putative glucosyltransferase. OSJNBa0040E01.15.

CAC09351.1 AL442007 *Oryza sativa*

5 DESCRIPTION: putative glucosyltransferase. H0212B02.7.

AAD04166.1 AF101972 *Phaseolus lunatus*

10 DESCRIPTION: catalyzes formation of O-glucosylzeatin from zeatin and
UDPG; catalyzes formation of O-xylosylzeatin from zeatin and UDPX. zeatin
O-glucosyltransferase. ZOG1. cytokinin O-glucosyltransferase.

AAF17077.1 AF199453 *Sorghum bicolor*

15 DESCRIPTION: UDP-glucose glucosyltransferase.
UDP-glucose:p-hydroxymandelonitrile-o- glucosyltransferase.

BAA12737.1 D85186 *Gentiana triflora*

20 DESCRIPTION: UDP-glucose:flavonoid-3-glucosyltransferase.

BAB07962.1 AP002524 *Oryza sativa*

25 DESCRIPTION: putative anthocyanin 5-O-glucosyltransferase. P0406H10.16.
contains ESTs AU067881(C10481),AU067882(C10481).

BAA36421.1 AB013596 *Perilla frutescens*

30 DESCRIPTION: UDP-glucose:anthocynsin 5-O-glucosyltransferase. PF3R4.

CAA54610.1 X77460 *Manihot esculenta*

DESCRIPTION: UTP-glucose glucosyltransferase. CGT4.

35 AAF98390.1 AF287143 *Brassica napus*

40 DESCRIPTION: catalyzes the transfer of glucose from UDP-glucose to
sinapate and some other hydroxycinnamates (4-coumarate, caffeate,
ferulate). UDP-glucose:sinapate glucosyltransferase. SGT1. SGT.

BAA36423.1 AB013598 *Verbena x hybrida*

DESCRIPTION: UDP-glucose:anthocyanin 5-O-glucosyltransferase. HGT8.

45 CAA30760.1 X07937 *Zea mays*

DESCRIPTION: UDPglucose flavonoid glycosyl transferase. Bz-W22.

CAA30761.1 X07940 Zea mays
5 DESCRIPTION: UDPglucose flavonoid glycosyl-transferase. Bz-McC.

CAA31855.1 X13500 Zea mays
10 DESCRIPTION: UDPglucose:flavonol 3-O-glucosyltransferase.

BAA19659.1 AB002818 Perilla frutescens
DESCRIPTION: flavonoid 3-O-glucosyltransferase. UDP glucose.

15 BAA89008.1 AB027454 Petunia x hybrida
DESCRIPTION: anthocyanidin 3-O-glucosyltransferase. PGT8.

20 AAK16172.1 AC079887 Oryza sativa
DESCRIPTION: putative glucosyltransferase. OSJNBa0040E01.14.

613

25 CAA54609.1 X77459 Manihot esculenta
DESCRIPTION: UTP-glucose glucosyltransferase. CGT1.

30 CAA54613.1 X77463 Manihot esculenta
DESCRIPTION: UTP-glucose glucosyltransferase. CGT6.

35 CAA54611.1 X77461 Manihot esculenta
DESCRIPTION: UTP-glucose glucosyltransferase. CGT2.

CAA54612.1 X77462 Manihot esculenta
DESCRIPTION: UTP-glucose glucosyltransferase. CGT5.

40 BAB17182.1 AP002843 Oryza sativa
DESCRIPTION: putative UTP-glucose glucosyltransferase. P0407B12.19.

45 BAB17176.1 AP002843 Oryza sativa
DESCRIPTION: putative UTP-glucose glucosyltransferase. P0407B12.13.

CAB56231.1 Y18871 *Dorotheanthus bellidiformis*
 DESCRIPTION: betanidin-5-O-glucosyltransferase.
 5

AAB36653.1 U32644 *Nicotiana tabacum*
 DESCRIPTION: immediate-early salicylate-induced glucosyltransferase.
 IS5a.
 10

AAK28303.1 AF346431 *Nicotiana tabacum*
 DESCRIPTION: phenylpropanoid:glucosyltransferase 1. togt1.
 glucosyltransferase.
 15

AAB36652.1 U32643 *Nicotiana tabacum*
 DESCRIPTION: immediate-early salicylate-induced glucosyltransferase.
 IS10a.
 20

AAK28304.1 AF346432 *Nicotiana tabacum*
 DESCRIPTION: phenylpropanoid:glucosyltransferase 2. togt2.
 glucosyltransferase.
 25

CAA59450.1 X85138 *Lycopersicon esculentum*
 DESCRIPTION: twi1. homologous to glucosyltransferases.
 30

BAA83484.1 AB031274 *Scutellaria baicalensis*
 DESCRIPTION: UDP-glucose: flavonoid 7-O-glucosyltransferase. ufgt.
 35

AAF61647.1 AF190634 *Nicotiana tabacum*
 DESCRIPTION: UDP-glucose:salicylic acid glucosyltransferase. SA-GTase.
 40

BAA93039.1 AB033758 *Citrus unshiu*
 DESCRIPTION: limonoid UDP-glucosyltransferase. LGTase.
 45

AAB48444.1 U82367 *Solanum tuberosum*
 DESCRIPTION: UDP-glucose glucosyltransferase.

- BAA89009.1 AB027455 *Petunia x hybrida*
DESCRIPTION: anthocyanin 5-O-glucosyltransferase. PH1.
- 5 BAA36421.1 AB013596 *Perilla frutescens*
DESCRIPTION: UDP-glucose:anthocynsin 5-O-glucosyltransferase. PF3R4.
- 10 CAC09351.1 AL442007 *Oryza sativa*
DESCRIPTION: putative glucosyltransferase. H0212B02.7.
- 15 BAA12737.1 D85186 *Gentiana triflora*
DESCRIPTION: UDP-glucose:flavonoid-3-glucosyltransferase.
- AAG25643.1 AF303396 *Phaseolus vulgaris*
DESCRIPTION: UDP-glucosyltransferase HRA25. putative; defense associated.
- 20 AAD04166.1 AF101972 *Phaseolus lunatus*
DESCRIPTION: catalyzes formation of O-glucosylzeatin from zeatin and
UDPG; catalyzes formation of O-xylosylzeatin from zeatin and UDPX. zeatin
O-glucosyltransferase. ZOG1. cytokinin O-glucosyltransferase.
- 25 CAA54610.1 X77460 *Manihot esculenta*
DESCRIPTION: UTP-glucose glucosyltransferase. CGT4.
- 30 AAF98390.1 AF287143 *Brassica napus*
DESCRIPTION: catalyzes the transfer of glucose from UDP-glucose to
sinapate and some other hydroxycinnamates (4-coumarate, caffeate,
ferulate). UDP-glucose:sinapate glucosyltransferase. SGT1. SGT.
- 35 AAK16172.1 AC079887 *Oryza sativa*
DESCRIPTION: putative glucosyltransferase. OSJNBa0040E01.14.
- 40 BAA36423.1 AB013598 *Verbena x hybrida*
DESCRIPTION: UDP-glucose:anthocyanin 5-O-glucosyltransferase. HGT8.
- 45 AAD21086.1 AF127218 *Forsythia x intermedia*
DESCRIPTION: adds glucose residue to position 3 of flavonoid compounds.

flavonoid 3-O-glucosyltransferase. UFGT.

- 5 AAF17077.1 AF199453 Sorghum bicolor
DESCRIPTION: UDP-glucose glucosyltransferase.
UDP-glucose:p-hydroxymandelonitrile-o- glucosyltransferase.
- 10 AAK16175.1 AC079887 Oryza sativa
DESCRIPTION: putative glucosyltransferase. OSJNBa0040E01.15.
- 15 BAB07962.1 AP002524 Oryza sativa
DESCRIPTION: putative anthocyanin 5-O-glucosyltransferase. P0406H10.16.
contains ESTs AU067881(C10481),AU067882(C10481).
- 20 CAA31855.1 X13500 Zea mays
DESCRIPTION: UDPglucose:flavonol 3-0-glucosyltransferase.
- 25 BAA36422.1 AB013597 Perilla frutescens
DESCRIPTION: UDP-glucose:anthocyanin 5-O-glucosyltransferase homologue.
PF3R6.
- 30 BAA89008.1 AB027454 Petunia x hybrida
DESCRIPTION: anthocyanidin 3-O-glucosyltransferase. PGT8.
614
-
- 35 AAD21872.1 AF078082 Phaseolus vulgaris
DESCRIPTION: receptor-like protein kinase homolog RK20-1.
- CAA73134.1 Y12531 Brassica oleracea
DESCRIPTION: serine/threonine kinase. BRLK.
- 40 AAB93834.1 U82481 Zea mays
DESCRIPTION: KI domain interacting kinase 1. KIK1. receptor-like protein
kinase; serine/threonine protein kinase.
- 45 AAA33008.1 M97667 Brassica napus
DESCRIPTION: serine/threonine kinase receptor.

- 5 CAB89179.1 AJ245479 Brassica napus subsp. napus
DESCRIPTION: ser /thr kinase. S-locus receptor kinase. srk.
- AAA33000.1 M76647 Brassica oleracea
DESCRIPTION: receptor protein kinase. SKR6.
- 10 BAA23676.1 AB000970 Brassica rapa
DESCRIPTION: receptor kinase 1. BcRK1.
- 15 BAA06285.1 D30049 Brassica rapa
DESCRIPTION: S-receptor kinase SRK9.
- 20 BAA21132.1 D88193 Brassica rapa
DESCRIPTION: S-receptor kinase. SRK9 (B.c).
- 25 CAA74661.1 Y14285 Brassica oleracea
DESCRIPTION: SFR1. extracellular S domain: 8-1342; transmembrane domain:
1343-1411; intracellular kinase domain: 1412-2554.
- 30 BAA92837.1 AB032474 Brassica oleracea
DESCRIPTION: S60 S-locus receptor kinase. SRK60.
- BAA07577.2 D38564 Brassica rapa
DESCRIPTION: receptor protein kinase SRK12.
- 35 BAA07576.1 D38563 Brassica rapa
DESCRIPTION: receptor protein kinase SRK8.
- 40 CAA73133.1 Y12530 Brassica oleracea
DESCRIPTION: serine /threonine kinase. ARLK.
- 45 AAC23542.1 U20948 Ipomoea trifida
DESCRIPTION: receptor protein kinase. IRK1.

CAA79355.1 Z18921 Brassica oleracea
DESCRIPTION: S-receptor kinase-like protein.

5

CAA67145.1 X98520 Brassica oleracea
DESCRIPTION: receptor-like kinase. SFR2.

10

CAA74662.1 Y14286 Brassica oleracea
DESCRIPTION: SFR3. extracellular S domain: 123-1346; transmembrane domain: 1347-1412; intracellular kinase domain: from 1413.

15

BAB21001.1 AB054061 Brassica rapa
DESCRIPTION: S locus receptor kinase. SRK22.

20

AAA62232.1 U00443 Brassica napus
DESCRIPTION: S-receptor kinase. protein contains an immunoglobulin-like domain.

25

CAB41879.1 Y18260 Brassica oleracea
DESCRIPTION: SRK15 protein. SRK15. receptor-like kinase.

30

CAB41878.1 Y18259 Brassica oleracea
DESCRIPTION: SRK5 protein. SRK5. receptor-like kinase.

35

BAA92836.1 AB032473 Brassica oleracea
DESCRIPTION: S18 S-locus receptor kinase. SRK18.

40

BAB18292.1 AP002860 Oryza sativa
DESCRIPTION: putative receptor-like protein kinase. P0409B08.19.

45

AAD52097.1 AF088885 Nicotiana tabacum
DESCRIPTION: receptor-like kinase CHRK1. Chrk1.

AAA33915.1 L27821 Oryza sativa
DESCRIPTION: receptor type serine/threonine kinase. protein kinase.

- 5 BAB39873.1 AP002882 *Oryza sativa*
DESCRIPTION: putative protein kinase. P0439B06.8. contains ESTs
AU056701(S20808),AU056702(S20808).
- 10 BAB16871.1 AP002537 *Oryza sativa*
DESCRIPTION: putative protein kinase APK1A*Arabidopsis thaliana*.
P0001B06.24. contains ESTs C22608(R3192),D25110(R3192).
- 15 AAK21965.1 AY028699 *Brassica napus*
DESCRIPTION: receptor protein kinase PERK1.
- 20 AAK00425.1 AC069324 *Oryza sativa*
DESCRIPTION: Putative protein kinase. OSJNBa0071K19.11.
- 25 BAA94529.2 AP001800 *Oryza sativa*
DESCRIPTION: Similar to *Zea mays* S-domain receptor-like protein kinase
(AJ010166).
- 30 BAA94509.1 AB041503 *Populus nigra*
DESCRIPTION: protein kinase 1. PnPK1.
- 35 BAA94510.1 AB041504 *Populus nigra*
DESCRIPTION: protein kinase 2. PnPK2.
- 40 BAA87853.1 AP000816 *Oryza sativa*
DESCRIPTION: EST AU030604(E51294) corresponds to a region of the
predicted gene. Similar to putative NAK-like Ser/Thr protein kinase.
(AF001308).
- 45 BAB39409.1 AP002901 *Oryza sativa*
DESCRIPTION: putative protein kinase. P0456F08.9. contains EST
C23560(R0290).
- AAG03090.1 AC073405 *Oryza sativa*
DESCRIPTION: Similar to an *Arabidopsis* somatic embryogenesis
receptor-like kinase (AC007504).

BAA92954.1 AP001551 *Oryza sativa*
 DESCRIPTION: Similar to *Oryza sativa* protein kinase (OSPK10) mRNA.
 5 (L27821).

BAA94518.1 AP001800 *Oryza sativa*
 DESCRIPTION: Similar to *Arabidopsis thaliana* chromosome 2 section 111 of
 10 255; putative receptor-like protein kinase (AC002392).

BAB07904.1 AP002835 *Oryza sativa*
 DESCRIPTION: putative S-receptor kinase. P0417G05.12.
 15 619

CAA72092.1 Y11209 *Nicotiana tabacum*
 DESCRIPTION: protein disulfide-isomerase precursor. PDI.
 20

AAG13988.1 AF298829 *Prunus avium*
 DESCRIPTION: putative protein disulfide-isomerase. PDI.
 25

AAD02069.1 AF036939 *Chlamydomonas reinhardtii*
 DESCRIPTION: redox-regulator of 5'UTR psbA mRNA binding complex and
 translation. protein disulfide isomerase. localized to ER and chloroplast.
 30

AAC49896.1 AF027727 *Chlamydomonas reinhardtii*
 DESCRIPTION: involved in the redox-regulated binding of chloroplast
 poly(A)-binding protein to the 5'-UTR of psbA mRNA; regulates chloroplast
 translational activation. protein disulfide isomerase RB60. PDI.
 35

AAD55566.1 AF110784 *Volvox carteri f. nagariensis*
 DESCRIPTION: protein disulfide isomerase precursor. pdi.
 40

AAB08519.1 L39014 *Zea mays*
 DESCRIPTION: protein disulfide isomerase. pdi. putative.
 45

AAA70344.1 L33250 *Hordeum vulgare*
 DESCRIPTION: catalyze the formation of disulfide bonds. disulfide

isomerase. PDI. putative.

- 5 AAA70345.1 L33251 Hordeum vulgare
DESCRIPTION: catalyze the formation of disulfide bonds. disulfide
isomerase. PDI. putative.
- 10 CAC21230.1 AJ277379 Triticum turgidum subsp. durum
DESCRIPTION: catalyzes formation of disulfide bonds. protein disulfide
isomerase. Pdi.
- 15 AAA19660.1 U11496 Triticum aestivum
DESCRIPTION: protein disulfide isomerase. PDI.
- 20 CAC21231.1 AJ277380 Triticum turgidum subsp. durum
DESCRIPTION: catalyzes formation of disulfide bonds. protein disulfide
isomerase. Pdi.
- 25 CAC21229.1 AJ277378 Triticum turgidum subsp. durum
DESCRIPTION: catalyzes formation of disulfide bonds. protein disulfide
isomerase. Pdi.
- 30 CAC21228.1 AJ277377 Triticum turgidum subsp. durum
DESCRIPTION: catalyzes the formation of disulfide bonds. protein
disulfide isomerase. Pdi.
- 35 AAB05641.1 U41385 Ricinus communis
DESCRIPTION: protein disulphide isomerase PDI. molecular chaperone.
- 40 CAA77575.1 Z11499 Medicago sativa
DESCRIPTION: protein disulfide isomerase.
- 45 AAD28260.1 AF131223 Datisca glomerata
DESCRIPTION: protein disulfide isomerase homolog. PDI.
- AAA70346.1 L33252 Hordeum vulgare
DESCRIPTION: catalyze the formation of disulfide bonds. disulfide

isomerase. PDI. putative.

5 BAA92322.1 AB039278 Oryza sativa
DESCRIPTION: protein disulfide isomerase. Pdi.

10 BAA77026.1 AB026252 Lithospermum erythrorhizon
DESCRIPTION: disulfide-isomerase precursor.

AAC79709.1 AF093614 Acetabularia acetabulum
DESCRIPTION: putative protein disulfide isomerase.

15 620

CAA64413.1 X94943 Lycopersicon esculentum
DESCRIPTION: peroxidase. cevil6.

20 AAA32676.1 M37637 Arachis hypogaea
DESCRIPTION: cationic peroxidase. PNC2.

25 BAA82307.1 AB027753 Nicotiana tabacum
DESCRIPTION: peroxidase.

30 AAB67737.1 L77080 Stylosanthes humilis
DESCRIPTION: cationic peroxidase.

AAD37429.2 AF149279 Phaseolus vulgaris
DESCRIPTION: peroxidase 4 precursor. FBP4. secretory peroxidase.
35

CAA71494.1 Y10468 Spinacia oleracea
DESCRIPTION: peroxidase. prxr7.

40 AAD37375.1 AF145349 Glycine max
DESCRIPTION: peroxidase. Prx3.

45 AAF63024.1 AF244921 Spinacia oleracea
DESCRIPTION: hydrogen peroxide catabolism. peroxidase prx12 precursor.

type III peroxidase.

CAA66037.1 X97351 Populus balsamifera subsp. trichocarpa
5 DESCRIPTION: signal for ER. peroxidase.

BAB39274.1 AP002971 Oryza sativa
10 DESCRIPTION: putative peroxidase. P0537A05.2.

AAA65637.1 L13654 Lycopersicon esculentum
DESCRIPTION: peroxidase. TPX1.

CAA40796.1 X57564 Armoracia rusticana
15 DESCRIPTION: peroxidase. peroxidase precursor.

AAD11482.1 U51192 Glycine max
20 DESCRIPTION: peroxidase precursor. sEPa2.

CAA80502.1 Z22920 Spirodela polyrrhiza
25 DESCRIPTION: peroxidase.

BAA77387.1 AB024437 Scutellaria baicalensis
30 DESCRIPTION: peroxidase 1.

CAA59485.1 X85228 Triticum aestivum
DESCRIPTION: peroxidase. POX2.

BAA07663.1 D42064 Nicotiana tabacum
35 DESCRIPTION: cationic peroxidase isozyme 38K precursor.

BAA11853.1 D83225 Populus nigra
40 DESCRIPTION: peroxidase.

BAA07664.1 D42065 Nicotiana tabacum
45 DESCRIPTION: cationic peroxidase isozyme 40K precursor.

- AAD37430.1 AF149280 *Phaseolus vulgaris*
DESCRIPTION: peroxidase 5 precursor. FBP5. secretory peroxidase.
- 5
- AAD11481.1 U51191 *Glycine max*
DESCRIPTION: peroxidase precursor. sEPa1.
- 10 CAB94692.1 AJ242742 *Ipomoea batatas*
DESCRIPTION: Removal of H₂O₂, oxidation of toxic reductants, defence response toward wounding. peroxidase. pod.
- 15 BAA03644.1 D14997 *Oryza sativa*
DESCRIPTION: peroxidase.
- AAD43561.1 AF155124 *Gossypium hirsutum*
20 DESCRIPTION: bacterial-induced peroxidase precursor. Perx_Goshiko.
- BAA06334.1 D30652 *Populus kitakamiensis*
DESCRIPTION: peroxidase.
25
- BAA92500.1 AP001383 *Oryza sativa*
DESCRIPTION: ESTs D39300(R3292),AU030751(E60187) correspond to a
region
30 of the predicted gene. Similar to peroxidase ATP6a. (X98774).
- BAA90365.1 AP001081 *Oryza sativa*
DESCRIPTION: ESTs D24550(R2151),D24265(R1609),AU031848(R2151)
35 correspond
to a region of the predicted gene. Similar to cationic peroxidase isozyme
40K precursor (D42065).
- 40 BAA89584.1 AP001073 *Oryza sativa*
DESCRIPTION: ESTs D24550(R2151),D24265(R1609),AU031848(R2151)
correspond
to a region of the predicted gene. Similar to cationic peroxidase isozyme
40K precursor (D42065).
45

- AAF34416.1 AF172282 *Oryza sativa*
DESCRIPTION: putative peroxidase. DUPR11.5.
- 5 AAC49820.1 AF014469 *Oryza sativa*
DESCRIPTION: peroxidase. POX5.1. wound inducible.
- 10 CAA66034.1 X97348 *Populus balsamifera* subsp. *trichocarpa*
DESCRIPTION: signal for ER. peroxidase.
- 15 BAB39281.1 AP002971 *Oryza sativa*
DESCRIPTION: putative peroxidase. P0537A05.10. contains ESTs
D24657(R2329),AU082066(R2329).
- 20 BAA14144.1 D90116 *Armoracia rusticana*
DESCRIPTION: peroxidase isozyme.
- 25 AAB97734.1 AF014502 *Glycine max*
DESCRIPTION: seed coat peroxidase precursor. Ep. H₂O₂ oxidoreductase;
class III plant peroxidase.
- 30 CAA37713.1 X53675 *Triticum aestivum*
DESCRIPTION: peroxidase.
- 35 AAC05277.1 AF049881 *Linum usitatissimum*
DESCRIPTION: peroxidase FLXPER4. PER4.
- 40 CAA66035.1 X97349 *Populus balsamifera* subsp. *trichocarpa*
DESCRIPTION: signal for ER. peroxidase.
- 45 BAA06335.1 D30653 *Populus kitakamiensis*
DESCRIPTION: peroxidase.
- CAA39486.1 X56011 *Triticum aestivum*
DESCRIPTION: peroxidase.

- BAA03911.1 D16442 *Oryza sativa*
DESCRIPTION: peroxidase.
- 5 BAA94962.1 AB042103 *Asparagus officinalis*
DESCRIPTION: peroxidase. AspPOX1.
- 10 AAC49821.1 AF014470 *Oryza sativa*
DESCRIPTION: peroxidase. POXgX9. expressed in roots.
- 15 AAD37427.1 AF149277 *Phaseolus vulgaris*
DESCRIPTION: peroxidase 1 precursor. FBP1. secretory peroxidase.
- CAA76374.2 Y16776 *Spinacia oleracea*
DESCRIPTION: peroxidase. prx10.
- 20 BAA08499.1 D49551 *Oryza sativa*
DESCRIPTION: peroxidase. poxN.
- 25 CAA66036.1 X97350 *Populus balsamifera* subsp. *trichocarpa*
DESCRIPTION: signal for ER. peroxidase.
- 30 AAA34108.1 J02979 *Nicotiana tabacum*
DESCRIPTION: lignin-forming peroxidase precursor (EC 1.11.1.7).
- 35 CAA62226.1 X90693 *Medicago sativa*
DESCRIPTION: peroxidase1B. prx1B.
- CAA59487.1 X85230 *Triticum aestivum*
DESCRIPTION: peroxidase. pox4.
- 40 626
-
- CAA98160.1 Z73932 *Lotus japonicus*
DESCRIPTION: GTP-binding protein. RAB1C. rab1C.
- 45 BAA76422.1 AB024994 *Cicer arietinum*

DESCRIPTION: rab-type small GTP-binding protein.

5 BAA02116.1 D12548 Pisum sativum
DESCRIPTION: GTP-binding protein.

10 CAA69701.1 Y08425 Nicotiana plumbaginifolia
DESCRIPTION: small GTP-binding protein. Rab1 subfamily.

15 AAA80678.1 U38464 Lycopersicon esculentum
DESCRIPTION: small GTP-binding protein. LeRab1A. ; YPT1/Rab1A
homolog
LeRab1A.

20 BAA02118.1 D12550 Pisum sativum
DESCRIPTION: GTP-binding protein.

25 AAB97115.1 U58854 Glycine max
DESCRIPTION: small GTP-binding protein. sra2.

CAA51011.1 X72212 Nicotiana tabacum
DESCRIPTION: ras-related GTP-binding protein. ypt2 homologue.

30 AAF65510.1 AF108883 Capsicum annuum
DESCRIPTION: small GTP-binding protein.

35 AAA80680.1 U38466 Lycopersicon esculentum
DESCRIPTION: small GTP-binding protein. LeRab1C. ; YPT1/Rab1A homolog
LeRab1C.

40 CAA98161.1 Z73933 Lotus japonicus
DESCRIPTION: GTP-binding protein. RAB1D. rab1D.

45 BAA02117.1 D12549 Pisum sativum
DESCRIPTION: GTP-binding protein.

- CAA98162.1 Z73934 Lotus japonicus
DESCRIPTION: GTP-binding protein. RAB1E. rab1E.
- 5 AAA50159.1 L27417 Glycine max
DESCRIPTION: GTP binding protein.
- 10 AAB28535.1 S66160 Oryza sativa
DESCRIPTION: ric1. ras-related GTP binding protein possessing GTPase activity; This sequence comes from Fig. 1.
- 15 CAA98159.1 Z73931 Lotus japonicus
DESCRIPTION: GTP-binding protein. RAB1B. rab1B.
- 20 BAA02115.1 D12547 Pisum sativum
DESCRIPTION: GTP-binding protein.
- 25 CAA66447.1 X97853 Lotus japonicus
DESCRIPTION: GTP-binding protein. RAB1A. rab1A.
- AAD10389.1 U35026 Petunia x hybrida
DESCRIPTION: Rab1-like small GTP-binding protein.
- 30 AAA80679.1 U38465 Lycopersicon esculentum
DESCRIPTION: small GTP-binding protein. LeRab1B. ; Ypt1/Rab1A homolog LeRab1B.
- 35 BAB07961.1 AP002524 Oryza sativa
DESCRIPTION: putative GTP-binding protein. P0406H10.17. contains ESTs D23874(R0480),AU031678(R0480).
- 40 CAA98176.1 Z73948 Lotus japonicus
DESCRIPTION: GTP-binding protein. RAB8E. rab8E.
- 45 CAA89021.1 Z49152 Beta vulgaris
DESCRIPTION: GTP-binding. small G protein.

- CAA98172.1 Z73944 Lotus japonicus
DESCRIPTION: GTP-binding protein. RAB8A. rab8A.
- 5 CAA04701.1 AJ001367 Daucus carota
DESCRIPTION: small GTP-binding protein. Dc-Rab8.
- 10 CAA90080.1 Z49900 Pisum sativum
DESCRIPTION: small GTP-binding protein.
- AAD46405.1 AF096249 Lycopersicon esculentum
15 DESCRIPTION: ethylene-responsive small GTP-binding protein. ER43.
- CAA98174.1 Z73946 Lotus japonicus
DESCRIPTION: GTP-binding protein. RAB8C. rab8C.
20
- CAA90082.1 Z49902 Pisum sativum
DESCRIPTION: small GTP-binding protein.
- 25 CAA49600.1 X69980 Lycopersicon esculentum
DESCRIPTION: GTP-binding protein. ypt2.
- 30 CAA98175.1 Z73947 Lotus japonicus
DESCRIPTION: GTP-binding protein. RAB8D. rab8D.
- CAA90081.1 Z49901 Pisum sativum
35 DESCRIPTION: small GTP-binding protein.
- AAB17726.1 U38471 Brassica rapa
DESCRIPTION: small GTP-binding protein rab. BRAB-1. small GTP-binding
40 protein rab family.
- AAA34251.1 L08128 Volvox carteri
DESCRIPTION: GTP-binding protein. yptV2.
45

CAA98173.1 Z73945 Lotus japonicus
DESCRIPTION: GTP-binding protein. RAB8B. rab8B.

5 CAA89049.1 Z49190 Beta vulgaris
DESCRIPTION: GTP-binding. small G protein.

10 CAA98179.1 Z73951 Lotus japonicus
DESCRIPTION: GTP-binding protein. RAB11C. rab11C.

15 AAA34253.1 L08130 Volvox carteri
DESCRIPTION: GTP-binding protein. yptV4.

CAA98165.1 Z73937 Lotus japonicus
DESCRIPTION: GTP-binding protein. RAB2A. rab2A.

20 AAA63902.1 U22433 Zea mays
DESCRIPTION: GTP binding protein. rab2.

25 AAA90955.1 U32185 Glycine max
DESCRIPTION: vesicular transport. guanine nucleotide regulatory protein.
rab2. GTP-binding protein; soyrab.

628

30 -----
AAA87456.1 U22147 Hevea brasiliensis
DESCRIPTION: beta-1,3-glucanase. HGN1. hydrolytic enzyme.

35 CAB38443.1 AJ133470 Hevea brasiliensis
DESCRIPTION: beta-1,3-glucanase. hgn1.

40 AAG24921.1 AF311749 Hevea brasiliensis
DESCRIPTION: beta-1,3-glucanase.

45 AAF44667.1 AF239617 Vitis vinifera
DESCRIPTION: hydrolysis of 1,3-beta-D-glucosidic linkages in
1,3-beta-D-glucans. beta-1,3-glucanase. fungal pathogen defense-related
protein.

- AAA33648.1 L02212 *Pisum sativum*
DESCRIPTION: beta-1,3-glucan hydrolysis. beta-1,3-glucanase. putative.
- 5
- AAB41551.1 U27179 *Medicago sativa* subsp. *sativa*
DESCRIPTION: acidic glucanase.
- 10
- AAB24398.1 S51479 *Pisum sativum*
DESCRIPTION: beta-1,3-glucanase. beta-1,3-glucanase. This sequence comes from Fig. 1B.
- 15
- CAA37289.1 X53129 *Phaseolus vulgaris*
DESCRIPTION: 1,3,-beta-D-glucanase.
- 20
- AAA34078.1 M63634 *Nicotiana plumbaginifolia*
DESCRIPTION: regulator of beta(1,3)-glucanase. beta(1,3)-glucanase regulator.
- 25
- AAA51643.1 M23120 *Nicotiana plumbaginifolia*
DESCRIPTION: beta-glucanase precursor.
- 30
- CAA30261.1 X07280 *Nicotiana plumbaginifolia*
DESCRIPTION: beta-glucanase.
- 35
- AAA03618.1 M80608 *Lycopersicon esculentum*
DESCRIPTION: beta-1,3-glucanase.
- 40
- AAC19114.1 AF067863 *Solanum tuberosum*
DESCRIPTION: 1,3-beta-glucan glucanohydrolase. glucanase.
- 45
- AAA18928.1 U01901 *Solanum tuberosum*
DESCRIPTION: catalyzes the hydrolysis of 1,3-beta-D-glucoside linkages in 1,3,-beta-D-glucans (such as laminarin). 1,3-beta-D-glucan glucanohydrolase; endo-1,3-beta-D-glucanase; 1,3-beta-glucanase (basic, class I). glub2. plant defense gene; induced expression in response to infection, elicitor, ethylene, wounding.

AAA63539.1 M60402 *Nicotiana tabacum*
 DESCRIPTION: glucan beta-1,3-glucanase. glucanase GLA.
 5

AAA63540.1 M60403 *Nicotiana tabacum*
 DESCRIPTION: glucan-1,3-beta-glucosidase. glucanase GLB.
 10

AAA88794.1 U01900 *Solanum tuberosum*
 DESCRIPTION: catalyzes the hydrolysis of 1,3-beta-D-glucoside linkages in
 1,3,-beta-D-glucans (such as laminarin). 1,3-beta-D-glucan
 glucanohydrolase; endo-1,3-beta-D-glucanase; 1,3-beta-glucanase (basic,
 15 class I). gluB1. plant defense gene; induced expression in response to
 infection, elicitor, ethylene, wounding.

AAA63541.1 M59442 *Nicotiana tabacum*
 20 DESCRIPTION: basic beta-1,3-glucanase. glucanase.

AAB82772.2 AF001523 *Musa acuminata*
 DESCRIPTION: beta-1, 3-glucanase. similar to beta-1, 3-glucanase.
 25

AAF08679.1 AF004838 *Musa acuminata*
 DESCRIPTION: beta-1,3-glucanase.
 30

AAA19111.1 U01902 *Solanum tuberosum*
 DESCRIPTION: catalyzes the hydrolysis of 1,3-beta-D-glucoside linkages in
 1,3,-beta-D-glucans (such as laminarin). 1,3-beta-D-glucan
 glucanohydrolase; endo-1,3-beta-D-glucanase; 1,3-beta-glucanase (basic,
 35 class I). gluB3. plant defense gene; induced expression in response to
 infection, elicitor, ethylene, wounding.

AAC04710.1 AF034106 *Glycine max*
 40 DESCRIPTION: beta-1,3-glucanase 1. SGlu1.

AAC04714.1 AF034113 *Glycine max*
 DESCRIPTION: beta-1,3-glucanase 8. SGlu8.
 45

- CAB91554.1 AJ277900 *Vitis vinifera*
DESCRIPTION: beta 1-3 glucanase. gl.
- 5 AAA34082.1 M20620 *Nicotiana tabacum*
DESCRIPTION: prepro-beta-1,3-glucanase precursor.
- 10 CAA03908.1 AJ000081 *Citrus sinensis*
DESCRIPTION: glucan hydrolase. beta-1,3-glucanase. gns1.
- 15 AAB03501.1 U41323 *Glycine max*
DESCRIPTION: beta-1,3-glucanase. SGN1.
- 20 AAA92013.1 U49454 *Prunus persica*
DESCRIPTION: beta-1,3-glucanase. Gns1.
- 25 AAA33946.1 M37753 *Glycine max*
DESCRIPTION: beta-1,3-endoglucanase (EC 3.2.1.39).
- 30 AAA63542.1 M59443 *Nicotiana tabacum*
DESCRIPTION: acidic beta-1,3-glucanase. glucanase.
- AAF34761.1 AF227953 *Capsicum annuum*
DESCRIPTION: basic beta-1,3-glucanase. BGLU.
- 35 AAD33881.1 AF141654 *Nicotiana tabacum*
DESCRIPTION: beta-1,3-glucanase. GGL4.
- AAG34080.1 AF294849 *Capsicum annuum*
DESCRIPTION: beta-1,3-glucanase-like protein.
- 40 AAF33405.1 AF230109 *Populus x canescens*
DESCRIPTION: beta-1,3 glucanase. BGLUC.
- 45 AAD33880.1 AF141653 *Nicotiana tabacum*
DESCRIPTION: beta-1,3-glucanase. GGL1.

CAA57255.1 X81560 *Nicotiana tabacum*
 DESCRIPTION: (1-)-beta-glucanase. Sp41a.

5

AAA34053.1 M60464 *Nicotiana tabacum*
 DESCRIPTION: beta-1,3-glucanase.

10 630

AAD37698.1 AF145729 *Oryza sativa*
 DESCRIPTION: homeodomain leucine zipper protein. Oshox5. transcription
 factor.

15

BAA05624.1 D26575 *Daucus carota*
 DESCRIPTION: transcriptional regulator. DNA-binding protein. homeodomain
 at nt 520-699; leucine zipper at nt 700-805.

20

AAF01765.1 AF184278 *Glycine max*
 DESCRIPTION: homeodomain-leucine zipper protein 57. Hdl57. transcription
 factor.

25

CAA64417.1 X94947 *Lycopersicon esculentum*
 DESCRIPTION: homeobox. VAHOX1.

30

BAA93465.1 AB028077 *Physcomitrella patens*
 DESCRIPTION: homeobox protein PpHB6. PpHB6. homeodomain-leucine
 zipper
 gene.

35

BAB18171.1 AB042769 *Zinnia elegans*
 DESCRIPTION: homeobox-leucine zipper protein. ZeHB3. full length.

40

BAA93460.1 AB028072 *Physcomitrella patens*
 DESCRIPTION: homeobox protein PpHB1. PpHB1. homeodomain-leucine
 zipper
 gene.

45

- 5 BAA93465.1 AB028078 *Physcomitrella patens*
DESCRIPTION: homeobox protein PpHB7. PpHB7. homeodomain-leucine zipper gene.
- 10 BAA93461.1 AB028073 *Physcomitrella patens*
DESCRIPTION: homeobox protein PpHB2. PpHB2. homeodomain-leucine zipper gene.
- 15 BAA05625.1 D26576 *Daucus carota*
DESCRIPTION: transcriptional regulator. DNA-binding protein. homeodomain at nt 300-479; leucine zipper at nt 480-587.
- 20 BAA05622.1 D26573 *Daucus carota*
DESCRIPTION: transcriptional regulator. DNA-binding protein. homeodomain at nt 585-764; leucine zipper at nt 765-851.
- 25 BAA93467.1 AB028079 *Physcomitrella patens*
DESCRIPTION: homeobox protein PpHB8. PpHB8. homeodomain-leucine zipper gene.
- 30 BAA93464.1 AB028076 *Physcomitrella patens*
DESCRIPTION: homeobox protein PpHB5. PpHB5. homeodomain-leucine zipper gene.
- 35 AAD37697.1 AF145728 *Oryza sativa*
DESCRIPTION: homeodomain leucine zipper protein. Oshox4. transcription factor.
- 40 AAF01764.2 AF184277 *Glycine max*
DESCRIPTION: homeodomain-leucine zipper protein 56. Hdl56. transcription factor.
- 45 BAA21017.1 D26578 *Daucus carota*
DESCRIPTION: transcriptional regulator. DNA-binding protein. homeodomain

at nt 761-940; leucine zipper at nt 941-1048.

BAB18168.1 AB042766 *Zinnia elegans*

5 DESCRIPTION: homeobox-leucine zipper protein. ZeHB7. 3'RACE product.

BAA93468.1 AB028080 *Physcomitrella patens*

10 DESCRIPTION: homeobox protein PpHB9. PpHB9. homeodomain-leucine zipper gene.

BAA05623.1 D26574 *Daucus carota*

15 DESCRIPTION: transcriptional regulator. DNA-binding protein. homeodomain at nt 498-677; leucine zipper at nt 678-785.

AAD37699.1 AF145730 *Oryza sativa*

20 DESCRIPTION: homeodomain leucine zipper protein. Oshox6. transcription factor.

AAD38144.1 AF139497 *Prunus armeniaca*

25 DESCRIPTION: DNA-binding protein. homeobox leucine zipper protein. HBLZP.

AAA63768.2 AF339748 *Helianthus annuus*

30 DESCRIPTION: homeobox-leucine zipper protein HAHB-4. Hahb-4.

BAA93463.1 AB028075 *Physcomitrella patens*

35 DESCRIPTION: homeobox protein PpHB4. PpHB4. homeodomain-leucine zipper gene.

CAA64491.1 X95193 *Pimpinella brachycarpa*

40 DESCRIPTION: transcription activator. homeobox-leucine zipper protein.

CAA64221.1 X94449 *Pimpinella brachycarpa*

45 DESCRIPTION: transcription activator. homeobox-leucine zipper protein. PHZ4.

AAG13983.1 AF297522 *Prunus avium*
DESCRIPTION: expansin 2. Exp2. PruavExp2.

5 AAF35902.1 AF230333 *Zinnia elegans*
DESCRIPTION: expansin 3.

10 AAF32409.1 AF230276 *Triphysaria versicolor*
DESCRIPTION: alpha-expansin 3.

AAC96080.1 AF049353 *Nicotiana tabacum*
DESCRIPTION: involved in acid-growth response. alpha-expansin precursor.
15 Nt-EXP4. cell wall protein.

AAG13982.1 AF297521 *Prunus avium*
DESCRIPTION: expansin 1. Exp1. PruavExp1.
20

AAC33529.1 U93167 *Prunus armeniaca*
DESCRIPTION: expansin. PA-Exp1.

25 AAF32411.1 AF230278 *Triphysaria versicolor*
DESCRIPTION: alpha-expansin 1.

30 AAF35901.1 AF230332 *Zinnia elegans*
DESCRIPTION: expansin 2.

35 AAF21101.1 AF159563 *Fragaria x ananassa*
DESCRIPTION: expansin. Exp2. ripening regulated.

BAB19676.1 AB029083 *Prunus persica*
DESCRIPTION: expansin. PchExp1.
40

AAD47901.1 AF085330 *Pinus taeda*
DESCRIPTION: expansin.

45 AAC33530.1 AF038815 *Prunus armeniaca*

DESCRIPTION: expansin. Exp2.

CAC19184.1 AJ291817 Cicer arietinum

5 DESCRIPTION: expansin.

AAB40635.1 U64891 Pinus taeda

10 DESCRIPTION: expansin. similar to Arabidopsis expansin encoded by
GenBank

Accession Numbers U30476, U30478, U30480 and U30481, to Cucumis sativus
expansin encoded by GenBank Accession Numbers U30382 and U30460, and to
rice expansin encoded by GenBank Accession Numbers U30477 and U30479.

15

AAG32921.1 AF184233 Lycopersicon esculentum

DESCRIPTION: expansin. Exp10.

20

AAD49956.1 AF167360 Rumex palustris

DESCRIPTION: expansin. EXP1.

25

AAB40637.1 U64893 Pinus taeda

DESCRIPTION: expansin. similar to Arabidopsis expansin encoded by
GenBank

Accession Numbers U30476, U30478, U30480 and U30481, to Cucumis sativus
expansin encoded by GenBank Accession Numbers U30382 and U30460, and to
rice expansin encoded by GenBank Accession Numbers U30477 and U30479.

30

AAB40634.1 U64890 Pinus taeda

DESCRIPTION: expansin. similar to Arabidopsis expansin encoded by
GenBank

35

Accession Numbers U30476, U30478, U30480 and U30481, to Cucumis sativus
expansin encoded by GenBank Accession Numbers U30382 and U30460, and to
rice expansin encoded by GenBank Accession Numbers U30477 and U30479.

40

AAB37746.1 U30382 Cucumis sativus

DESCRIPTION: expansin S1 precursor. Cs-EXP1. similar to pollen allergen
Lol pI, Lolium perenne, Swiss-Prot Accession Number P14946; former gene
name CuExS1; expansin-29 (Ex29) protein.

45

AAB40636.1 U64892 Pinus taeda

DESCRIPTION: expansin. similar to Arabidopsis expansin encoded by
GenBank

Accession Numbers U30476, U30478, U30480 and U30481, to Cucumis sativus
expansin encoded by GenBank Accession Numbers U30382 and U30460, and to
5 rice expansin encoded by GenBank Accession Numbers U30477 and U30479.

AAC39512.1 AF043284 Gossypium hirsutum

DESCRIPTION: expansin. GhEX1. contains N-terminal signal peptide.
10

CAB43197.1 AJ239068 Lycopersicon esculentum

DESCRIPTION: cell wall loosening enzyme. expansin2. exp2.

15

AAC64201.1 AF096776 Lycopersicon esculentum

DESCRIPTION: expansin. LeEXP2.

20 AAC96081.1 AF049354 Nicotiana tabacum

DESCRIPTION: involved in acid-growth response. alpha-expansin precursor.
Nt-EXP5. cell wall protein.

25 CAB46492.1 AJ243340 Lycopersicon esculentum

DESCRIPTION: expansin9. exp9.

30 AAF17570.1 AF202119 Marsilea quadrifolia

DESCRIPTION: alpha-expansin. EXP1. Mq-EXP1.

AAB81662.1 U85246 Oryza sativa

DESCRIPTION: expansin. Os-EXP4.
35

AAF62180.1 AF247162 Oryza sativa

DESCRIPTION: alpha-expansin OsEXP5. cell wall loosening factor; expressed
in internodes, leaves, coleoptiles, and roots.
40

AAB38074.1 U30477 Oryza sativa

DESCRIPTION: induces extension (creep) in plant cell walls. expansin
Os-EXP2. Os-EXP2. former gene name RiExB.
45

- AAD13632.1 AF059488 *Lycopersicon esculentum*
DESCRIPTION: expansin precursor. Exp4.
- 5 AAF32410.1 AF230277 *Triphysaria versicolor*
DESCRIPTION: alpha-expansin 2.
- 10 AAG01875.1 AF291659 *Striga asiatica*
DESCRIPTION: alpha-expansin 3. Exp3.
- 15 CAA04385.1 AJ000885 *Brassica napus*
DESCRIPTION: Cell wall extension in plants. Expansin.
- 20 CAA06271.2 AJ004997 *Lycopersicon esculentum*
DESCRIPTION: expansin18. exp18.
- BAB32732.1 AB049406 *Eustoma grandiflorum*
DESCRIPTION: expansin. Eg Expansin.
- 25 AAC63088.1 U82123 *Lycopersicon esculentum*
DESCRIPTION: expansin. LeEXP1. fruit ripening regulated expansin.
- 30 AAF62182.1 AF247164 *Oryza sativa*
DESCRIPTION: alpha-expansin OsEXP7. cell wall loosening factor; expressed in internodes and leaves.
- 35 AAB37749.1 U30460 *Cucumis sativus*
DESCRIPTION: expansin S2 precursor. Cs-EXP2. similar to pollen allergen Lol pI, *Lolium perenne*, Swiss-Prot Accession Number P14946; former gene name CuExS2; expansin-30 (Ex30) protein.
- 40 AAG32920.1 AF184232 *Lycopersicon esculentum*
DESCRIPTION: expansin. Exp8.
- 45 CAC06433.1 AJ276007 *Festuca pratensis*
DESCRIPTION: expansin. exp2.

AAF62181.1 AF247163 *Oryza sativa*
DESCRIPTION: alpha-expansin OsEXP6. cell wall loosening factor; expressed
in internodes and leaves.

AAC96079.1 AF049352 *Nicotiana tabacum*
DESCRIPTION: involved in acid-growth response. alpha-expansin precursor.
Nt-EXP3. cell wall protein.

AAC96077.1 AF049350 *Nicotiana tabacum*
DESCRIPTION: involved in acid-growth response. alpha-expansin precursor.
Nt-EXP1. cell wall protein.

BAA88200.1 AP000837 *Oryza sativa*
DESCRIPTION: EST AU078708(E60526) corresponds to a region of the
predicted gene. Similar to expansin (U85246).

AAF17571.1 AF202120 *Regnellidium diphyllum*
DESCRIPTION: alpha-expansin. EXP1. Rd-EXP1.

AAC96078.1 AF049351 *Nicotiana tabacum*
DESCRIPTION: involved in acid-growth response. alpha-expansin precursor.
Nt-EXP2. cell wall protein.

AAG01874.1 AF291658 *Striga asiatica*
DESCRIPTION: alpha-expansin 2. Exp2.

634

AAF63205.1 AF245119 *Mesembryanthemum crystallinum*
DESCRIPTION: AP2-related transcription factor. CDBP. stress induced
transcription factor.

BAA97122.1 AB016264 *Nicotiana sylvestris*
DESCRIPTION: ERF (EREBP); ethylene-responsive element binding factor for
basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive
element binding factor. nserf2.

- BAA07321.1 D38123 *Nicotiana tabacum*
DESCRIPTION: ERF1. ethylene-responsive transcription factor.
- 5 AAG43545.1 AF211527 *Nicotiana tabacum*
DESCRIPTION: Avr9/Cf-9 rapidly elicited protein 1. ACRE1. similar to EREBP transcription factors.
- 10 BAA87068.1 AB035270 *Matricaria chamomilla*
DESCRIPTION: ethylene-responsive element binding protein1 homolog. McEREBP1.
- 15 BAA97124.1 AB016266 *Nicotiana sylvestris*
DESCRIPTION: ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf4.
- 20 AAC62619.1 AF057373 *Nicotiana tabacum*
DESCRIPTION: transcription factor. ethylene response element binding protein 1. EREBP1.
- 25 CAB93940.1 AJ238740 *Catharanthus roseus*
DESCRIPTION: putative transcription factor. AP2-domain DNA-binding protein. orca2.
- 30 AAK31279.1 AC079890 *Oryza sativa*
DESCRIPTION: putative ethylene-responsive element binding protein. OSJNBb0089A17.16.
- 35 AAG60182.1 AC084763 *Oryza sativa*
DESCRIPTION: putative ethylene-responsive element binding protein. OSJNBa0027P10.12.
- 40 CAB96900.1 AJ251250 *Catharanthus roseus*
DESCRIPTION: transcription factor. AP2-domain DNA-binding protein. orca3.
- 45 CAB96899.1 AJ251249 *Catharanthus roseus*
DESCRIPTION: transcription factor. AP2-domain DNA-binding protein. orca3.

5 CAC12822.1 AJ299252 *Nicotiana tabacum*
 DESCRIPTION: AP2 domain-containing transcription factor. ap2.

10 AAF23899.1 AF193803 *Oryza sativa*
 DESCRIPTION: transcription factor EREBP1. EREBP/AP2-like transcription factor.

15 AAF05606.1 AF190770 *Oryza sativa*
 DESCRIPTION: EREBP-like protein. tsh1. TSH1; induced by ethylene.

20 BAA97123.1 AB016265 *Nicotiana sylvestris*
 DESCRIPTION: ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf3.

25 BAA76734.1 AB024575 *Nicotiana tabacum*
 DESCRIPTION: ethylene responsive element binding factor.

30 BAB03248.1 AB037183 *Oryza sativa*
 DESCRIPTION: ERF protein transcriptional repressor. ethylene responsive element binding factor3. osERF3.

35 CAB93939.1 AJ238739 *Catharanthus roseus*
 DESCRIPTION: putative transcription factor. AP2-domain DNA-binding protein. orca1.

40 AAD00708.1 U91857 *Stylosanthes hamata*
 DESCRIPTION: ethylene-responsive element binding protein homolog. similar to EREBP1, -2, -3 and -4 proteins encoded by GenBank Accession Numbers D38123, D38126, D38124, and D38125 respectively.

45 AAG43548.1 AF211530 *Nicotiana tabacum*
 DESCRIPTION: Avr9/Cf-9 rapidly elicited protein 111A. ACRE111A. similar to EREBP transcription factors.

- AAAG43549.1 AF211531 *Nicotiana tabacum*
 DESCRIPTION: Avr9/Cf-9 rapidly elicited protein 111B. ACRE111B. similar
 to EREBP transcription factors.
- 5 AAK31271.1 AC079890 *Oryza sativa*
 DESCRIPTION: putative transcriptional factor. OSJNBb0089A17.22.
- 10 AAK01088.1 AF298230 *Hordeum vulgare*
 DESCRIPTION: CBF1-like protein BCBF1. BCBF1. AP2 domain protein;
 putative
 DRE binding factor.
- 15 AAC49567.1 U41466 *Zea mays*
 DESCRIPTION: Glossy15. Glossy15. AP2 DNA-binding domain protein;
 similar
 to the Arabidopsis floral homeotic gene APETALA2; maize AP2-domain
 20 regulator of leaf epidermal traits; homeotic regulator of leaf epidermal
 cell identity; allele: W64A; putative transcription factor.
- 635

- 25 CAC19789.1 AJ251686 *Catharanthus roseus*
 DESCRIPTION: putative transcription factor. MYB-like DNA-binding protein.
 bpf-1.
- 30 CAA55693.1 X79086 *Zea mays*
 DESCRIPTION: initiator-binding protein. IBP2.
- 35 CAA55691.1 X79085 *Zea mays*
 DESCRIPTION: initiator binding protein. IBP1.
- AAF97508.1 AF242298 *Oryza sativa*
 DESCRIPTION: telomere binding protein-1. TBP1.
- 40 636

- 45 CAB43505.1 AJ239051 *Cicer arietinum*
 DESCRIPTION: cytochrome P450. cyp81E2.

- BAA22422.1 AB001379 *Glycyrrhiza echinata*
DESCRIPTION: cytochrome P450. CYP81E1.
- 5 BAA74465.1 AB022732 *Glycyrrhiza echinata*
DESCRIPTION: cytochrome P450. CYP Ge-31.
- 10 CAA10067.1 AJ012581 *Cicer arietinum*
DESCRIPTION: cytochrome P450. cyp81E3.
- 15 CAB41490.1 AJ238439 *Cicer arietinum*
DESCRIPTION: cytochrome P450 monooxygenase. cyp81E3v2.
- BAA93634.1 AB025016 *Lotus japonicus*
DESCRIPTION: cytochrome P450.
- 20 CAA04117.1 AJ000478 *Helianthus tuberosus*
DESCRIPTION: fatty acid in-chain hydroxylase. cytochrome P450. CYP81B1l.
chimeric sequence (from 5'-race).
- 25 CAA04116.1 AJ000477 *Helianthus tuberosus*
DESCRIPTION: fatty acid in-chain hydroxylase. cytochrome P450. CYP81B1c.
- 30 AAK38080.1 AF321856 *Lolium rigidum*
DESCRIPTION: putative cytochrome P450.
- 35 AAK38079.1 AF321855 *Lolium rigidum*
DESCRIPTION: putative cytochrome P450.
- 40 AAK38081.1 AF321857 *Lolium rigidum*
DESCRIPTION: putative cytochrome P450.
- 45 AAC34853.1 AF082028 *Hemerocallis* hybrid cultivar
DESCRIPTION: putative cyt P450-containing fatty acid hydroxylase.
senescence-associated protein 3. SA3. mRNA accumulates in senescing
petals.

CAA65580.1 X96784 *Nicotiana tabacum*
DESCRIPTION: cytochrome P450. hsr515.

5

CAB56742.1 AJ249800 *Cicer arietinum*
DESCRIPTION: cytochrome P450 monooxygenase. cyp81E5.

10 AAA32913.1 M32885 *Persea americana*
DESCRIPTION: cytochrome P-450LXXIA1 (cyp71A1).

15 BAA12159.1 D83968 *Glycine max*
DESCRIPTION: Cytochrome P-450 (CYP93A1).

20 AAD56282.1 AF155332 *Petunia x hybrida*
DESCRIPTION: flavonoid 3'-hydroxylase. Ht1. cytochrome P450; CYP75B2.

CAA71515.1 Y10491 *Glycine max*
DESCRIPTION: putative cytochrome P450.

25 AAB94590.1 AF022461 *Glycine max*
DESCRIPTION: CYP82C1p. CYP82C1. cytochrome P450 monooxygenase.

30 CAA71516.1 Y10492 *Glycine max*
DESCRIPTION: putative cytochrome P450.

35 CAA64635.1 X95342 *Nicotiana tabacum*
DESCRIPTION: cytochrome P450. hsr515. hypersensitivity-related gene.

40 BAA13076.1 D86351 *Glycine max*
DESCRIPTION: cytochrome P-450 (CYP93A2).

AAG44132.1 AF218296 *Pisum sativum*
DESCRIPTION: cytochrome P450. P450 isolog.

45 AAG09208.1 AF175278 *Pisum sativum*

DESCRIPTION: wound-inducible P450 hydroxylase. CYP82A1.

- 5 AAC49188.2 U29333 *Pisum sativum*
DESCRIPTION: cytochrome P450 monooxygenase. CYP82. new cytochrome P450 family.
- 10 AAD38930.1 AF135485 *Glycine max*
DESCRIPTION: cytochrome P450 monooxygenase CYP93D1. CYP93E1.
- 15 CAA71876.1 Y10982 *Glycine max*
DESCRIPTION: putative cytochrome P450.
- 20 CAA70575.1 Y09423 *Nepeta racemosa*
DESCRIPTION: cytochrome P450. CYP71A5.
- CAA70576.1 Y09424 *Nepeta racemosa*
DESCRIPTION: cytochrome P450. CYP71A6.
- 25 CAA71513.1 Y10489 *Glycine max*
DESCRIPTION: putative cytochrome P450.
- 30 CAA71877.1 Y10983 *Glycine max*
DESCRIPTION: putative cytochrome P450.
- 35 AAB94587.1 AF022458 *Glycine max*
DESCRIPTION: CYP98A2p. CYP98A2. cytochrome P450 monooxygenase.
- 40 AAC39454.1 AF014802 *Eschscholzia californica*
DESCRIPTION: (S)-N-methylcoclaurine 3'-hydroxylase. CYP82B1. cytochrome P-450-dependent monooxygenase; methyl jasmonate-inducible cytochrome P-450-dependent, homologous to wound-inducible CYP82A1 of *Pisum sativum* GenBank Accession Number U29333.
- 45 BAA92894.1 AB006790 *Petunia x hybrida*
DESCRIPTION: cytochrome P450. IMT-2.

5 BAA84072.1 AB028152 *Torenia hybrida*
DESCRIPTION: flavone synthase II. cytochrome P450. TFNS5.

BAA35080.1 AB015762 *Nicotiana tabacum*
DESCRIPTION: putative cytochrome P450. CYP82E1.

10 CAB56743.1 AJ249801 *Cicer arietinum*
DESCRIPTION: cytochrome P450 monooxygenase. cyp81E4.

15 AAB17562.1 U72654 *Eustoma grandiflorum*
DESCRIPTION: flavonoid 3'5'-hydroxylase. F3'5'H. cytochrome P450; CYP75.

20 AAG34695.1 AF313492 *Matthiola incana*
DESCRIPTION: putative cytochrome P450.

25 BAA74466.1 AB022733 *Glycyrrhiza echinata*
DESCRIPTION: cytochrome P450. CYP Ge-51.

BAA22423.1 AB001380 *Glycyrrhiza echinata*
DESCRIPTION: cytochrome P450. CYP93B1.

30 639

AAC06319.1 AF053084 *Malus x domestica*
DESCRIPTION: putative cinnamyl alcohol dehydrogenase. CAD.

35 CAA61275.1 X88797 *Eucalyptus gunnii*
DESCRIPTION: cinnamyl alcohol dehydrogenase. CAD1.

40 640

BAA92916.1 AP001539 *Oryza sativa*
DESCRIPTION: EST C26826(C50159) corresponds to a region of the predicted
gene. Similar to *Arabidopsis thaliana* chromosome II BAC F13A10; putative
ARF1 family auxin responsive transcription factor. (AC006418).

45

AAK21342.1 AC024594 *Oryza sativa*
DESCRIPTION: putative transcription factor. OSJNBa0093B11.2.

5 AAG43286.1 AF140228 *Oryza sativa*
DESCRIPTION: auxin response factor 1.

641

10 CAC24691.1 AJ132363 *Brassica juncea*
DESCRIPTION: efflux carrier of polar auxin transport. pina.

15 AAG17172.1 AF190881 *Populus tremula* x *Populus tremuloides*
DESCRIPTION: PIN1-like auxin transport protein. ppl1.

20 AAC39514.1 AF056027 *Oryza sativa*
DESCRIPTION: auxin transport protein REH1. REH1. potential membrane protein.

642

25 AAG22044.1 AF305783 *Pisum sativum*
DESCRIPTION: apyrase 2. apy2. phosphatase.

30 AAF00610.1 AF156781 *Dolichos biflorus*
DESCRIPTION: apyrase. apyrase-2.

AAG32959.1 AF207687 *Glycine soja*
DESCRIPTION: apyrase GS50.

35 AAG32960.1 AF207688 *Glycine soja*
DESCRIPTION: apyrase GS52.

40 AAF00609.1 AF156780 *Lotus japonicus*
DESCRIPTION: apyrase. nod factor binding lectin-nucleotide phosphohydrolase. LNP.

45 AAD31285.1 AF139807 *Dolichos biflorus*
DESCRIPTION: apyrase. nod factor binding lectin-nucleotide

phosphohydrolase. LNP.

5 AAF00611.1 AF156782 *Medicago sativa*
DESCRIPTION: apyrase. nod factor binding lectin-nucleotide
phosphohydrolase. LNP.

10 AAK15160.1 AF288132 *Medicago truncatula*
DESCRIPTION: putative apyrase. apy1. nucleotide phosphohydrolase; Mtapyl.

15 BAB18896.1 AB038669 *Pisum sativum*
DESCRIPTION: apyrase.

BAB18895.1 AB038668 *Pisum sativum*
DESCRIPTION: apyrase.

20 BAB18894.1 AB038555 *Pisum sativum*
DESCRIPTION: apyrase H-type.

25 BAB18893.1 AB038554 *Pisum sativum*
DESCRIPTION: apyrase S-type.

30 BAB18900.1 AB027614 *Pisum sativum*
DESCRIPTION: apyrase.

35 BAB40230.1 AB027613 *Pisum sativum*
DESCRIPTION: S-type apyras. ATP diphosphohydrolase (apyrase) S-type.

BAB18890.1 AB023621 *Pisum sativum*
DESCRIPTION: apyrase S-type. ATP diphosphohydrolase (apyrase) S-type.

40 BAA75506.1 AB022319 *Pisum sativum*
DESCRIPTION: apyrase. cytoskeleton associated.

45 BAA89275.1 AB027616 *Pisum sativum*
DESCRIPTION: apyrase.

- 5 BAB40231.1 AB027615 *Pisum sativum*
DESCRIPTION: S-type apyrase. ATP diphosphohydrolase (apyrase) S-type.
- AAB02720.1 U58597 *Solanum tuberosum*
DESCRIPTION: catalyzes the hydrolysis of phosphoanhydride bonds of
nucleoside tri- and di- phosphates in the presence of divalent cations.
10 ATP-diphosphohydrolase. RROP1. apyrase, Ecto-ATPase, E-type ATPase;
NTP-diphosphohydrolase.
- 15 AAK15161.1 AF288133 *Medicago truncatula*
DESCRIPTION: putative apyrase. apy4. nucleotide phosphohydrolase; Mtap4.
- 20 BAB18891.1 AB030444 *Pisum sativum*
DESCRIPTION: apyrase. ATP diphosphohydrolase, (EC 3.6.1.5) this sequence
is reported in Acc#:AB022319.
- 25 BAB18892.1 AB030445 *Pisum sativum*
DESCRIPTION: apyrase. ATP diphosphohydrolase, EC 3.6.1.5 this sequence is
reported in Acc#:AB022319, Acc#:AB027613.
- 645

- 30 AAG22044.1 AF305783 *Pisum sativum*
DESCRIPTION: apyrase 2. apy2. phosphatase.
- 35 AAF00610.1 AF156781 *Dolichos biflorus*
DESCRIPTION: apyrase. apyrase-2.
- 40 AAG32959.1 AF207687 *Glycine soja*
DESCRIPTION: apyrase GS50.
- 45 AAG32960.1 AF207688 *Glycine soja*
DESCRIPTION: apyrase GS52.
- 45 AAD31285.1 AF139807 *Dolichos biflorus*
DESCRIPTION: apyrase. nod factor binding lectin-nucleotide

phosphohydrolase. LNP.

5 AAK15160.1 AF288132 *Medicago truncatula*
DESCRIPTION: putative apyrase. apy1. nucleotide phosphohydrolase; Mtapy1.

10 AAF00609.1 AF156780 *Lotus japonicus*
DESCRIPTION: apyrase. nod factor binding lectin-nucleotide
phosphohydrolase. LNP.

15 BAB18896.1 AB038669 *Pisum sativum*
DESCRIPTION: apyrase.

BAB18895.1 AB038668 *Pisum sativum*
DESCRIPTION: apyrase.

20 BAB18894.1 AB038555 *Pisum sativum*
DESCRIPTION: apyrase H-type.

25 BAB18893.1 AB038554 *Pisum sativum*
DESCRIPTION: apyrase S-type.

30 BAB18900.1 AB027614 *Pisum sativum*
DESCRIPTION: apyrase.

35 BAB40230.1 AB027613 *Pisum sativum*
DESCRIPTION: S-type apyras. ATP diphosphohydrolase (apyrase) S-type.

BAB18890.1 AB023621 *Pisum sativum*
DESCRIPTION: apyrase S-type. ATP diphosphohydrolase (apyrase) S-type.

40 BAA75506.1 AB022319 *Pisum sativum*
DESCRIPTION: apyrase. cytoskeleton associated.

45 AAF00611.1 AF156782 *Medicago sativa*
DESCRIPTION: apyrase. nod factor binding lectin-nucleotide

phosphohydrolase. LNP.

- 5 BAA89275.1 AB027616 Pisum sativum
DESCRIPTION: apyrase.
- 10 BAB40231.1 AB027615 Pisum sativum
DESCRIPTION: S-type apyrase. ATP diphosphohydrolase (apyrase) S-type.
- 15 AAB02720.1 U58597 Solanum tuberosum
DESCRIPTION: catalyzes the hydrolysis of phosphoanhydride bonds of
nucleoside tri- and di- phosphates in the presence of divalent cations.
ATP-diphosphohydrolase. RROP1. apyrase, Ecto-ATPase, E-type ATPase;
NTP-diphosphohydrolase.
- 20 AAK15161.1 AF288133 Medicago truncatula
DESCRIPTION: putative apyrase. apy4. nucleotide phosphohydrolase; Mtap4.
- 25 BAB18891.1 AB030444 Pisum sativum
DESCRIPTION: apyrase. ATP diphosphohydrolase, (EC 3.6.1.5) this sequence
is reported in Acc#:AB022319.
- 30 BAB18892.1 AB030445 Pisum sativum
DESCRIPTION: apyrase. ATP diphosphohydrolase, EC 3.6.1.5 this sequence is
reported in Acc#:AB022319, Acc#:AB027613.
- 646

- 35 AAB80947.1 AF022915 Triticum aestivum
DESCRIPTION: ornithine/acetylornithine aminotransferase.
- 40 CAA69936.1 Y08680 Alnus glutinosa
DESCRIPTION: acetylornithine aminotransferase. ag118.
- 45 AAK11219.1 AF324485 Oryza sativa
DESCRIPTION: aminotransferase-like protein.
- AAG09278.1 AF177590 Vitis vinifera

DESCRIPTION: ornithine aminotransferase.

AAC78480.1 AF085149 Capsicum chinense

5 DESCRIPTION: putative aminotransferase. pyridoxal phosphate dependent.

AAA02916.1 L08400 Vigna aconitifolia

10 DESCRIPTION: production of pyrroline-5-carboxylate by deamination of
ornithine. ornithine aminotransferase.

AAB59330.1 M31545 Hordeum vulgare

15 DESCRIPTION: glutamate 1-semialdehyde aminotransferase. GSA. precursor.

AAA18861.1 U03632 Chlamydomonas reinhardtii

20 DESCRIPTION: glutamate-1-semialdehyde aminotransferase. gsa.

AAA33968.1 L12453 Glycine max

25 DESCRIPTION: catalyzes 5-aminolevulinic acid formation from GSA.
glutamate 1-semialdehyde aminotransferase. Gsa. putative.

AAC48996.1 U20260 Glycine max

30 DESCRIPTION: converts GSA to 5-aminolevulinic acid. glutamate
1-semialdehyde aminotransferase. Gsa1.

650

AAF66982.1 AF247646 Zea mays

DESCRIPTION: transposase. similar to Mutator family transposases.

35 652

AAB41812.1 L36158 Medicago sativa

40 DESCRIPTION: peroxidase. pxdD. amino acid feature: conserved domains, aa
120 .. 126, 188 .. 195; amino acid feature: heme-binding domain, aa 63 ..
68.

CAA71495.1 Y10469 Spinacia oleracea

45 DESCRIPTION: peroxidase. prxr8.

CAA09881.1 AJ011939 *Trifolium repens*
DESCRIPTION: peroxidase. prx2.

5 CAA62228.1 X90695 *Medicago sativa*
DESCRIPTION: peroxidase2. prx2.

10 AAA98491.1 L36981 *Petroselinum crispum*
DESCRIPTION: anionic peroxidase.

15 BAB39281.1 AP002971 *Oryza sativa*
DESCRIPTION: putative peroxidase. P0537A05.10. contains ESTs
D24657(R2329),AU082066(R2329).

20 AAB02926.1 U59284 *Linum usitatissimum*
DESCRIPTION: peroxidase. FLXPER3.

BAA77387.1 AB024437 *Scutellaria baicalensis*
DESCRIPTION: peroxidase 1.

25 CAA66037.1 X97351 *Populus balsamifera* subsp. *trichocarpa*
DESCRIPTION: signal for ER. peroxidase.

30 CAA71488.1 Y10462 *Spinacia oleracea*
DESCRIPTION: peroxidase. prxr1.

35 BAA01950.1 D11337 *Vigna angularis*
DESCRIPTION: peroxidase.

40 BAA14143.1 D90115 *Armoracia rusticana*
DESCRIPTION: peroxidase isozyme.

CAA71490.1 Y10464 *Spinacia oleracea*
DESCRIPTION: peroxidase. prxr3.

45 CAB94692.1 AJ242742 *Ipomoea batatas*

DESCRIPTION: Removal of H₂O₂, oxidation of toxic reductants, defence response toward wounding. peroxidase. pod.

- 5 BAA92497.1 AP001383 *Oryza sativa*
DESCRIPTION: ESTs AU081576(R0541),AU032412(R4029) correspond to a region
of the predicted gene. Similar to peroxidase ATP18a. (X98804).
- 10 AAC36707.1 AF078691 *Manihot esculenta*
DESCRIPTION: peroxidase.
- 15 BAA92422.1 AP001366 *Oryza sativa*
DESCRIPTION: ESTs AU081576(R0541),AU032412(R4029) correspond to a region
of the predicted gene. Similar to *A.thaliana* mRNA for peroxidase ATP18a.
(X98804).
- 20 CAA62226.1 X90693 *Medicago sativa*
DESCRIPTION: peroxidase1B. prx1B.
- 25 AAF63024.1 AF244921 *Spinacia oleracea*
DESCRIPTION: hydrogen peroxide catabolism. peroxidase prx12 precursor.
type III peroxidase.
- 30 AAA32676.1 M37637 *Arachis hypogaea*
DESCRIPTION: cationic peroxidase. PNC2.
- 35 BAA11853.1 D83225 *Populus nigra*
DESCRIPTION: peroxidase.
- 40 CAC21393.1 AJ401276 *Zea mays*
DESCRIPTION: peroxidase. pox3.
- 45 AAA65636.1 L13653 *Lycopersicon esculentum*
DESCRIPTION: peroxidase. TPX2.

- CAB67121.1 Y19023 *Lycopersicon esculentum*
DESCRIPTION: peroxidase. cevi-1.
- 5 CAA62227.1 X90694 *Medicago sativa*
DESCRIPTION: peroxidase1C. prx1C.
- 10 CAA50597.1 X71593 *Lycopersicon esculentum*
DESCRIPTION: peroxidase. CEVI-1.
- 15 AAD37376.1 AF145350 *Glycine max*
DESCRIPTION: peroxidase. Prx4.
- AAB67737.1 L77080 *Stylosanthes humilis*
DESCRIPTION: cationic peroxidase.
- 20 CAA71489.1 Y10463 *Spinacia oleracea*
DESCRIPTION: peroxidase. prxr2.
- 25 CAA71496.1 Y10470 *Spinacia oleracea*
DESCRIPTION: peroxidase. prxr9.
- 30 CAA71494.1 Y10468 *Spinacia oleracea*
DESCRIPTION: peroxidase. prxr7.
- 35 BAA06334.1 D30652 *Populus kitakamiensis*
DESCRIPTION: peroxidase.
- CAA66034.1 X97348 *Populus balsamifera* subsp. *trichocarpa*
DESCRIPTION: signal for ER. peroxidase.
- 40 BAA94962.1 AB042103 *Asparagus officinalis*
DESCRIPTION: peroxidase. AspPOX1.
- 45 CAA80502.1 Z22920 *Spirodela polyrrhiza*
DESCRIPTION: peroxidase.

- CAA66035.1 X97349 *Populus balsamifera* subsp. *trichocarpa*
DESCRIPTION: signal for ER. peroxidase.
- 5
- BAA11852.1 D83224 *Populus nigra*
DESCRIPTION: peroxidase.
- 10
- CAA66036.1 X97350 *Populus balsamifera* subsp. *trichocarpa*
DESCRIPTION: signal for ER. peroxidase.
- 15
- BAA07241.1 D38051 *Populus kitakamiensis*
DESCRIPTION: peroxidase. prxA4a.
- 20
- AAD11481.1 U51191 *Glycine max*
DESCRIPTION: peroxidase precursor. sEPa1.
- 25
- AAC98519.1 AF007211 *Glycine max*
DESCRIPTION: peroxidase precursor. GMIPER1. pathogen-induced.
- 30
- AAA32973.1 M73234 *Hordeum vulgare*
DESCRIPTION: peroxidase BP 1. Prx5.
- 35
- AAB47602.1 L07554 *Linum usitatissimum*
DESCRIPTION: peroxidase. FLXPER1.
- 40
- AAB41810.1 L36156 *Medicago sativa*
DESCRIPTION: peroxidase. pxdA. amino acid feature: conserved motifs, aa 181 .. 188; amino acid feature: heme-binding domain, aa 60 .. 65.
- 45
- AAF63027.1 AF244924 *Spinacia oleracea*
DESCRIPTION: hydrogen peroxide catabolism. peroxidase prx15 precursor. type III peroxidase.
- AAA34108.1 J02979 *Nicotiana tabacum*
DESCRIPTION: lignin-forming peroxidase precursor (EC 1.11.1.7).

- AAD43561.1 AF155124 *Gossypium hirsutum*
 DESCRIPTION: bacterial-induced peroxidase precursor. Perx_Goshiko.
- 5 653
-
- AAB97617.1 U83687 *Apium graveolens*
 DESCRIPTION: NADPH-dependent mannose 6-phosphate reductase. m6pr.
 10 aldo-keto reductase; similar to aldose 6-phosphate reductase also known as
 NADP-sorbitol-6-phosphate dehydrogenase encoded by GenBank Accession
 Number D11080.
- 15 BAA01853.1 D11080 *Malus x domestica*
 DESCRIPTION: NADP-dependent D-sorbitol-6-phosphate dehydrogenase.
 S6PDH.
- 20 AAC97607.1 AF057134 *Malus x domestica*
 DESCRIPTION: synthesizes sorbitol, a major photosynthetic product in many
 members of the Rosaceae family. NADP-dependent sorbitol 6-phosphate
 dehydrogenase. S6PDH.
- 25 654
-
- BAA82556.1 AB030083 *Populus nigra*
 DESCRIPTION: lectin-like protein kinase. PnLPK.
- 30
- AAB61708.1 U93048 *Daucus carota*
 DESCRIPTION: somatic embryogenesis receptor-like kinase. SERK.
- 35 BAB19337.1 AP003044 *Oryza sativa*
 DESCRIPTION: putative protein kinase. P0038C05.10. contains ESTs
 AU056335(S20481),AU056336(S20481).
- 40 AAK21965.1 AY028699 *Brassica napus*
 DESCRIPTION: receptor protein kinase PERK1.
- 45 BAB39873.1 AP002882 *Oryza sativa*
 DESCRIPTION: putative protein kinase. P0439B06.8. contains ESTs
 AU056701(S20808),AU056702(S20808).

AAB93834.1 U82481 Zea mays
 DESCRIPTION: KI domain interacting kinase 1. KIK1. receptor-like protein
 5 kinase; serine/threonine protein kinase.

BAB18292.1 AP002860 Oryza sativa
 DESCRIPTION: putative receptor-like protein kinase. P0409B08.19.
 10

AAK00425.1 AC069324 Oryza sativa
 DESCRIPTION: Putative protein kinase. OSJNBa0071K19.11.
 15

AAD21872.1 AF078082 Phaseolus vulgaris
 DESCRIPTION: receptor-like protein kinase homolog RK20-1.
 20

AAC23542.1 U20948 Ipomoea trifida
 DESCRIPTION: receptor protein kinase. IRK1.
 25

CAA73134.1 Y12531 Brassica oleracea
 DESCRIPTION: serine/threonine kinase. BRLK.
 30

CAB51480.1 Y14600 Sorghum bicolor
 DESCRIPTION: putative protein serine /threonine kinase. RLK1. accumulates
 in mesophyll cells.
 35

AAG59657.1 AC084319 Oryza sativa
 DESCRIPTION: putative protein kinase. OSJNBa0004B24.20.
 40

BAB16871.1 AP002537 Oryza sativa
 DESCRIPTION: putative protein kinase APK1AArabidopsis thaliana.
 P0001B06.24. contains ESTs C22608(R3192),D25110(R3192).
 45

CAB51834.1 00069 Oryza sativa
 DESCRIPTION: I1332.5. contains eukaryotic protein kinase domain PF.
 50

BAA94509.1 AB041503 Populus nigra
 55

DESCRIPTION: protein kinase 1. PnPK1.

5 AAG16628.1 AY007545 Brassica napus
DESCRIPTION: protein serine/threonine kinase BNK1.

10 BAA87853.1 AP000816 Oryza sativa
DESCRIPTION: EST AU030604(E51294) corresponds to a region of the
predicted gene. Similar to putative NAK-like Ser/Thr protein kinase.
(AF001308).

15 BAB03429.1 AP002817 Oryza sativa
DESCRIPTION: EST C22619(S11214) corresponds to a region of the predicted
gene. Similar to Arabidopsis thaliana chromosome 2, BAC clone T17D12;
putative protein kinase (AC006587).

20 BAB07999.1 AP002525 Oryza sativa
DESCRIPTION: putative protein kinase. P0462H08.22. contains EST
C22619(S11214).

25 BAB21240.1 AP002953 Oryza sativa
DESCRIPTION: Putative protein kinase. P0426D06.20. contains ESTs
C22359(C11461),C22360(C11461).

30 BAA92954.1 AP001551 Oryza sativa
DESCRIPTION: Similar to Oryza sativa protein kinase (OSPK10) mRNA.
(L27821).

35 BAA94510.1 AB041504 Populus nigra
DESCRIPTION: protein kinase 2. PnPK2.

40 AAG03090.1 AC073405 Oryza sativa
DESCRIPTION: Similar to an Arabidopsis somatic embryogenesis
receptor-like kinase (AC007504).

45 AAF91322.1 AF244888 Glycine max
DESCRIPTION: receptor-like protein kinase 1. RLK1. GmRLK1.

- 5 BAA94517.1 AP001800 *Oryza sativa*
DESCRIPTION: Similar to *Zea mays* S-domain receptor-like protein kinase (AJ010166).
- 10 BAB07905.1 AP002835 *Oryza sativa*
DESCRIPTION: putative S-receptor kinase. P0417G05.13.
- 15 CAB51836.1 AJ243961 *Oryza sativa*
DESCRIPTION: Putative Ser/Thr protein kinase. 11332.7.
- 20 BAA78764.1 AB023482 *Oryza sativa*
DESCRIPTION: ESTs C98382(C2985),D22444(C11129) correspond to a region of
the predicted gene.; Similar to *Arabidopsis thaliana* APK1 gene for protein
tyrosine-serine-threonine kinase.(D12522).
- 25 AAA33915.1 L27821 *Oryza sativa*
DESCRIPTION: receptor type serine/threonine kinase. protein kinase.
- 30 AAF91323.1 AF244889 *Glycine max*
DESCRIPTION: receptor-like protein kinase 2. RLK2. GmRLK2.
- 35 CAA67145.1 X98520 *Brassica oleracea*
DESCRIPTION: receptor-like kinase. SFR2.
- 40 CAA73133.1 Y12530 *Brassica oleracea*
DESCRIPTION: serine /threonine kinase. ARLK.
- 45 AAF91324.1 AF244890 *Glycine max*
DESCRIPTION: receptor-like protein kinase 3. RLK3. GmRLK3.
- CAA74661.1 Y14285 *Brassica oleracea*
DESCRIPTION: SFR1. extracellular S domain: 8-1342; transmembrane domain: 1343-1411; intracellular kinase domain: 1412-2554.

BAA92953.1 AP001551 *Oryza sativa*
 DESCRIPTION: Similar to *Arabidopsis thaliana* chromosome 4 BAC clone
 F10M6
 ; S-receptor kinase -like protein. (AL021811).
 5

BAB40094.1 AP003210 *Oryza sativa*
 DESCRIPTION: putative receptor protein kinase. OSJNBa0010K01.7.
 10

AAF43496.1 AF131222 *Lophopyrum elongatum*
 DESCRIPTION: protein serine/threonine kinase. ESI47. induced in roots by
 salt stress, osmotic stress, and ABA treatment.
 15

AAK11674.1 AF339747 *Lophopyrum elongatum*
 DESCRIPTION: protein kinase. ESI47.
 20

BAB07906.1 AP002835 *Oryza sativa*
 DESCRIPTION: putative S-receptor kinase. P0417G05.14.
 25

BAA94516.1 AP001800 *Oryza sativa*
 DESCRIPTION: Similar to *Zea mays* S-domain receptor-like protein kinase
 (AJ010166).
 30

CAB41878.1 Y18259 *Brassica oleracea*
 DESCRIPTION: SRK5 protein. SRK5. receptor-like kinase.
 35

BAA23676.1 AB000970 *Brassica rapa*
 DESCRIPTION: receptor kinase 1. BcRK1.
 40

CAB41879.1 Y18260 *Brassica oleracea*
 DESCRIPTION: SRK15 protein. SRK15. receptor-like kinase.
 45

655

 AAD21872.1 AF078082 *Phaseolus vulgaris*
 DESCRIPTION: receptor-like protein kinase homolog RK20-1.
 45

CAA73134.1 Y12531 *Brassica oleracea*

DESCRIPTION: serine/threonine kinase. BRLK.

CAA67145.1 X98520 Brassica oleracea
5 DESCRIPTION: receptor-like kinase. SFR2.

CAA73133.1 Y12530 Brassica oleracea
10 DESCRIPTION: serine /threonine kinase. ARLK.

AAB93834.1 U82481 Zea mays
15 DESCRIPTION: KI domain interacting kinase 1. KIK1. receptor-like protein
kinase; serine/threonine protein kinase.

BAA23676.1 AB000970 Brassica rapa
20 DESCRIPTION: receptor kinase 1. BcRK1.

AAC23542.1 U20948 Ipomoea trifida
DESCRIPTION: receptor protein kinase. IRK1.

25 CAB41879.1 Y18260 Brassica oleracea
DESCRIPTION: SRK15 protein. SRK15. receptor-like kinase.

CAA74662.1 Y14286 Brassica oleracea
30 DESCRIPTION: SFR3. extracellular S domain: 123-1346; transmembrane
domain: 1347-1412; intracellular kinase domain: from 1413.

CAB89179.1 AJ245479 Brassica napus subsp. napus
35 DESCRIPTION: ser /thr kinase. S-locus receptor kinase. srk.

AAA33008.1 M97667 Brassica napus
40 DESCRIPTION: serine/threonine kinase receptor.

AAA62232.1 U00443 Brassica napus
45 DESCRIPTION: S-receptor kinase. protein contains an immunoglobulin-like
domain.

CAA74661.1 Y14285 Brassica oleracea
DESCRIPTION: SFR1. extracellular S domain: 8-1342; transmembrane domain:
1343-1411; intracellular kinase domain: 1412-2554.

5

AAA33000.1 M76647 Brassica oleracea
DESCRIPTION: receptor protein kinase. SKR6.

10

CAA79355.1 Z18921 Brassica oleracea
DESCRIPTION: S-receptor kinase-like protein.

15

CAB41878.1 Y18259 Brassica oleracea
DESCRIPTION: SRK5 protein. SRK5. receptor-like kinase.

20

BAA07576.1 D38563 Brassica rapa
DESCRIPTION: receptor protein kinase SRK8.

25

BAA06285.1 D30049 Brassica rapa
DESCRIPTION: S-receptor kinase SRK9.

BAA21132.1 D88193 Brassica rapa
DESCRIPTION: S-receptor kinase. SRK9 (B.c).

30

BAA07577.2 D38564 Brassica rapa
DESCRIPTION: receptor protein kinase SRK12.

35

BAA92836.1 AB032473 Brassica oleracea
DESCRIPTION: S18 S-locus receptor kinase. SRK18.

40

BAB21001.1 AB054061 Brassica rapa
DESCRIPTION: S locus receptor kinase. SRK22.

BAA92837.1 AB032474 Brassica oleracea
DESCRIPTION: S60 S-locus receptor kinase. SRK60.

45

BAB18292.1 AP002860 Oryza sativa

DESCRIPTION: putative receptor-like protein kinase. P0409B08.19.

AAD52097.1 AF088885 *Nicotiana tabacum*

5 DESCRIPTION: receptor-like kinase CHRK1. Chrkl.

BAB39873.1 AP002882 *Oryza sativa*

10 DESCRIPTION: putative protein kinase. P0439B06.8. contains ESTs
AU056701(S20808),AU056702(S20808).

AAK21965.1 AY028699 *Brassica napus*

15 DESCRIPTION: receptor protein kinase PERK1.

AAA33915.1 L27821 *Oryza sativa*

20 DESCRIPTION: receptor type serine/threonine kinase. protein kinase.

AAK00425.1 AC069324 *Oryza sativa*

DESCRIPTION: Putative protein kinase. OSJNBa0071K19.11.

25 BAA94529.2 AP001800 *Oryza sativa*

DESCRIPTION: Similar to *Zea mays* S-domain receptor-like protein kinase
(AJ010166).

30 BAB16871.1 AP002537 *Oryza sativa*

DESCRIPTION: putative protein kinase APK1A*Arabidopsis thaliana*.
P0001B06.24. contains ESTs C22608(R3192),D25110(R3192).

35 AAF34428.1 AF172282 *Oryza sativa*

DESCRIPTION: receptor-like protein kinase. DUPR11.18.

AAG03090.1 AC073405 *Oryza sativa*

40 DESCRIPTION: Similar to an *Arabidopsis* somatic embryogenesis
receptor-like kinase (AC007504).

BAB21240.1 AP002953 *Oryza sativa*

45 DESCRIPTION: Putative protein kinase. P0426D06.20. contains ESTs
C22359(C11461),C22360(C11461).

- 5 BAA87853.1 AP000816 *Oryza sativa*
DESCRIPTION: EST AU030604(E51294) corresponds to a region of the
predicted gene. Similar to putative NAK-like Ser/Thr protein kinase.
(AF001308).
- 10 BAA94516.1 AP001800 *Oryza sativa*
DESCRIPTION: Similar to *Zea mays* S-domain receptor-like protein kinase
(AJ010166).
- 15 BAB07905.1 AP002835 *Oryza sativa*
DESCRIPTION: putative S-receptor kinase. P0417G05.13.
- 20 BAB07906.1 AP002835 *Oryza sativa*
DESCRIPTION: putative S-receptor kinase. P0417G05.14.
657

- 25 AAF43869.1 AF166114 Chloroplast *Mesostigma viride*
DESCRIPTION: probable transport protein. cysA.
- 30 BAB17113.1 AP002866 *Oryza sativa*
DESCRIPTION: putative white protein; ATP-binding cassette transporter.
P0410E01.34.
- 35 BAA57907.1 AB001684 *Chlorella vulgaris*
DESCRIPTION: sulfate transport system permease protein. cysA.
- AAD54843.1 AF137379 Chloroplast *Nephroselmis olivacea*
DESCRIPTION: probable transport protein. cysA.
- 40 BAA90508.1 AP001111 *Oryza sativa*
DESCRIPTION: similar to ABC transporter of *Arabidopsis thaliana*
(AC004697).
- 45 BAA90507.1 AP001111 *Oryza sativa*
DESCRIPTION: similar to ABC transporter of *Arabidopsis thaliana*

(AC004697).

- 5 BAA83352.1 AP000391 *Oryza sativa*
DESCRIPTION: ESTs AU067992(C11433),AU077424(C11433) correspond to
a region of the predicted gene.; Similar to ABC transporter-7 (U43892).
- 10 AAG49003.1 AY013246 *Hordeum vulgare*
DESCRIPTION: putative ABC transporter. 635P2.4b; GC splice donor
confirmed by cDNA alignment and comparative sequence.
- 15 AAD10836.1 U52079 *Solanum tuberosum*
DESCRIPTION: P-glycoprotein. pmdr1. binds ATP; ATPase; transporter;
transmembrane protein.
- 20 BAA96612.1 AP002482 *Oryza sativa*
DESCRIPTION: Similar to *Arabidopsis thaliana* chromosome 2, BAC F14M4 ;
putative ABC transporter (AC004411).
- 25 BAB40032.1 AP003046 *Oryza sativa*
DESCRIPTION: putative ABC transporter. P0445D12.3.
- 30 AAG45492.1 AY013245 *Oryza sativa*
DESCRIPTION: 36I5.4. putative ABC transporter; GC splice donor confirmed
by cDNA alignment and comparative sequence.
- 35 AAG49002.1 AY013246 *Hordeum vulgare*
DESCRIPTION: putative ABC transporter. 635P2.4a; GC splice donor
confirmed by cDNA and comparative sequencing.
- 40 BAB21275.1 AP002844 *Oryza sativa*
DESCRIPTION: putative ABC transporter protein. P0410E03.6.
- 45 BAB21273.1 AP002844 *Oryza sativa*
DESCRIPTION: putative ABC transporter protein. P0410E03.4.

- 5 AAA51643.1 M23120 *Nicotiana plumbaginifolia*
DESCRIPTION: beta-glucanase precursor.
- 10 AAA34078.1 M63634 *Nicotiana plumbaginifolia*
DESCRIPTION: regulator of beta(1,3)-glucanase. beta(1,3)-glucanase
regulator.
- 15 AAB82772.2 AF001523 *Musa acuminata*
DESCRIPTION: beta-1, 3-glucanase. similar to beta-1, 3-glucanase.
- 20 AAF08679.1 AF004838 *Musa acuminata*
DESCRIPTION: beta-1,3-glucanase.
- 25 CAB71021.1 AJ271598 *Hieracium piloselloides*
DESCRIPTION: putative role in callose degradation. putative
beta-1,3-glucanase. gluc.
- 30 AAD10383.1 U72252 *Oryza sativa*
DESCRIPTION: beta-1,3-glucanase precursor. Gns6.
- AAD28732.1 AF112965 *Triticum aestivum*
DESCRIPTION: beta-1,3-glucanase precursor. Glb3.
- 35 BAB40807.1 AB052291 *Pyrus pyrifolia*
DESCRIPTION: catalyzing the hydrolysis of 1,3-beta-glucosyl linkages.
endo-1,3-beta-glucanase-like protein. bgn-1. Amino acid alignment of the
protein(BGN-1) encoded by pear pollen bgn-1 with barley
endo-1,3-beta-glucanase(GII. accession number: pdb/1GHS-B/2.3/2/306/N/)(40%
identity) and their hydrophobic cluster analysis(HCA)(a overall HCA
homology score of 87.1%) showed that it was most likely that the bgn-1
40 encoded a endo-1,3-beta-glucanase. A higher identity(59.3%) was found
between BGN-1 and a putative pea endo-1,3-beta-glucanase (accession
number:dad/AJ251646-1).
- 45 AAA63539.1 M60402 *Nicotiana tabacum*
DESCRIPTION: glucan beta-1,3-glucanase. glucanase GLA.

AAA63541.1 M59442 *Nicotiana tabacum*
 DESCRIPTION: basic beta-1,3-glucanase. glucanase.
 5

AAA63540.1 M60403 *Nicotiana tabacum*
 DESCRIPTION: glucan-1,3-beta-glucosidase. glucanase GLB.
 10

AAA32939.1 M62907 *Hordeum vulgare*
 DESCRIPTION: hydrolysis of beta-(1-3)-glucan. (1-3)-beta-glucanase.
 cBGL32.
 15

AAC14399.1 AF030771 *Hordeum vulgare*
 DESCRIPTION: beta-1,3-glucanase 2. BGL32.
 20

AAA87456.1 U22147 *Hevea brasiliensis*
 DESCRIPTION: beta-1,3-glucanase. HGN1. hydrolytic enzyme.
 25

BAA77784.1 AB027429 *Oryza sativa*
 DESCRIPTION: beta-1,3-glucanase.
 30

BAA77785.1 AB027430 *Oryza sativa*
 DESCRIPTION: beta-1,3-glucanase.
 35

CAB91554.1 AJ277900 *Vitis vinifera*
 DESCRIPTION: beta 1-3 glucanase. gl.
 40

AAD10381.1 U72250 *Oryza sativa*
 DESCRIPTION: beta-1,3-glucanase precursor. Gns4.
 45

AAA33946.1 M37753 *Glycine max*
 DESCRIPTION: beta-1,3-endoglucanase (EC 3.2.1.39).
 45

AAD33881.1 AF141654 *Nicotiana tabacum*
 DESCRIPTION: beta-1,3-glucanase. GGL4.

AAB86541.1 AF030166 *Oryza sativa*
DESCRIPTION: glucanase. glu1.

5

AAD10384.1 U72253 *Oryza sativa*
DESCRIPTION: beta-1,3-glucanase precursor. Gns7.

10 CAB38443.1 AJ133470 *Hevea brasiliensis*
DESCRIPTION: beta-1,3-glucanase. hgn1.

15 AAB03501.1 U41323 *Glycine max*
DESCRIPTION: beta-1,3-glucanase. SGN1.

20 AAA18928.1 U01901 *Solanum tuberosum*
DESCRIPTION: catalyzes the hydrolysis of 1,3-beta-D-glucoside linkages in
1,3,-beta-D-glucans (such as laminarin). 1,3-beta-D-glucan
glucanohydrolase; endo-1,3-beta-D-glucanase; 1,3-beta-glucanase (basic,
class I). glub2. plant defense gene; induced expression in response to
infection, elicitor, ethylene, wounding.

25

AAA88794.1 U01900 *Solanum tuberosum*
DESCRIPTION: catalyzes the hydrolysis of 1,3-beta-D-glucoside linkages in
1,3,-beta-D-glucans (such as laminarin). 1,3-beta-D-glucan
glucanohydrolase; endo-1,3-beta-D-glucanase; 1,3-beta-glucanase (basic,
class I). gluB1. plant defense gene; induced expression in response to
infection, elicitor, ethylene, wounding.

35 AAC19114.1 AF067863 *Solanum tuberosum*
DESCRIPTION: 1,3-beta-glucan glucanohydrolase. glucanase.

40 AAG24921.1 AF311749 *Hevea brasiliensis*
DESCRIPTION: beta-1,3-glucanase.

CAA03908.1 AJ000081 *Citrus sinensis*
DESCRIPTION: glucan hydrolase. beta-1,3-glucanase. gns1.

45

CAA37289.1 X53129 *Phaseolus vulgaris*

DESCRIPTION: 1,3,-beta-D-glucanase.

CAA57255.1 X81560 Nicotiana tabacum
5 DESCRIPTION: (1-)-beta-glucanase. Sp41a.

659

AAB65776.1 U97521 Vitis vinifera
10 DESCRIPTION: class IV endochitinase. VvChi4A.

AAB65777.1 U97522 Vitis vinifera
15 DESCRIPTION: class IV endochitinase. VvChi4B.

BAA03751.1 D16223 Oryza sativa
20 DESCRIPTION: endochitinase. Cht-3.

CAA30142.1 X07130 Solanum tuberosum
DESCRIPTION: endochitinase.

BAA03749.1 D16221 Oryza sativa
25 DESCRIPTION: endochitinase. Cht-1.

660

30 AAF07221.1 AF072519 Nicotiana tabacum
DESCRIPTION: centrin. CEN1. caltractin; EF-hand domain calcium-binding
protein.

35 AAF07222.1 AF072520 Nicotiana tabacum
DESCRIPTION: centrin. CEN2. caltractin; EF-hand domain calcium-binding
protein.

40 CAA49153.1 X69220 Scherffelia dubia
DESCRIPTION: caltractin.

AAC04626.1 U92973 Marsilea vestita
45 DESCRIPTION: calcium-binding protein. centrin. MvCen1. caltractin.

AAB67855.1 U53812 *Dunaliella salina*
DESCRIPTION: caltractin-like protein.

5

CAA41039.1 X57973 *Chlamydomonas reinhardtii*
DESCRIPTION: caltractin.

10 CAA31163.1 X12634 *Chlamydomonas reinhardtii*
DESCRIPTION: caltractin (AA 1 - 169).

664

15 BAB16432.1 AB041520 *Nicotiana tabacum*
DESCRIPTION: WRKY transcription factor Nt-SubD48. Nt-SubD48.

20 AAC49528.1 U56834 *Petroselinum crispum*
DESCRIPTION: DNA-binding. WRKY3. WRKY-type DNA-binding protein.

25 AAD27591.1 AF121354 *Petroselinum crispum*
DESCRIPTION: binds sequence specifically to W Boxes (TTGACC).
transcription factor. WRKY3. sequence specific DNA-binding protein.

30 AAD32676.1 AF140553 *Avena sativa*
DESCRIPTION: DNA-binding protein WRKY3. wrky3. putative transcription
factor.

35 BAA77358.1 AB020023 *Nicotiana tabacum*
DESCRIPTION: WRKY domain Zn-finger type DNA-binding protein. DNA-
binding
protein NtWRKY3.

40 AAG46150.1 AC018727 *Oryza sativa*
DESCRIPTION: putative DNA-binding protein. OSJNBa0056G17.18.

45 BAB40073.1 AP003074 *Oryza sativa*
DESCRIPTION: putative WRKY DNA binding protein. OSJNBa0004G10.20.
contains EST C26525(C12525).

- BAB18313.1 AP002865 *Oryza sativa*
 DESCRIPTION: putative WRKY DNA binding protein. P0034C11.1. contains
 EST
 5 C26525(C12525).
- AAD38283.1 AC007789 *Oryza sativa*
 DESCRIPTION: putative WRKY DNA binding protein. OSJNBa0049B20.9.
 10
- BAA77383.1 AB020590 *Nicotiana tabacum*
 DESCRIPTION: transcription factor NtWRKY2.
 15
- BAA82107.1 AB022693 *Nicotiana tabacum*
 DESCRIPTION: transcription factor. NtWRKY1.
 20
- CAA88326.1 Z48429 *Avena fatua*
 DESCRIPTION: binds conserved cis-element from cereal alpha-Amy2
 promoters. DNA-binding protein.
 25
- AAD32677.1 AF140554 *Avena sativa*
 DESCRIPTION: DNA-binding protein WRKY1. wrky1. putative transcription
 factor.
 30
- AAD55974.1 AF121353 *Petroselinum crispum*
 DESCRIPTION: zinc-finger type transcription factor WRKY1. WRKY1.
 35
- AAC49529.1 U58540 *Petroselinum crispum*
 DESCRIPTION: WRKY2. Contains two WRKY domains; WRKY-type DNA-
 binding
 protein.
 40
- AAC49527.1 U48831 *Petroselinum crispum*
 DESCRIPTION: WRKY1. contains two WRKY domains; WRKY-type DNA-
 binding
 protein; sequence-specific DNA-binding protein.
 45
- AAC31956.1 AF080595 *Pimpinella brachycarpa*

DESCRIPTION: zinc finger protein. ZFP1. WRKY1.

5 BAA86031.1 AB026890 *Nicotiana tabacum*
DESCRIPTION: transcription factor NtWRKY4.

10 AAD16139.1 AF096299 *Nicotiana tabacum*
DESCRIPTION: DNA-binding protein 2. WRKY2. transcription factor.

AAF23898.1 AF193802 *Oryza sativa*
DESCRIPTION: zinc finger transcription factor WRKY1.

15 AAD16138.1 AF096298 *Nicotiana tabacum*
DESCRIPTION: DNA-binding protein 1. WRKY1. transcription factor.

20 AAC37515.1 L44134 *Cucumis sativus*
DESCRIPTION: SPF1-like DNA-binding protein.

25 AAG35658.1 AF204925 *Petroselinum crispum*
DESCRIPTION: transcription factor WRKY4. WRKY4. binds to W box
(TTGACC)
elements.

30 CAA88331.1 Z48431 *Avena fatua*
DESCRIPTION: binds conserved cis-element from cereal alpha-Amy2
promoters. DNA-binding protein.

35 BAB19075.1 AP002744 *Oryza sativa*
DESCRIPTION: putative DNA-binding protein homolog. P0006C01.17.

40 BAB19096.1 AP002839 *Oryza sativa*
DESCRIPTION: putative DNA-binding protein homolog. P0688A04.2.

45 AAK16170.1 AC079887 *Oryza sativa*
DESCRIPTION: putative DNA binding protein. OSJNBa0040E01.4.

AAK16171.1 AC079887 *Oryza sativa*
DESCRIPTION: putative DNA-binding protein. OSJNBa0040E01.10.

5 AAG35659.1 AF204926 *Petroselinum crispum*
DESCRIPTION: transcription factor WRKY5. WRKY5. binds to W box
(TTGACC)
elements.

10 CAB97004.1 AJ278507 *Solanum tuberosum*
DESCRIPTION: putative transcription factor. WRKY DNA binding protein.
WRKY1.

15 AAF61864.1 AF193771 *Nicotiana tabacum*
DESCRIPTION: DNA-binding protein 4. WRKY4. transcription factor.

20 BAA87069.1 AB035271 *Matricaria chamomilla*
DESCRIPTION: elicitor-induced DNA-binding protein homolog. McWRKY1.

25 AAF61863.1 AF193770 *Nicotiana tabacum*
DESCRIPTION: DNA-binding protein 3. WRKY3. transcription factor.

665

30 AAD02558.1 AF049933 *Petunia x hybrida*
DESCRIPTION: PGPS/NH17. PGPS/NH17. protein sec61 gamma subunit
homolog;
protein transport to ER.

667

35 AAD51623.1 AF169020 *Glycine max*
DESCRIPTION: seed maturation protein PM35. PM35. similar to *Phaseolus*
vulgaris putative osmoprotector PvLEA-18.

40 AAC49859.1 U72764 *Phaseolus vulgaris*
DESCRIPTION: putative osmoprotector. PvLEA-18. Pvlea-18. atypical late
embryogenesis abundant protein.

45 AAF81194.1 AF240774 *Phaseolus vulgaris*

DESCRIPTION: starch branching enzyme 2. Sbe2. glucosyltransferase.

- CAA72154.1 Y11282 Triticum aestivum
5 DESCRIPTION: 1,4-alpha-glucan branching enzyme II. sbe2.
- AAK26821.1 AF338431 Aegilops tauschii
10 DESCRIPTION: starch branching enzyme IIa. SBEIIa.
- AAK26822.1 AF338432 Triticum aestivum
DESCRIPTION: starch branching enzyme IIa variant. SBEIIa variant.
- 15 AAC33764.1 AF072725 Zea mays
DESCRIPTION: starch branching enzyme IIb. ae. SBEIIb.
- 20 AAA18571.1 L08065 Zea mays
DESCRIPTION: starch branching enzyme II.
- BAA82828.1 AB023498 Oryza sativa
25 DESCRIPTION: starch branching enzyme rbe4. RBE4.
- AAC69753.1 AF064560 Hordeum vulgare
30 DESCRIPTION: starch branching enzyme IIa. sbellla.
- CAA56320.1 X80010 Pisum sativum
DESCRIPTION: starch branching enzyme II. SBEII.
- 35 AAC69754.1 AF064561 Hordeum vulgare
DESCRIPTION: starch branching enzyme IIb. sbelllb.
- 40 AAC36471.1 AF072724 Zea mays
DESCRIPTION: starch branching enzyme I. sbe1. confirmed by partial
peptide sequencing.
- 45 AAA82735.1 U17897 Zea mays
DESCRIPTION: starch branching enzyme I. sbe1.

- 5 AAD50279.2 AF169833 *Sorghum bicolor*
DESCRIPTION: seed starch branching enzyme. SBE.
- 10 BAA01854.1 D11081 *Zea mays*
DESCRIPTION: branching enzyme-I precursor.
- 15 CAA49463.1 X69805 *Solanum tuberosum*
DESCRIPTION: 1,4-alpha-glucan branching enzyme. SBE.
- 20 AAB17086.1 U66376 *Triticum aestivum*
DESCRIPTION: 1,4-alpha-D-glucan
6-alpha-D-(1,4-alpha-D-glucanotransferase. branching enzyme.
- 25 AAB67316.1 U65948 *Zea mays*
DESCRIPTION: formation of alpha-1-6 glucosidic linkage in starch
biosynthesis. starch branching enzyme IIa. Sbe2a. starch branching enzyme
isozyme SBEIIa.
- 30 BAB40334.1 AB042937 *Ipomoea batatas*
DESCRIPTION: starch branching enzyme. IBE.
- 35 BAA01584.1 D10752 *Oryza sativa*
DESCRIPTION: branching enzyme.
- 40 AAD28284.1 AF136268 *Oryza sativa* subsp. japonica
DESCRIPTION: starch-branching enzyme I. Rbe1.
- 45 BAA01616.1 D10838 *Oryza sativa*
DESCRIPTION: 1,4-alpha-glucan branching enzyme. sbe1.
- BAA01855.1 D11082 *Oryza sativa*

DESCRIPTION: branching enzyme-I precursor.

5 CAB40981.1 AJ237897 Triticum aestivum
DESCRIPTION: starch branching enzyme I. sbel. alternative.

10 CAB40979.1 AJ237897 Triticum aestivum
DESCRIPTION: starch branching enzyme I. sbel.

15 CAB40980.1 AJ237897 Triticum aestivum
DESCRIPTION: starch branching enzyme I. sbel. alternative.

15 AAG27622.1 AF286318 Triticum aestivum
DESCRIPTION: starch branching enzyme 1. Sbe1A. glucosyltransferase.

20 CAA54308.1 X77012 Manihot esculenta
DESCRIPTION: 1,4-alpha-glucan branching enzyme. SBE.

25 CAA72987.1 Y12320 Triticum aestivum
DESCRIPTION: starch branching enzyme I. Sbe1.

30 AAG27621.1 AF286317 Triticum aestivum
DESCRIPTION: starch branching enzyme 1. Sbe1D. glucosyltransferase.

35 BAA82349.1 AB029549 Phaseolus vulgaris
DESCRIPTION: branching enzyme 3. kbe3.

AAB61925.1 AF002820 Triticum aestivum
DESCRIPTION: starch branching enzyme I. wSBE I-D2.

40 CAB40749.1 AJ011891 Solanum tuberosum
DESCRIPTION: starch branching enzyme II. SBE II.

45 CAB40745.1 AJ011887 Solanum tuberosum
DESCRIPTION: starch branching enzyme II. SBE II.

CAB40744.1 AJ011886 *Solanum tuberosum*
DESCRIPTION: starch branching enzyme II. SBE II.

5 BAA85762.1 AB028067 *Nicotiana tabacum*
DESCRIPTION: starch branching enzyme. SBE.

10 CAA49371.1 X69713 *Manihot esculenta*
DESCRIPTION: branching enzyme. r-2.

15 BAB40335.1 AB042940 *Ipomoea batatas*
DESCRIPTION: starch branching enzyme. IBE.

20 CAA49370.1 X69712 *Manihot esculenta*
DESCRIPTION: branching enzyme. r-1.

AAC72336.1 AF064563 *Hordeum vulgare*
DESCRIPTION: starch branching enzyme IIb. sbellb.

25 673

CAA09881.1 AJ011939 *Trifolium repens*
DESCRIPTION: peroxidase. prx2.

30 CAA62228.1 X90695 *Medicago sativa*
DESCRIPTION: peroxidase2. prx2.

35 CAA71495.1 Y10469 *Spinacia oleracea*
DESCRIPTION: peroxidase. prxr8.

40 AAB41812.1 L36158 *Medicago sativa*
DESCRIPTION: peroxidase. pxdD. amino acid feature: conserved domains, aa
120 .. 126, 188 .. 195; amino acid feature: heme-binding domain, aa 63 ..
68.

45 BAA77387.1 AB024437 *Scutellaria baicalensis*
DESCRIPTION: peroxidase 1.

AAF63024.1 AF244921 *Spinacia oleracea*
DESCRIPTION: hydrogen peroxide catabolism. peroxidase prx12 precursor.
type III peroxidase.

AAD11483.1 U51193 *Glycine max*
DESCRIPTION: peroxidase. sEPb1.

AAB67737.1 L77080 *Stylosanthes humilis*
DESCRIPTION: cationic peroxidase.

BAA07663.1 D42064 *Nicotiana tabacum*
DESCRIPTION: cationic peroxidase isozyme 38K precursor.

BAA07664.1 D42065 *Nicotiana tabacum*
DESCRIPTION: cationic peroxidase isozyme 40K precursor.

CAB94692.1 AJ242742 *Ipomoea batatas*
DESCRIPTION: Removal of H₂O₂, oxidation of toxic reductants, defence
response toward wounding. peroxidase. pod.

CAB67121.1 Y19023 *Lycopersicon esculentum*
DESCRIPTION: peroxidase. cevi-1.

CAA62226.1 X90693 *Medicago sativa*
DESCRIPTION: peroxidase1B. prx1B.

CAA50597.1 X71593 *Lycopersicon esculentum*
DESCRIPTION: peroxidase. CEVI-1.

AAD11481.1 U51191 *Glycine max*
DESCRIPTION: peroxidase precursor. sEPa1.

AAD11484.1 U51194 *Glycine max*
DESCRIPTION: peroxidase. sEPb2.

BAA82306.1 AB027752 *Nicotiana tabacum*
 DESCRIPTION: peroxidase.
 5

AAA65637.1 L13654 *Lycopersicon esculentum*
 DESCRIPTION: peroxidase. TPX1.
 10

AAD11482.1 U51192 *Glycine max*
 DESCRIPTION: peroxidase precursor. sEPa2.
 15

CAA62225.1 X90692 *Medicago sativa*
 DESCRIPTION: peroxidase1A. prx1A.
 20

AAC98519.1 AF007211 *Glycine max*
 DESCRIPTION: peroxidase precursor. GMIPER1. pathogen-induced.
 25

AAD37427.1 AF149277 *Phaseolus vulgaris*
 DESCRIPTION: peroxidase 1 precursor. FBP1. secretory peroxidase.
 30

BAA14144.1 D90116 *Armoracia rusticana*
 DESCRIPTION: peroxidase isozyme.
 35

AAA98491.1 L36981 *Petroselinum crispum*
 DESCRIPTION: anionic peroxidase.
 40

CAA71488.1 Y10462 *Spinacia oleracea*
 DESCRIPTION: peroxidase. prxr1.
 45

AAD43561.1 AF155124 *Gossypium hirsutum*
 DESCRIPTION: bacterial-induced peroxidase precursor. Perx_Goshiko.
 50

BAA14143.1 D90115 *Armoracia rusticana*
 DESCRIPTION: peroxidase isozyme.
 55

- CAA71490.1 Y10464 *Spinacia oleracea*
DESCRIPTION: peroxidase. prxr3.
- 5 AAB02554.1 L37790 *Stylosanthes humilis*
DESCRIPTION: cationic peroxidase.
- 10 CAA66037.1 X97351 *Populus balsamifera* subsp. *trichocarpa*
DESCRIPTION: signal for ER. peroxidase.
- 15 BAA01877.1 D11102 *Populus kitakamiensis*
DESCRIPTION: peroxidase. prxA1.
- CAA62227.1 X90694 *Medicago sativa*
DESCRIPTION: peroxidase1C. prx1C.
- 20 BAA07241.1 D38051 *Populus kitakamiensis*
DESCRIPTION: peroxidase. prxA4a.
- 25 BAA01950.1 D11337 *Vigna angularis*
DESCRIPTION: peroxidase.
- 30 AAF65464.2 AF247700 *Oryza sativa*
DESCRIPTION: peroxidase POC1.
- 35 AAF63027.1 AF244924 *Spinacia oleracea*
DESCRIPTION: hydrogen peroxide catabolism. peroxidase prx15 precursor.
type III peroxidase.
- 40 CAC21393.1 AJ401276 *Zea mays*
DESCRIPTION: peroxidase. pox3.
- CAA59487.1 X85230 *Triticum aestivum*
DESCRIPTION: peroxidase. pox4.
- 45 AAD37430.1 AF149280 *Phaseolus vulgaris*

DESCRIPTION: peroxidase 5 precursor. FBP5. secretory peroxidase.

CAA71491.1 Y10465 Spinacia oleracea
5 DESCRIPTION: peroxidase. prxr4.

AAB41811.1 L36157 Medicago sativa
10 DESCRIPTION: peroxidase. pxdC. amino acid feature: conserved domains, aa
123 .. 129, 191 .. 198; amino acid feature: heme-binding domain, aa 68 ..
73.

BAA03644.1 D14997 Oryza sativa
15 DESCRIPTION: peroxidase.

AAA32676.1 M37637 Arachis hypogaea
20 DESCRIPTION: cationic peroxidase. PNC2.

CAA71494.1 Y10468 Spinacia oleracea
25 DESCRIPTION: peroxidase. prxr7.

AAA34050.1 M74103 Nicotiana sylvestris
DESCRIPTION: anionic peroxidase.

CAA40796.1 X57564 Armoracia rusticana
30 DESCRIPTION: peroxidase. peroxidase precursor.

674

35 AAG31438.1 AF241793 Perilla frutescens
DESCRIPTION: limonene synthase.

BAA08367.1 D49368 Perilla frutescens
40 DESCRIPTION: limonene cyclase.

BAA21629.1 AB005744 Perilla frutescens
45 DESCRIPTION: catalyzing the cyclization of geranyl pyrophosphate to
1-limonene. 1-limonene synthase. gPFLC. similar to perilla PFLC-1:DDBJ
Acc#D49368.

- 5 AAG31437.1 AF241792 *Perilla frutescens*
DESCRIPTION: limonene synthase.
- 10 AAK06663.1 AF317695 *Perilla frutescens* var. *frutescens*
DESCRIPTION: limonene synthase.
- 15 AAG31435.1 AF241790 *Perilla citriodora*
DESCRIPTION: limonene synthase.
- 20 AAF65545.1 AF233894 *Perilla citriodora*
DESCRIPTION: limonene synthase.
- 25 AAD50304.1 AF175323 *Mentha longifolia*
DESCRIPTION: limonene synthase. monoterpene synthase.
- AAC37366.1 L13459 *Mentha spicata*
DESCRIPTION: 4S-limonene synthase.
- 30 AAG01140.1 AF282875 *Schizonepeta tenuifolia*
DESCRIPTION: (+)-4R-limonene synthase.
- AAC61260.1 AF061285 *Capsicum annuum*
DESCRIPTION: sesquiterpene cyclase. UV induced.
- 35 AAG09949.1 AF171216 *Lycopersicon esculentum*
DESCRIPTION: vetispiradiene synthase. LEVS2. sesquiterpene cyclase.
- 40 AAF74977.1 AF270425 *Gossypium hirsutum*
DESCRIPTION: (E,E)-farnesyl diphosphate cyclase. (+)-delta-cadinene synthase. cdn2. sesquiterpene cyclase.
- 45 BAA82141.1 AB023816 *Solanum tuberosum*
DESCRIPTION: vetispiradiene synthase. PVS4. potato sesquiterpene cyclase.

BAA82092.1 AB022598 Solanum tuberosum
DESCRIPTION: vetispiradiene synthase. PVS1. potato sesquiterpene cyclase.

5

AAF21053.1 AF212433 Capsicum annuum
DESCRIPTION: UV-induced sesquiterpene cyclase. SC2.

10 BAA82109.1 AB022720 Solanum tuberosum
DESCRIPTION: vetispiradiene synthase. PVS3. potato sesquiterpene cyclase;
PVS3.

15 BAA82108.1 AB022719 Solanum tuberosum
DESCRIPTION: vetispiradiene synthase. PVS2. potato sesquiterpene cyclase;
PVS2.

20 AAC12784.1 U88318 Gossypium hirsutum
DESCRIPTION: (E,E)-farnesyl diphosphate cyclizing. (+)-delta-cadinene
synthase. cdn1. sesquiterpene cyclase; delta-cadinene synthase.

25 AAG24640.2 AF304444 Artemisia annua
DESCRIPTION: sesquiterpene cyclase.

30 AAK15641.1 AF326117 Capsicum annuum
DESCRIPTION: sesquiterpene cyclase. PSC2.

CAC12731.1 AJ271792 Artemisia annua
DESCRIPTION: putative sesquiterpene cyclase. cASC125.

35

675

CAA50609.1 X71609 Nicotiana tabacum
DESCRIPTION: ras-related GTP-binding protein.

40

CAA98166.1 Z73938 Lotus japonicus
DESCRIPTION: GTP-binding protein. RAB5A. rab5A.

45

CAC24477.1 AJ296336 Cichorium intybus x Cichorium endivia

BAA84717.1 AB032761 *Oryza sativa*
 DESCRIPTION: GTP-binding protein. rab5B.
 5

AAG24438.1 AF304518 *Oryza sativa*
 DESCRIPTION: small GTP-binding protein RAB5B. rab5B.

10 CAB57221.1 AJ249867 *Cichorium intybus* x *Cichorium endivia*
 DESCRIPTION: GTP binding protein. b1.5.

15 CAA98180.1 Z73952 *Lotus japonicus*
 DESCRIPTION: GTP-binding protein. RAB11D. rab11D.

20 CAA98181.1 Z73953 *Lotus japonicus*
 DESCRIPTION: GTP-binding protein. RAB11E. rab11E.

BAA02114.1 D12546 *Pisum sativum*
 DESCRIPTION: GTP-binding protein.
 25

BAA02113.1 D12545 *Pisum sativum*
 DESCRIPTION: GTP-binding protein.

30 BAA02116.1 D12548 *Pisum sativum*
 DESCRIPTION: GTP-binding protein.

35 BAA02112.1 D12544 *Pisum sativum*
 DESCRIPTION: GTP-binding protein.

40 BAA02118.1 D12550 *Pisum sativum*
 DESCRIPTION: GTP-binding protein.

CAA98159.1 Z73931 *Lotus japonicus*
 DESCRIPTION: GTP-binding protein. RAB1B. rab1B.
 45

CAB65172.1 AJ245570 *Lycopersicon esculentum*
DESCRIPTION: putative role in secretion of cell wall modifying enzymes.
Rab11 GTPase. Rab11a.

5 CAA89049.1 Z49190 *Beta vulgaris*
DESCRIPTION: GTP-binding. small G protein.

10 BAA02110.1 D12542 *Pisum sativum*
DESCRIPTION: GTP-binding protein.

15 AAB97114.1 U58853 *Glycine max*
DESCRIPTION: small GTP-binding protein. sra1.

20 BAA02904.1 D13758 *Oryza sativa*
DESCRIPTION: ras-related GTP binding protein. ss230.

25 CAA98178.1 Z73950 *Lotus japonicus*
DESCRIPTION: GTP-binding protein. RAB11B. rab11B.
CAA98177.1 Z73949 *Lotus japonicus*
DESCRIPTION: GTP-binding protein. RAB11A. rab11A.

30 AAK15703.1 AF327517 *Oryza sativa*
DESCRIPTION: GTP-binding protein.

35 AAF65510.1 AF108883 *Capsicum annuum*
DESCRIPTION: small GTP-binding protein.

40 BAA76422.1 AB024994 *Cicer arietinum*
DESCRIPTION: rab-type small GTP-binding protein.

CAA98160.1 Z73932 *Lotus japonicus*
DESCRIPTION: GTP-binding protein. RAB1C. rab1C.

45 AAA80680.1 U38466 *Lycopersicon esculentum*

DESCRIPTION: small GTP-binding protein. LeRab1C. ; YPT1/Rab1A homolog
LeRab1C.

5 AAA80678.1 U38464 Lycopersicon esculentum
DESCRIPTION: small GTP-binding protein. LeRab1A. ; YPT1/Rab1A
homolog
LeRab1A.

10 676

AAA80499.1 U20594 Lycopersicon esculentum
DESCRIPTION: leucine aminopeptidase.

15

CAA54314.1 X77015 Solanum tuberosum
DESCRIPTION: leucine aminopeptidase. LAP.

20

CAA48038.1 X67845 Solanum tuberosum
DESCRIPTION: leucine aminopeptidase. LAP.

25

AAC49457.1 U50152 Lycopersicon esculentum
DESCRIPTION: peptidase. leucine aminopeptidase. lap2.

30

AAC49456.1 U50151 Lycopersicon esculentum
DESCRIPTION: exoprotease in the defense response. leucine aminopeptidase.
lap.

35

AAA80498.1 U20593 Lycopersicon esculentum
DESCRIPTION: leucine aminopeptidase.

40

CAA68143.1 X99825 Petroselinum crispum
DESCRIPTION: cytosol aminopeptidase. leucine aminopeptidase.

45

678

CAC09580.1 AJ298992 Fagus sylvatica

DESCRIPTION: Absciscic acid (ABA) and calcium induced protein kinase.
protein kinase (PK). pk1.

5 AAA34002.1 M67449 Glycine max
DESCRIPTION: protein kinase. PK6.

10 AAK11734.1 AY027437 Arachis hypogaea
DESCRIPTION: serine/threonine/tyrosine kinase.

15 BAB16918.1 AP002863 Oryza sativa
DESCRIPTION: putative protein kinase. P0005A05.22.

20 CAA06334.1 AJ005077 Lycopersicon esculentum
DESCRIPTION: protein kinase. TCTR2 protein. TCTR2.

25 AAG31141.1 AF305911 Oryza sativa
DESCRIPTION: EDR1. EDR1. MAP kinase kinase kinase; similar to
Arabidopsis
thaliana EDR1.

CAA73722.1 Y13273 Lycopersicon esculentum
DESCRIPTION: putative protein kinase.

30 AAD46406.1 AF096250 Lycopersicon esculentum
DESCRIPTION: ethylene-responsive protein kinase TCTR1. ER50.
serine/threonine kinase; similar to Arabidopsis thaliana negative
regulator of the ethylene response pathway encoded by GenBank Accession
35 Number L08789.

40 AAG31142.1 AF305912 Hordeum vulgare
DESCRIPTION: EDR1. EDR1. MAP kinase kinase kinase; similar to
Arabidopsis
thaliana EDR1.

45 AAD10056.1 AF110518 Lycopersicon esculentum
DESCRIPTION: ethylene-inducible CTR1-like protein kinase. protein kinase
homolog; ethylene and fruit ripening inducible CTR1-like protein kinase;

TCTR1.

- 5 AAD10057.1 AF110519 *Lycopersicon esculentum*
DESCRIPTION: ethylene-inducible CTR1-like protein kinase. protein kinase homolog; ethylene and fruit ripening inducible CTR1-like protein kinase; TCTR1v.
- 10 AAK30005.1 AY029067 *Rosa hybrid cultivar*
DESCRIPTION: CTR2 protein kinase.
- 15 BAB39409.1 AP002901 *Oryza sativa*
DESCRIPTION: putative protein kinase. P0456F08.9. contains EST C23560(R0290).
- 20 BAA87853.1 AP000816 *Oryza sativa*
DESCRIPTION: EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative NAK-like Ser/Thr protein kinase. (AF001308).
- 25 BAA06538.1 D31737 *Nicotiana tabacum*
DESCRIPTION: protein-serine/threonine kinase.
- 30 BAB21240.1 AP002953 *Oryza sativa*
DESCRIPTION: Putative protein kinase. P0426D06.20. contains ESTs C22359(C11461),C22360(C11461).
- 35 BAA94528.1 AP001800 *Oryza sativa*
DESCRIPTION: Similar to *Arabidopsis thaliana* chromosome 2 BAC T20K24; putative receptor-like protein kinase (AC002392).
- 40 BAB17126.1 AP002867 *Oryza sativa*
DESCRIPTION: putative receptor kinase. P0463F06.16.
- 45 BAB39451.1 AP003338 *Oryza sativa*
DESCRIPTION: putative receptor kinase. OJ1212_B09.24.

BAB17348.1 AP002747 *Oryza sativa*
DESCRIPTION: putative receptor kinase. P0698G03.32.

5 BAB17321.1 AP002747 *Oryza sativa*
DESCRIPTION: putative receptor kinase. P0698G03.1.

10 BAB17129.1 AP002867 *Oryza sativa*
DESCRIPTION: putative receptor kinase. P0463F06.20.

15 AAF68398.1 AF237568 *Oryza sativa*
DESCRIPTION: receptor-like protein kinase. RLG2.

BAB07905.1 AP002835 *Oryza sativa*
DESCRIPTION: putative S-receptor kinase. P0417G05.13.

20 BAA94517.1 AP001800 *Oryza sativa*
DESCRIPTION: Similar to *Zea mays* S-domain receptor-like protein kinase
(AJ010166).

25 BAB17335.1 AP002747 *Oryza sativa*
DESCRIPTION: putative receptor kinase. P0698G03.17. contains ESTs
D47575(S13157),AU032665(S13157).

30 BAB39441.1 AP003338 *Oryza sativa*
DESCRIPTION: putative receptor kinase. OJ1212_B09.11.

35 BAB17116.1 AP002867 *Oryza sativa*
DESCRIPTION: putative receptor kinase. P0463F06.3.

40 AAF78044.1 AF248493 *Oryza sativa*
DESCRIPTION: receptor-like kinase. RLG18. protein kinase.

45 CAB51834.1 00069 *Oryza sativa*
DESCRIPTION: 11332.5. contains eukaryotic protein kinase domain PF.

BAB17127.1 AP002867 *Oryza sativa*
DESCRIPTION: putative receptor kinase. P0463F06.17.

5 AAF78021.1 AF238477 *Oryza sativa*
DESCRIPTION: receptor-like kinase. RLG5. protein kinase.

10 AAD46420.1 AF100771 *Hordeum vulgare*
DESCRIPTION: receptor-like kinase. Hv3ARK. similar to wheat ARK1AS.

15 AAD46917.1 AF164021 *Oryza sativa*
DESCRIPTION: receptor kinase.

20 BAB17345.1 AP002747 *Oryza sativa*
DESCRIPTION: putative receptor kinase. P0698G03.29.

25 BAB39438.1 AP003338 *Oryza sativa*
DESCRIPTION: putative receptor kinase. OJ1212_B09.7.

30 AAF78018.1 AF238474 *Oryza sativa*
DESCRIPTION: receptor-like kinase. RLG16. protein kinase.

35 AAC01746.1 AF044489 *Oryza sativa*
DESCRIPTION: receptor-like protein kinase. drpk1.

40 BAB17337.1 AP002747 *Oryza sativa*
DESCRIPTION: putative receptor kinase. P0698G03.21. contains ESTs
D47575(S13157),AU032665(S13157).

45 BAB17347.1 AP002747 *Oryza sativa*
DESCRIPTION: putative receptor kinase. P0698G03.31. contains ESTs
D47575(S13157),AU032665(S13157).

BAB17344.1 AP002747 *Oryza sativa*
DESCRIPTION: putative receptor kinase. P0698G03.28. contains ESTs
D47575(S13157),AU032665(S13157).

BAB39437.1 AP003338 *Oryza sativa*
DESCRIPTION: receptor-like kinase. OJ1212_B09.6.

5

AAF78019.1 AF238475 *Oryza sativa*
DESCRIPTION: receptor-like kinase. RLG17. protein kinase.

10 BAA05648.1 D26601 *Nicotiana tabacum*
DESCRIPTION: protein kinase.

15 BAB17332.1 AP002747 *Oryza sativa*
DESCRIPTION: putative receptor kinase. P0698G03.13. contains ESTs
D47575(S13157),AU032665(S13157).

20 BAB39435.1 AP003338 *Oryza sativa*
DESCRIPTION: putative receptor kinase. OJ1212_B09.2.

679

25 CAA78386.1 Z13996 *Petunia x hybrida*
DESCRIPTION: DNA binding protein; transcriptional activator. protein 1.
myb.Ph3. Product related to animal myb proto-oncoproteins. Sequence from
nucleotide 992 is not included in clone cPF1 and has been obtained by PCR
amplification of cDNA.

30

CAB43399.1 AJ006292 *Antirrhinum majus*
DESCRIPTION: Myb-related transcription factor mixta-like 1. mybm11.

35 CAA67600.1 X99210 *Lycopersicon esculentum*
DESCRIPTION: myb-related transcription factor. THM16.

40 BAA23337.1 D88617 *Oryza sativa*
DESCRIPTION: transfactor. OSMYB1. Osmyb1.

45 AAA82943.1 U39448 *Picea mariana*
DESCRIPTION: MYB-like transcriptional factor MBF1. putative DNA binding
region highly similar to the maize C1.

CAA64614.1 X95296 *Lycopersicon esculentum*
DESCRIPTION: transcription factor. THM27. myb-related.

5 BAA93038.1 AP001552 *Oryza sativa*
DESCRIPTION: EST AU082058(C12976) corresponds to a region of the
predicted gene. Similar to *Arabidopsis thaliana* putative transcription
factor (AF062916).

10 AAC04720.1 AF034134 *Gossypium hirsutum*
DESCRIPTION: putative MYB-like transcription factor. MYB-like DNA-
binding
15 domain protein. Cmy-O. similar to MYB A encoded by GenBank Accession
Number L04497.

20 CAA72186.1 Y11351 *Oryza sativa*
DESCRIPTION: myb factor. myb.

25 AAF22256.1 AF161711 *Pimpinella brachycarpa*
DESCRIPTION: myb-related transcription factor.

30 BAB39987.1 AP003020 *Oryza sativa*
DESCRIPTION: putative transcription factor (myb). P0498A12.16. contains
ESTs AU097474(S5087),D40175(S1959).

35 BAB39972.1 AP003018 *Oryza sativa*
DESCRIPTION: putative transcription factor (myb). OSJNBa0004B13.27.
contains ESTs AU097474(S5087),D40175(S1959).

40 BAA23338.1 D88618 *Oryza sativa*
DESCRIPTION: transfactor. OSMYB2. Osmyb2.

BAA88222.1 AB028650 *Nicotiana tabacum*
DESCRIPTION: myb-related transcription factor LBM2. lbm2.

45 CAA67575.1 X99134 *Lycopersicon esculentum*
DESCRIPTION: transcription factor. THM6. myb-related.

CAA78387.1 Z13997 Petunia x hybrida
 DESCRIPTION: DNA-binding protein, transcriptional activator. protein 2.
 5 myb.Ph2. related to animal myb proto-oncoproteins.

CAA66952.1 X98308 Lycopersicon esculentum
 DESCRIPTION: THM18. myb-related transcription factor.
 10

BAA23339.1 D88619 Oryza sativa
 DESCRIPTION: transfactor. OSMYB3. Osmyb3.
 15

AAC49394.1 U57002 Zea mays
 DESCRIPTION: P protein. P. allele P-wr; Myb-like transcriptional
 regulator with a putative zinc-finger at the C-terminal.
 20

AAB41101.1 U72762 Nicotiana tabacum
 DESCRIPTION: transcription factor Myb1. myb1. TMV-inducible Myb
 homolog;
 contains helix-turn-helix motif; contains redox-sensitive cysteine.
 25

AAA33500.1 M73028 Zea mays
 DESCRIPTION: myb-like transcription factor. P.
 30

AAG36774.1 AF210616 Zea mays
 DESCRIPTION: P2 protein. P2. myb-like transcriptional factor; similar to
 Zea mays P gene.
 35

BAA88223.1 AB028651 Nicotiana tabacum
 DESCRIPTION: myb-related transcription factor LBM3. lbm3.
 40

BAA88224.1 AB028652 Nicotiana tabacum
 DESCRIPTION: myb-related transcription factor LBM4. lbm4.
 45

CAA72187.1 Y11352 Oryza sativa
 DESCRIPTION: myb factor. myb.

CAA46150.1 X65016 *Oryza sativa*
DESCRIPTION: calmodulin. cam.

5

AAC36058.1 AF042839 *Oryza sativa*
DESCRIPTION: calmodulin. CaM2.

10

AAD10246.1 AF030034 *Phaseolus vulgaris*
DESCRIPTION: calmodulin. CaM. EF-hand protein; calcium-dependent
protein;
functions in calcium signal transduction pathways.

15

CAA54583.1 X77397 *Zea mays*
DESCRIPTION: calmodulin. CaM2.

20

BAA87825.1 AP000815 *Oryza sativa*
DESCRIPTION: ESTs AU030013(E50493),AU081341(E50493) correspond to
a
region of the predicted gene. Similar to O.sativa gene encoding
25 calmodulin. (Z12828).

30

AAA92681.1 U13882 *Pisum sativum*
DESCRIPTION: calcium-binding protein. calmodulin.

35

AAA33706.1 M80836 *Petunia x hybrida*
DESCRIPTION: calmodulin. CAM81.

40

CAA43143.1 X60738 *Malus x domestica*
DESCRIPTION: Calmodulin. CaM.

45

CAA78301.1 Z12839 *Lilium longiflorum*
DESCRIPTION: calcium binding protein, signal transduction. calmodulin.

AAC49582.1 U48691 *Triticum aestivum*
DESCRIPTION: calmodulin TaCaM2-2. calcium-binding protein.

5 AAC49580.1 U48689 *Triticum aestivum*
DESCRIPTION: calmodulin TaCaM1-3. calcium-binding protein.

10 AAC49579.1 U48688 *Triticum aestivum*
DESCRIPTION: calmodulin TaCaM1-2. calcium binding protein.

15 AAC49578.1 U48242 *Triticum aestivum*
DESCRIPTION: calmodulin TaCaM1-1. calcium-binding.

20 AAA03580.1 L01431 *Glycine max*
DESCRIPTION: calcium-binding regulatory protein. calmodulin. SCaM-2.
putative.

25 AAB36130.1 S81594 *Vigna radiata*
DESCRIPTION: auxin-regulated calmodulin. auxin-regulated calmodulin,
arCaM. This sequence comes from Fig. 1; arCaM.

30 AAA33901.1 L18913 *Oryza sativa*
DESCRIPTION: calcium binding protein, signal transduction. calmodulin.
putative.

35 CAA78287.1 Z12827 *Oryza sativa*
DESCRIPTION: calcium binding protein, signal transduction. calmodulin.

AAB46588.1 U83402 *Capsicum annuum*
DESCRIPTION: calmodulin.

40 CAA61980.1 X89890 *Bidens pilosa*
DESCRIPTION: Calmodulin.

45 AAA32938.1 M27303 *Hordeum vulgare*
DESCRIPTION: calmodulin.

BAA88540.1 AP000969 *Oryza sativa*
 DESCRIPTION: ESTs AU081349(E61253), D41425(S3918) correspond to a
 region
 5 of the predicted gene. Similar to calmodulin. (AF042840).

AAF65511.1 AF108889 *Capsicum annuum*
 DESCRIPTION: calmodulin.
 10

AAC36059.1 AF042840 *Oryza sativa*
 DESCRIPTION: calmodulin. CaM1.

15
 AAA33900.1 L18914 *Oryza sativa*
 DESCRIPTION: calcium binding protein, signal transduction. calmodulin.

20
 CAA78288.1 Z12828 *Oryza sativa*
 DESCRIPTION: calcium binding protein, signal transduction. calmodulin.

25
 AAA34015.1 L01433 *Glycine max*
 DESCRIPTION: calcium-binding regulatory protein. calmodulin. SCaM-4.
 putative.

30
 AAA16320.1 L14071 *Bryonia dioica*
 DESCRIPTION: calmodulin. Bc329. calcium-binding sites (amino acid #): 1.
 (21..33); 2. (57..68); 3. (94..106); 4. (130..141).

35
 AAA19571.1 U10150 *Brassica napus*
 DESCRIPTION: calcium binding. calmodulin. bcm1.

40
 AAA87347.1 M88307 *Brassica juncea*
 DESCRIPTION: calmodulin.

CAA52602.1 X74490 *Zea mays*
 DESCRIPTION: Calmodulin. ZMCALM1.

45 683

- CAA71800.1 Y10847 *Brassica juncea*
DESCRIPTION: O-acetylserine(thiol) lyase.
- 5 CAA71798.1 Y10845 *Brassica juncea*
DESCRIPTION: O-acetylserine(thiol) lyase.
- 10 AAC25635.1 AF044172 *Solanum tuberosum*
DESCRIPTION: cysteine synthase. CS-A; O-acetylserine (thiol) lyase;
cytosolic isoform.
- 15 BAA01279.1 D10476 *Spinacia oleracea*
DESCRIPTION: O-acetylserine(thiol) lyase.
- 20 BAA02438.1 D13153 *Triticum aestivum*
DESCRIPTION: O-acetylserine (thiol) lyase. cys1.
- 25 CAA59798.1 X85803 *Zea mays*
DESCRIPTION: O-acetylserine (thiol) lyase. Mcysp. cysteine synthase.
- AAD23907.1 AF073695 *Oryza sativa*
DESCRIPTION: cysteine synthase. rcs1. O-acetylserine(thiol)-lyase.
- 30 AAD23909.1 AF073697 *Oryza sativa*
DESCRIPTION: cysteine synthase. rcs3. O-acetylserine(thiol)-lyase.
- 35 AAC25636.1 AF044173 *Solanum tuberosum*
DESCRIPTION: cysteine synthase. CS-B; O-acetylserine (thiol) lyase;
plastidic isoform.
- 40 AAC27794.1 AF078693 *Chlamydomonas reinhardtii*
DESCRIPTION: cysteine biosynthesis. putative O-acetylserine(thiol)lyase
precursor. Crcys-1A.
- 45 CAA06819.1 AJ006024 *Cicer arietinum*
DESCRIPTION: cysteine synthase, O-acetyl-L-serine (thiol)-lyase.

CAA46086.1 X64874 Capsicum annuum
DESCRIPTION: O-acetylserine (thiol)-lyase.

5 CAA71799.1 Y10846 Brassica juncea
DESCRIPTION: O-acetylserine(thiol) lyase.

10 AAA16973.1 L05184 Chloroplast Spinacia oleracea
DESCRIPTION: O-acetylserine-(thiol)-lyase.

AAD23908.1 AF073696 Oryza sativa
15 DESCRIPTION: cysteine synthase. rcs2. O-acetylserine(thiol)-lyase.

AAD23910.1 AF073698 Oryza sativa
DESCRIPTION: cysteine synthase. rcs4. O-acetylserine(thiol)-lyase.

20 684

AAA68983.1 L12395 Brassica napus
DESCRIPTION: signal transduction, membrane vehicle traffic. small
25 GTP-binding protein. bra. putative.

685

AAB61961.1 L81152 Oryza sativa
30 DESCRIPTION: integral membrane protein. OsNramp2.

AAB36424.1 S81897 Oryza sativa
DESCRIPTION: OsNramp1. OsNramp1. Nramp1 homolog/Bcg product
35 homolog; This
sequence comes from Fig. 2.

AAB62273.1 L41217 Oryza sativa
40 DESCRIPTION: integral membrane protein. OsNramp1. putative.

AAC49720.1 U60767 Oryza sativa
DESCRIPTION: integral membrane protein OsNramp3. OsNramp3.

45 686

-
- AAC04719.1 AF034133 *Gossypium hirsutum*
DESCRIPTION: putative MYB-like transcription factor. MYB-like DNA-binding
5 domain protein. Cmy-N. similar to MYB A encoded by GenBank Accession Number L04497.
- AAB58314.1 U33917 *Craterostigma plantagineum*
10 DESCRIPTION: Cpm7. cpm7. putative DNA-binding protein; Description: myb-like gene; myb-related transcription factor.
- AAB58313.1 U33916 *Craterostigma plantagineum*
15 DESCRIPTION: Cpm5. cpm5. putative DNA-binding protein; Description: myb-related gene; myb-related transcription factor.
- AAC13876.1 U33915 *Craterostigma plantagineum*
20 DESCRIPTION: myb-related transcription factor Cpm10. cpm10. putative DNA-binding protein.
- AAK08983.1 AY026332 *Oryza sativa*
25 DESCRIPTION: Myb transcription factor JAMyb. related to host cell death and defense responses; induced by jasmonic acid, wounding, or infection of rice blast fungus, but not by salicylic acid or abscisic acid.
- BAB18296.1 AP002860 *Oryza sativa*
30 DESCRIPTION: putative myb-related transcription factor. P0409B08.23.
- CAA71992.1 Y11105 *Pisum sativum*
35 DESCRIPTION: Myb26.
- BAB40790.1 AB058642 *Lilium hybrid division I*
40 DESCRIPTION: LhMyb.
- AAK19618.1 AF336285 *Gossypium hirsutum*
DESCRIPTION: GHMYB38. ghmyb38. similar to myb.
- 45 CAA78387.1 Z13997 *Petunia x hybrida*

DESCRIPTION: DNA-binding protein, transcriptional activator. protein 2.
myb.Ph2. related to animal myb proto-oncoproteins.

5 BAA88221.1 AB028649 *Nicotiana tabacum*
DESCRIPTION: myb-related transcription factor LBM1. lbm1.

10 BAA88224.1 AB028652 *Nicotiana tabacum*
DESCRIPTION: myb-related transcription factor LBM4. lbm4.

15 AAK19617.1 AF336284 *Gossypium hirsutum*
DESCRIPTION: GHMYB36. ghmyb36. similar to myb.

20 AAA33067.1 L04497 *Gossypium hirsutum*
DESCRIPTION: MYB A; putative.

AAK19615.1 AF336282 *Gossypium hirsutum*
DESCRIPTION: GHMYB10. ghmyb10. similar to myb.

25 BAA81733.2 AB029162 *Glycine max*
DESCRIPTION: GmMYB29A2.

30 BAA81732.1 AB029161 *Glycine max*
DESCRIPTION: GmMYB29A2.

35 BAA81730.1 AB029159 *Glycine max*
DESCRIPTION: GmMYB29A1.

BAA88223.1 AB028651 *Nicotiana tabacum*
DESCRIPTION: myb-related transcription factor LBM3. lbm3.

40 AAB41101.1 U72762 *Nicotiana tabacum*
DESCRIPTION: transcription factor Myb1. myb1. TMV-inducible Myb
homolog;
contains helix-turn-helix motif; contains redox-sensitive cysteine.

45

- BAA81736.1 AB029165 Glycine max
DESCRIPTION: GmMYB29B2.
- 5 BAA81731.1 AB029160 Glycine max
DESCRIPTION: GmMYB29A1.
- 10 CAA72218.1 Y11415 Oryza sativa
DESCRIPTION: myb.
- 15 CAA67000.1 X98355 Oryza sativa
DESCRIPTION: activator of alpha-amylase gene promoter. transcription factor GAMyb. Gam1. Myb-like; expression is regulated by gibberellin.
- 20 AAK19611.1 AF336278 Gossypium hirsutum
DESCRIPTION: BNLGHi233. bnlghi6233. similar to myb.
- 25 CAA67575.1 X99134 Lycopersicon esculentum
DESCRIPTION: transcription factor. THM6. myb-related.
- CAA64614.1 X95296 Lycopersicon esculentum
DESCRIPTION: transcription factor. THM27. myb-related.
- 30 AAD31395.1 AF114162 Lolium temulentum
DESCRIPTION: gibberellin MYB transcription factor. GAMyb. R2/R3-MYB.
- 35 BAA93038.1 AP001552 Oryza sativa
DESCRIPTION: EST AU082058(C12976) corresponds to a region of the predicted gene. Similar to Arabidopsis thaliana putative transcription factor (AF062916).
- 40 AAG22863.1 AY008692 Hordeum vulgare
DESCRIPTION: transcription factor GAMyb. Gamyb.
- 45 BAA96421.1 AB044084 Triticum aestivum
DESCRIPTION: transcription activator for gibberellin response. GAMyb protein. Ta-GAMyb.

- AAC04716.1 AF034130 *Gossypium hirsutum*
 DESCRIPTION: putative MYB-like transcription factor. MYB-like DNA-binding
 5 domain protein. CmY-D. similar to MYB A encoded by GenBank Accession Number L04497.
- 10 AAG28526.1 AF198499 *Nicotiana tabacum*
 DESCRIPTION: anther-specific myb-related protein 1. mybAS1. NtMYBAS1; contains N-terminal R2, R3 myb domain repeats similar to c-myb.
- 15 CAA78388.1 Z13998 *Petunia x hybrida*
 DESCRIPTION: DNA-binding protein; transcriptional activator. protein 3. myb.Ph3. related to animal myb proto-oncoproteins.
- 20 AAA33482.1 M37153 *Zea mays*
 DESCRIPTION: c1 locus myb homologue; putative.
- AAK09327.1 AF320614 *Zea mays*
 25 DESCRIPTION: activates anthocyanin transcription. anthocyanin regulatory C1. c1. transcription factor.
- AAK09326.1 AF320613 *Zea mays*
 30 DESCRIPTION: activates anthocyanin transcription. anthocyanin regulatory C1. c1. transcription factor.
- 687

- 35 BAA92972.1 AP001551 *Oryza sativa*
 DESCRIPTION: ESTs AU056183(S20356),AU056881(S20950) correspond to a region of the predicted gene. Similar to Arabidopsis thaliana chromosome 4 BAC clone F6I18 ; putative protein kinase. (AL022198).
- 40 BAA83689.1 AB011968 *Oryza sativa*
 DESCRIPTION: OsPK7. OsPK7. protein kinase.
- 45 BAA83688.1 AB011967 *Oryza sativa*
 DESCRIPTION: OsPK4. OsPK4. protein kinase.

- AAAF22219.1 AF141378 Zea mays
DESCRIPTION: protein kinase PK4. ZmPK4.
- 5
- BAA34675.1 AB011670 Triticum aestivum
DESCRIPTION: wpk4 protein kinase. wpk4.
- 10
- CAA73068.1 Y12465 Sorghum bicolor
DESCRIPTION: serine/threonine kinase. SNFL2.
- 15
- CAA73067.1 Y12464 Sorghum bicolor
DESCRIPTION: serine/threonine kinase. SNFL1.
- 20
- BAA92970.1 AP001551 Oryza sativa
DESCRIPTION: Similar to Arabidopsis thaliana chromosome 4 BAC clone
F28A21 ; putative protein kinase. (AL035526).
- 25
- CAA74646.1 Y14274 Sorghum bicolor
DESCRIPTION: putative serine/threonine protein kinase. SNFL3.
- 30
- AAD31900.1 AF145482 Mesembryanthemum crystallinum
DESCRIPTION: putative serine/threonine protein kinase.
- 35
- AAB62693.1 AF004947 Oryza sativa
DESCRIPTION: protein kinase.
- 40
- BAA96628.1 AP002482 Oryza sativa
DESCRIPTION: ESTs D41739(S4522),AU055999(S20214),
AU057588(S21592
correspond to a region of the predicted gene. Similar to Sorghum bicolor
serine/threonine kinase (Y12465).
- 45
- AAD23582.1 AF128443 Glycine max
DESCRIPTION: probably involved in plant stress responses possibly
regulates gene expression. SNF-1-like serine/threonine protein kinase.
expressed in nodules, roots and leaves.

- 5 BAA05649.1 D26602 *Nicotiana tabacum*
DESCRIPTION: protein kinase.
- CAA71142.1 Y10036 *Cucumis sativus*
DESCRIPTION: SNF1-related protein kinase.
- 10 AAC99329.1 AF062479 *Oryza sativa*
DESCRIPTION: protein kinase SNF1. Snf1. similar to yeast SNF1.
- 15 CAA65244.1 X95997 *Solanum tuberosum*
DESCRIPTION: SNF1-related protein kinase. PKIN1.
- 20 CAA57898.1 X82548 *Hordeum vulgare*
DESCRIPTION: SNF1-related protein kinase. BKIN2.
- 25 CAA07813.1 AJ007990 *Hordeum vulgare*
DESCRIPTION: SnRK1-type protein kinase. kin12a.
- CAA46556.1 X65606 *Hordeum vulgare*
DESCRIPTION: protein kinase. BKIN12.
- 30 AAB05457.1 U55768 *Oryza sativa*
DESCRIPTION: SNF1-related protein kinase. RSk1. Ser/Thr protein kinase homolog.
- 35 CAA46554.1 X65604 *Hordeum vulgare*
DESCRIPTION: protein kinase. BKIN12.
- 40 AAD00239.1 U73938 *Nicotiana tabacum*
DESCRIPTION: protein kinase. PK11-C1. PK11-C1. induced at the transcriptional level by the abscisic acid plant hormone; similar to serine/threonine protein kinase.
- 45 AAC69450.1 AF032465 *Nicotiana tabacum*

DESCRIPTION: putative serine/threonine protein kinase. WAPK.

- 5 AAD00240.1 U73939 *Nicotiana tabacum*
DESCRIPTION: protein kinase. PK11-C5. PK11-C5. induced at the transcriptional level by the abscisic acid plant hormone; similar to serine/threonine protein kinase.
- 10 BAA13608.1 D88399 *Oryza sativa*
DESCRIPTION: serine-threonine kinase. endosperm kinase. REK.
- 15 AAA34017.1 L19360 *Glycine max*
DESCRIPTION: protein kinase 2. SPK-2. putative.
- 20 AAG60195.1 AC084763 *Oryza sativa*
DESCRIPTION: protein kinase REK. OSJNBa0027P10.6.
- 25 AAA33004.1 L12394 *Brassica napus*
DESCRIPTION: serine/threonine protein kination. serine/threonine protein kinase. BSK2. putative.
- 30 BAA19573.1 AB002109 *Oryza sativa*
DESCRIPTION: protein kinase. a novel protein kinase.
- 35 AAA33979.1 L01453 *Glycine max*
DESCRIPTION: protein phosphorylation, regulatory protein. protein kinase. SPK-1. putative.
- 40 AAA33003.1 L12393 *Brassica napus*
DESCRIPTION: protein kination. serine/threonine protein kinase. BSK1. putative.
- 45 AAB68962.1 L38855 *Glycine max*
DESCRIPTION: protein kinase. SPK-4.
- 45 AAB68961.1 L19361 *Glycine max*
DESCRIPTION: protein kinase 3. SPK-3. putative.

- 5 AAB58348.1 U29095 *Triticum aestivum*
DESCRIPTION: serine-threonine protein kinase. TaPK3.
- AAF27340.1 AF186020 *Vicia faba*
DESCRIPTION: abscisic acid-activated protein kinase. AAPK.
- 10 AAA96325.1 M94726 *Triticum aestivum*
DESCRIPTION: protein kinase. abscisic acid inducible.
- 15 CAA81443.1 Z26846 *Mesembryanthemum crystallinum*
DESCRIPTION: protein kinase. MCPK9.
- 20 AAG31326.1 AF178575 *Vitis vinifera*
DESCRIPTION: putative serine/threonine kinase GDBrPK. GDBrPK. similar to
SNF protein kinase.
- 25 CAA06503.1 AJ005373 *Craterostigma plantagineum*
DESCRIPTION: protein kinase. cppk1.
- 30 AAF21062.1 AF216527 *Dunaliella tertiolecta*
DESCRIPTION: calcium-dependent protein kinase. CPK1; CDPK.
- CAA89202.1 Z49233 *Chlamydomonas eugametos*
DESCRIPTION: calcium-stimulated protein kinase.
- 35 689

- AAC49826.1 U71604 *Catharanthus roseus*
DESCRIPTION: involved in the second to last step in vindoline
biosynthesis. desacetoxyvindoline 4-hydroxylase. CRSD4H. 2-oxoglutarate
40 dependent dioxygenase.
- AAB97311.1 AF008597 *Catharanthus roseus*
DESCRIPTION: desacetoxyvindoline-4-hydroxylase. CRSD4H. 2-oxoglutarate
45 dependent dioxygenase; involved in the second to last step in vindoline
biosynthesis.

- AAC49827.1 U71605 Catharanthus roseus
 DESCRIPTION: involved in the second to last step in vindoline
 biosynthesis. desacetoxyvindoline 4-hydroxylase. CRSD4H. 2-oxoglutarate
 dependent dioxygenase.
- BAA37127.1 AB012203 Lactuca sativa
 DESCRIPTION: 2-oxoglutarate-dependent dioxygenase. gibberelin 20-oxidase.
 Ls20ox1.
- BAA95828.1 AP002069 Oryza sativa
 DESCRIPTION: ESTs D47168(S12332),D46350(S10967) correspond to a
 region of
 the predicted gene. Similar to Prunus armeniaca
 ethylene-forming-enzyme-like dioxygenase. (U97530).
- AAD56580.1 AF184273 Daucus carota
 DESCRIPTION: leucoanthocyanidin dioxygenase 1. LDOX1. 2-oxoglutarate
 dependent dioxygenase.
- AAB39995.1 U82432 Dianthus caryophyllus
 DESCRIPTION: anthocyanidin synthase. allele: S; 2-oxoglutarat-dependent
 dioxygenase.
- AAD56581.1 AF184274 Daucus carota
 DESCRIPTION: leucoanthocyanidin dioxygenase 2. LDOX. 2-oxoglutarate
 dependent dioxygenase.
- 691

 AAA34002.1 M67449 Glycine max
 DESCRIPTION: protein kinase. PK6.
- CAC09580.1 AJ298992 Fagus sylvatica
 DESCRIPTION: Absciscic acid (ABA) and calcium induced protein kinase.
 protein kinase (PK). pk1.
- AAK11734.1 AY027437 Arachis hypogaea

DESCRIPTION: serine/threonine/tyrosine kinase.

5 BAB16918.1 AP002863 *Oryza sativa*
DESCRIPTION: putative protein kinase. P0005A05.22.

10 CAA06334.1 AJ005077 *Lycopersicon esculentum*
DESCRIPTION: protein kinase. TCTR2 protein. TCTR2.

15 AAD10057.1 AF110519 *Lycopersicon esculentum*
DESCRIPTION: ethylene-inducible CTR1-like protein kinase. protein kinase
homolog; ethylene and fruit ripening inducible CTR1-like protein kinase;
TCTR1v.

20 AAD10056.1 AF110518 *Lycopersicon esculentum*
DESCRIPTION: ethylene-inducible CTR1-like protein kinase. protein kinase
homolog; ethylene and fruit ripening inducible CTR1-like protein kinase;
TCTR1.

25 CAA73722.1 Y13273 *Lycopersicon esculentum*
DESCRIPTION: putative protein kinase.

30 AAD46406.1 AF096250 *Lycopersicon esculentum*
DESCRIPTION: ethylene-responsive protein kinase TCTR1. ER50.
serine/threonine kinase; similar to *Arabidopsis thaliana* negative
regulator of the ethylene response pathway encoded by GenBank Accession
Number L08789.

35 AAG31141.1 AF305911 *Oryza sativa*
DESCRIPTION: EDR1. EDR1. MAP kinase kinase kinase; similar to
Arabidopsis thaliana EDR1.

40 AAG31142.1 AF305912 *Hordeum vulgare*
DESCRIPTION: EDR1. EDR1. MAP kinase kinase kinase; similar to
Arabidopsis thaliana EDR1.

45

AAK30005.1 AY029067 Rosa hybrid cultivar
DESCRIPTION: CTR2 protein kinase.

5 AAK21965.1 AY028699 Brassica napus
DESCRIPTION: receptor protein kinase PERK1.

10 BAB16871.1 AP002537 Oryza sativa
DESCRIPTION: putative protein kinase APK1AArabidopsis thaliana.
P0001B06.24. contains ESTs C22608(R3192),D25110(R3192).

15 AAF91323.1 AF244889 Glycine max
DESCRIPTION: receptor-like protein kinase 2. RLK2. GmRLK2.

20 AAF91324.1 AF244890 Glycine max
DESCRIPTION: receptor-like protein kinase 3. RLK3. GmRLK3.

25 AAK00425.1 AC069324 Oryza sativa
DESCRIPTION: Putative protein kinase. OSJNBa0071K19.11.

30 BAB39409.1 AP002901 Oryza sativa
DESCRIPTION: putative protein kinase. P0456F08.9. contains EST
C23560(R0290).

35 AAF91322.1 AF244888 Glycine max
DESCRIPTION: receptor-like protein kinase 1. RLK1. GmRLK1.

40 BAB18292.1 AP002860 Oryza sativa
DESCRIPTION: putative receptor-like protein kinase. P0409B08.19.

45 AAK16409.1 AF320086 Zea mays
DESCRIPTION: serine threonine kinase 1. stk1. expressed in mature tassel.

45 BAA06538.1 D31737 Nicotiana tabacum
DESCRIPTION: protein-serine/threonine kinase.

BAA21132.1 D88193 Brassica rapa
DESCRIPTION: S-receptor kinase. SRK9 (B.c).

5 BAA06285.1 D30049 Brassica rapa
DESCRIPTION: S-receptor kinase SRK9.

10 BAB39873.1 AP002882 Oryza sativa
DESCRIPTION: putative protein kinase. P0439B06.8. contains ESTs
AU056701(S20808),AU056702(S20808).

15 CAB54520.1 AJ238845 Brassica napus
DESCRIPTION: putative role in cell cycle control. MAP3K epsilon 1 protein
kinase. MAP3Kel.

20 CAA97692.1 Z73295 Catharanthus roseus
DESCRIPTION: receptor-like protein kinase. CRPK1. Autophosphorylation
predominantly on Thr, less on Ser. Mechanism: autophosphorylation in cis.

25 CAA08995.1 AJ010091 Brassica napus
DESCRIPTION: MAP3K alpha 1 protein kinase. MAP3K alpha 1.

30 BAB40094.1 AP003210 Oryza sativa
DESCRIPTION: putative receptor protein kinase. OSJNBa0010K01.7.

35 CAB51834.1 00069 Oryza sativa
DESCRIPTION: 11332.5. contains eukaryotic protein kinase domain PF.

BAB40021.1 AP003021 Oryza sativa
DESCRIPTION: putative wall-associated kinase 2. P0503E05.25. contains EST
C24950(S16264).

40 AAF43496.1 AF131222 Lophopyrum elongatum
DESCRIPTION: protein serine/threonine kinase. ESI47. induced in roots by
salt stress, osmotic stress, and ABA treatment.

45 AAK11674.1 AF339747 Lophopyrum elongatum

DESCRIPTION: protein kinase. ESI47.

- 5 AAA62232.1 U00443 Brassica napus
DESCRIPTION: S-receptor kinase. protein contains an immunoglobulin-like domain.
- 10 BAB40010.1 AP003021 Oryza sativa
DESCRIPTION: putative wall-associated kinase 2. P0503E05.12.
- 15 AAC36318.1 AF053127 Malus x domestica
DESCRIPTION: leucine-rich receptor-like protein kinase. LRPKm1.
- 20 AAC23542.1 U20948 Ipomoea trifida
DESCRIPTION: receptor protein kinase. IRK1.
- 25 BAA23676.1 AB000970 Brassica rapa
DESCRIPTION: receptor kinase 1. BcRK1.
- 30 BAB18321.1 AP002865 Oryza sativa
DESCRIPTION: putative receptor protein kinase. P0034C11.11.
- 35 BAA92836.1 AB032473 Brassica oleracea
DESCRIPTION: S18 S-locus receptor kinase. SRK18.
- 40 AAA33915.1 L27821 Oryza sativa
DESCRIPTION: receptor type serine/threonine kinase. protein kinase.
- 45 BAB40081.1 AP003074 Oryza sativa
DESCRIPTION: putative receptor protein kinase. OSJNBa0004G10.30.
- AAD38286.1 AC007789 Oryza sativa
DESCRIPTION: putative protein kinase. OSJNBa0049B20.13.
- 45 BAA92837.1 AB032474 Brassica oleracea
DESCRIPTION: S60 S-locus receptor kinase. SRK60.

-
- 5 AAK16172.1 AC079887 *Oryza sativa*
DESCRIPTION: putative glucosyltransferase. OSJNBa0040E01.14.
- 10 AAF17077.1 AF199453 *Sorghum bicolor*
DESCRIPTION: UDP-glucose glucosyltransferase.
UDP-glucose:p-hydroxymandelonitrile-o- glucosyltransferase.
- 15 AAF61647.1 AF190634 *Nicotiana tabacum*
DESCRIPTION: UDP-glucose:salicylic acid glucosyltransferase. SA-GTase.
- 20 BAA89009.1 AB027455 *Petunia x hybrida*
DESCRIPTION: anthocyanin 5-O-glucosyltransferase. PH1.
- 25 AAF98390.1 AF287143 *Brassica napus*
DESCRIPTION: catalyzes the transfer of glucose from UDP-glucose to
sinapate and some other hydroxycinnamates (4-coumarate, caffeate,
ferulate). UDP-glucose:sinapate glucosyltransferase. SGT1. SGT.
- 30 AAD21086.1 AF127218 *Forsythia x intermedia*
DESCRIPTION: adds glucose residue to position 3 of flavonoid compounds.
flavonoid 3-O-glucosyltransferase. UFGT.
- 35 BAA93039.1 AB033758 *Citrus unshiu*
DESCRIPTION: limonoid UDP-glucosyltransferase. LGTase.
- 40 BAA12737.1 D85186 *Gentiana triflora*
DESCRIPTION: UDP-glucose:flavonoid-3-glucosyltransferase.
- 45 CAA54612.1 X77462 *Manihot esculenta*
DESCRIPTION: UTP-glucose glucosyltransferase. CGT5.

BAA19155.1 AB000623 *Nicotiana tabacum*
DESCRIPTION: glucosyl transferase. JIGT.

5

BAA89008.1 AB027454 *Petunia x hybrida*
DESCRIPTION: anthocyanidin 3-O-glucosyltransferase. PGT8.

10 BAB17060.1 AP002523 *Oryza sativa*
DESCRIPTION: putative glucosyl transferase. P0013F10.6.

15 BAA90787.1 AB038248 *Ipomoea batatas*
DESCRIPTION: UDP glucose: flavonoid 3-O-glucosyltransferase. uf3gt.

20 AAK16178.1 AC079887 *Oryza sativa*
DESCRIPTION: putative glucosyltransferase. OSJNBa0040E01.5.

AAK16175.1 AC079887 *Oryza sativa*
DESCRIPTION: putative glucosyltransferase. OSJNBa0040E01.15.

25 AAB36653.1 U32644 *Nicotiana tabacum*
DESCRIPTION: immediate-early salicylate-induced glucosyltransferase.
IS5a.

30 AAB36652.1 U32643 *Nicotiana tabacum*
DESCRIPTION: immediate-early salicylate-induced glucosyltransferase.
IS10a.

35 AAK28303.1 AF346431 *Nicotiana tabacum*
DESCRIPTION: phenylpropanoid:glucosyltransferase 1. togt1.
glucosyltransferase.

40 AAK28304.1 AF346432 *Nicotiana tabacum*
DESCRIPTION: phenylpropanoid:glucosyltransferase 2. togt2.
glucosyltransferase.

45 BAB17061.1 AP002523 *Oryza sativa*

DESCRIPTION: putative glucosyl transferase. P0013F10.7. contains EST C73149(E2992).

5 CAA30761.1 X07940 Zea mays

DESCRIPTION: UDPglucose flavonoid glycosyl-transferase. Bz-McC.

10 AAK16410.1 AF320086 Zea mays

DESCRIPTION: UDPG-flavonoid 3-O-glucosyl transferase. bz.

15 CAA31855.1 X13500 Zea mays

DESCRIPTION: UDPglucose:flavonol 3-O-glucosyltransferase.

20 BAB17059.1 AP002523 Oryza sativa

DESCRIPTION: putative glucosyl transferase. P0013F10.5.

BAA36421.1 AB013596 Perilla frutescens

DESCRIPTION: UDP-glucose:anthocynin 5-O-glucosyltransferase. PF3R4.

25 AAB86473.1 AF028237 Ipomoea purpurea

DESCRIPTION: UDP glucose: flavonoid 3-O-glucosyltransferase. UF3GT-FL1.

30 CAA30760.1 X07937 Zea mays

DESCRIPTION: UDPglucose flavonoid glycosyl transferase. Bz-W22.

35 BAB41021.1 AB047094 Vitis vinifera

DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. RuUFGT1.

BAB41019.1 AB047092 Vitis vinifera

DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. ItUFGT1.

40 BAB41025.1 AB047098 Vitis vinifera

DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. FIUFGT1.

45 AAD55985.1 AF165148 Petunia x hybrida

DESCRIPTION: catalyzes the penultimate step of flavonol

glucosylgalactoside biosynthesis from UDP-galactose and flavonol aglycones
in petunia pollen. UDP-galactose:flavonol 3-O-galactosyltransferase.
F3galtase.

5

BAB41018.1 AB047091 Vitis labrusca x Vitis vinifera
DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. KyUFGT2.
The
gene originated in one of the parents V. vinifera cv. Centennial.

10

BAB41017.1 AB047090 Vitis labrusca x Vitis vinifera
DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. KyUFGT1.
The
gene was derived from one of the parents V. labruscana cv. Ishiharawase.

15

AAK16181.1 AC079887 Oryza sativa
DESCRIPTION: putative glucosyltransferase. OSJNBa0040E01.16.

20

BAB41023.1 AB047096 Vitis vinifera
DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. AlUFGT1.

25

CAA59450.1 X85138 Lycopersicon esculentum
DESCRIPTION: twi1. homologous to glucosyltransferases.

30

CAA54614.1 X77464 Manihot esculenta
DESCRIPTION: UTP-glucose glucosyltransferase. CGT7.

35

AAB81682.1 AF000371 Vitis vinifera
DESCRIPTION: UDP glucose:flavonoid 3-o-glucosyltransferase.

40

AAB81683.1 AF000372 Vitis vinifera
DESCRIPTION: UDP glucose:flavonoid 3-o-glucosyltransferase.

45

BAB41024.1 AB047097 Vitis vinifera
DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. AlUFGT2.

CAA54558.1 X77369 Solanum melongena

DESCRIPTION: glycosyl transferase. GT.

5 BAB41026.1 AB047099 Vitis vinifera
DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. FIUFGT2.

10 BAB41020.1 AB047093 Vitis vinifera
DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. ItUFGT2.

BAB41022.1 AB047095 Vitis vinifera
DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. RuUFGT2.

15 BAA19659.1 AB002818 Perilla frutescens
DESCRIPTION: flavonoid 3-O-glucosyltransferase. UDP glucose.

20 AAG25643.1 AF303396 Phaseolus vulgaris
DESCRIPTION: UDP-glucosyltransferase HRA25. putative; defense associated.
694

25 BAB40923.1 AB059401 Oryza sativa
DESCRIPTION: putative selenium binding protein. Os SBP.
695

30 AAD26942.1 AF119050 Datisca glomerata
DESCRIPTION: zinc-finger protein 1. zfp1. DgZFP1.

35 BAA05079.1 D26086 Petunia x hybrida
DESCRIPTION: zinc-finger protein.

40 AAB39638.1 U68763 Glycine max
DESCRIPTION: putative transcription factor. SCOF-1. scof-1. zinc-finger protein.

45 CAB77055.1 Y18788 Medicago sativa
DESCRIPTION: putative TFIIIA (or kruppel)-like zinc finger protein.

AAC06243.1 AF053077 *Nicotiana tabacum*
DESCRIPTION: transcription factor. osmotic stress-induced zinc-finger protein. zfp.

5

BAA05077.1 D26084 *Petunia x hybrida*
DESCRIPTION: zinc-finger DNA binding protein.

10 BAA05076.1 D26083 *Petunia x hybrida*
DESCRIPTION: zinc-finger DNA binding protein.

15 AAB53260.1 U76554 *Brassica rapa*
DESCRIPTION: transcription factor. zinc-finger protein-1. BR42.

20 BAA05078.1 D26085 *Petunia x hybrida*
DESCRIPTION: zinc-finger DNA binding protein.

AAB53261.1 U76555 *Brassica rapa*
DESCRIPTION: zinc-finger protein BcZFP1. BcZFP1(3-2z).

25

AAK01713.1 AF332876 *Oryza sativa*
DESCRIPTION: zinc finger transcription factor ZF1.

30 BAA21920.1 AB006598 *Petunia x hybrida*
DESCRIPTION: ZPT2-11. C2H2 zinc finger protein, 2finger.

35 BAA21922.1 AB006600 *Petunia x hybrida*
DESCRIPTION: ZPT2-13. C2H2 zinc finger protein, 2finger.

40 BAA19112.1 AB000453 *Petunia x hybrida*
DESCRIPTION: PETHy;ZPT3-1. Cys(2) His(2) zinc finger protein, 3 fingers.

BAA21927.1 AB006605 *Petunia x hybrida*
DESCRIPTION: ZPT3-3. C2H2 zinc finger protein, 3 finger.

45

BAA96071.1 AB035133 *Petunia x hybrida*

DESCRIPTION: C2H2 zinc-finger protein ZPT3-3. ZPT3-3.

5 BAA96070.1 AB035132 Petunia x hybrida
DESCRIPTION: C2H2 zinc-finger protein ZPT2-10. PETHy;ZPT2-10.

10 BAA21919.1 AB006597 Petunia x hybrida
DESCRIPTION: ZPT2-10. C2H2 zinc finger protein, 2 finger.

BAA19114.1 AB000455 Petunia x hybrida
DESCRIPTION: PETHy;ZPT4-1. Cys(2) His(2) zinc finger protein, 4 fingers.

15 BAA21921.1 AB006599 Petunia x hybrida
DESCRIPTION: ZPT2-12. C2H2 zinc finger protein, 2 finger.

20 BAA21928.1 AB006606 Petunia x hybrida
DESCRIPTION: ZPT4-4. C2H2 zinc finger protein, 4 finger.

25 CAA60828.1 X87374 Pisum sativum
DESCRIPTION: putative zinc finger protein.

30 BAA21925.1 AB006603 Petunia x hybrida
DESCRIPTION: ZPT2-8. C2H2 zinc finger protein, 2 finger.

BAA19111.1 AB000452 Petunia x hybrida
DESCRIPTION: PETHy;ZPT2-6. Cys(2) His(2) zinc finger protein, 2 fingers.

35 BAA19926.1 AB000456 Petunia x hybrida
DESCRIPTION: PETHy; ZPT4-2. C2H2 zinc finger protein, 4 finger.

40 BAA21924.1 AB006602 Petunia x hybrida
DESCRIPTION: ZPT2-7. C2H2 zinc finger protein, 2finger.

45 BAA21923.1 AB006601 Petunia x hybrida
DESCRIPTION: ZPT2-14. C2H2 zinc finger protein, 2 finger.

BAA21926.1 AB006604 Petunia x hybrida
DESCRIPTION: ZPT2-9. C2H2 zinc finger protein, 2 finger.

5

BAA19110.1 AB000451 Petunia x hybrida
DESCRIPTION: PETHy;ZPT2-5. Cys(2) His(2) zinc finger protein, 2 fingers.

10 BAA19113.1 AB000454 Petunia x hybrida
DESCRIPTION: PETHy;ZPT3-2. Cys(2) His(2) zinc finger protein, 3 fingers.

702

15 AAK29419.1 AF348319 Zea mays
DESCRIPTION: TERMINAL EAR1. tel. RNA-binding protein; 3 putative
RRM
motifs; similar to Schizosaccharomyces pombe Mei2 and Arabidopsis AML1;
tel cDNA sequence is presented in GenBank Accession Number AF047852.

20

CAA57551.1 X82030 Phaseolus vulgaris
DESCRIPTION: chloroplast RNA binding protein. RNP1.

25

CAA66479.1 X97905 Vicia faba
DESCRIPTION: RNA- or ssDNA-binding protein.

30 CAC01237.1 AJ292767 Nicotiana plumbaginifolia
DESCRIPTION: nuclear RNA binding protein. RNA Binding Protein 45. rbp45.

35 AAF66823.1 AF190655 Nicotiana tabacum
DESCRIPTION: poly(A)-binding protein. PABP.

AAK30205.1 AF349964 Daucus carota
DESCRIPTION: poly(A)-binding protein. Translin1P.

40

AAG59664.1 AC084319 Oryza sativa
DESCRIPTION: putative RNA binding protein. OSJNBa0004B24.1.

45

AAB38974.1 U81318 *Triticum aestivum*
DESCRIPTION: poly(A)-binding protein. wheatpab.

5 CAA81127.1 Z26042 *Anemia phyllitidis*
DESCRIPTION: Binding to the poly(A)-tail of eukaryotic mRNAs.
poly(A)-mRNA binding protein.

10 AAA79045.1 U34742 *Spinacia oleracea*
DESCRIPTION: 24 kDa RNA binding protein.

AAC39368.1 AF043297 *Chlamydomonas reinhardtii*
15 DESCRIPTION: poly(A) binding protein RB47. PABP.

AAF63202.1 AF240679 *Cucumis sativus*
20 DESCRIPTION: poly(A)-binding protein.

CAA11894.1 AJ224325 *Hordeum vulgare*
DESCRIPTION: nucleic acid-binding protein. cp33Hv.

25 AAF66825.1 AF190657 *Nicotiana tabacum*
DESCRIPTION: poly(A)-binding protein. PABP.

30 CAA06469.1 AJ005286 *Hordeum vulgare*
DESCRIPTION: nucleic acid-binding protein. cp31AHv protein.

709

35 AAB36546.1 U77940 *Phaseolus vulgaris*
DESCRIPTION: polyubiquitin. expression is regulated by heavy metal
stress, UV, virus infection, heat shock and wounding treatment, this
suggests that ubiquitin plays a role in plant defense.

40 714

CAA61946.1 X89828 *Pisum sativum*
DESCRIPTION: fructose-1,6-bisphosphate aldolase.

45 AAB61592.1 AF003124 *Mesembryanthemum crystallinum*

DESCRIPTION: fructose-bisphosphate aldolase.

- 5 CAB77243.2 AJ133146 *Persea americana*
DESCRIPTION: glycolytic enzyme, sixth step in glycolysis.
fructose-bisphosphate aldolase. alf.
- 10 BAA08845.1 D50307 *Oryza sativa*
DESCRIPTION: aldolase C-1.
- 15 BAA08830.1 D50301 *Oryza sativa*
DESCRIPTION: aldolase C-1.
- 20 CAA46649.1 X65742 *Spinacia oleracea*
DESCRIPTION: fructose-bisphosphate aldolase.
- 25 BAA02729.1 D13512 *Oryza sativa*
DESCRIPTION: cytoplasmic aldolase.
- 30 AAG21429.1 AF308587 *Fragaria x ananassa*
DESCRIPTION: cytosolic aldolase. SCA1.
- 35 CAA37290.1 X53130 *Oryza sativa*
DESCRIPTION: fructose-diphosphate aldolase (AA 1-358).
- 40 CAA31366.1 X12872 *Zea mays*
DESCRIPTION: fructose bisphosphate aldolase.
- 45 AAA33435.1 M16220 *Zea mays*
DESCRIPTION: aldolase.
- CAA61947.1 X89829 *Pisum sativum*
DESCRIPTION: fructose-1,6-bisphosphate aldolase.
- CAA06308.1 AJ005041 *Cicer arietinum*
DESCRIPTION: cytosolic fructose-1,6-bisphosphate aldolase.

- AAK19324.1 AF329673 *Dunaliella salina*
DESCRIPTION: fructose-bisphosphate aldolase isoenzyme 1. salt-induced.
- 5
- CAA71408.1 Y10380 *Solanum tuberosum*
DESCRIPTION: homologous to plastidic aldolases.
- 10
- BAA77603.1 AB027002 *Nicotiana paniculata*
DESCRIPTION: plastidic aldolase.
- 15
- BAA77604.1 AB027001 *Nicotiana paniculata*
DESCRIPTION: plastidic aldolase NPALDP1. NpAldP1.
- 20
- AAA33642.1 M97476 *Pisum sativum*
DESCRIPTION: aldolase.
- 25
- AAA33643.1 M97477 *Pisum sativum*
DESCRIPTION: aldolase.
- 30
- BAA02730.1 D13513 *Oryza sativa*
DESCRIPTION: chloroplastic aldolase.
- 35
- CAA47293.1 X66814 *Spinacia oleracea*
DESCRIPTION: fructose-bisphosphate aldolase.
- 40
- AAK19325.1 AF329674 *Dunaliella salina*
DESCRIPTION: fructose-bisphosphate aldolase isoenzyme 2. salt-induced.
- 45
- CAB46520.1 AJ243524 *Phleum pratense*
DESCRIPTION: sixth step in glycolysis. putative fructose-bisphosphate aldolase.

CAA09669.1 AJ011516 Scherffelia dubia
DESCRIPTION: fructose-bisphosphate aldolase.

5

CAA49590.1 X69969 Chlamydomonas reinhardtii
DESCRIPTION: fructose-bisphosphate aldolase. ALDCHL.

10 AAC60574.1 S72951 Chloroplast Chlamydomonas reinhardtii
DESCRIPTION: fructosediphosphate aldolase. fructosediphosphate aldolase.
This sequence comes from Fig. 4.

15 AAB70542.1 AF017362 Oryza sativa
DESCRIPTION: aldolase.

20 BAA76430.1 AB025002 Cicer arietinum
DESCRIPTION: fructose-bisphosphate aldolase.

25 AAD20818.1 AF107590 Dendrobium grex Madame Thong-In
DESCRIPTION: putative fructose-bisphosphate aldolase. otg11.

30 BAA11395.1 D78500 Brassica rapa
DESCRIPTION: putative aldolase. Sequence homologous to cytoplasmic
aldolase of rice (D13512).

BAA78593.1 AU066535 Chlamydomonas sp. HS-5
DESCRIPTION: fructose-bisphosphate aldolase precursor. NaCl inducible.

35 CAC34412.1 Y18576 Flaveria trinervia
DESCRIPTION: fructose-bisphosphate aldolase. alf.

715
40 -----
AAK07429.1 AF321287 Musa acuminata
DESCRIPTION: beta-glucosidase.

45 AAC69619.1 AF072736 Pinus contorta
DESCRIPTION: beta-glucosidase.

- AAF04007.1 AF163097 *Dalbergia cochinchinensis*
DESCRIPTION: beta-fucosidase beta-glucosidase. daltrochitin
8'-O-beta-glucoside beta-glucosidase precursor. BGLU1. rotenoid
beta-glucosidase.
- AAA93032.1 U50201 *Prunus serotina*
DESCRIPTION: hydrolysis of the cyanogenic glucoside (R)-prunasin.
prunasin hydrolase precursor. located in protein bodies of *Prunus* seeds;
encodes 8 putative N-glycosylation sites (N-X-S/T); encodes NEP and ITENG
motifs characteristic of the BGA family of beta-glucosidases.
- BAA78708.1 AB003089 *Polygonum tinctorium*
DESCRIPTION: beta-glucosidase.
- AAA91166.1 U39228 *Prunus avium*
DESCRIPTION: beta-glucosidase.
- BAA11831.1 D83177 *Costus speciosus*
DESCRIPTION: saponin metabolite. furostanol glycoside
26-O-beta-glucosidase (F26G). functional expression in *E. coli*; one of the
F26G isozymes.
- AAF34650.1 AF221526 *Prunus serotina*
DESCRIPTION: hydrolysis of the cyanogenic glucoside (R)-prunasin.
prunasin hydrolase isoform PHA precursor. beta-glucosidase; contains 6
potential N-glycosylation sites (N-X-S/T); glycosyl hydrolase family 1
member.
- AAG25897.1 AF170087 *Cucurbita pepo*
DESCRIPTION: silverleaf whitefly-induced protein 3. SLW3. similar to
beta-glucosidase.
- AAG00614.1 AF293849 *Secale cereale*
DESCRIPTION: beta-glucosidase.
- AAB22162.1 S35175 *Manihot esculenta*

DESCRIPTION: linamarase. linamarase. beta-glucosidase; Method: conceptual translation with partial peptide sequencing; This sequence comes from Fig. 4.

5

AAF03675.1 AF149311 Rauvolfia serpentina

DESCRIPTION: hydrolyses the glucoalkaloid raucaffricine.
raucaffricine-O-beta-D-glucosidase. beta glucosidase; RG; part of the
Ajmaline biosynthesis pathway; belongs to family 1 of the glucosyl
hydrolases.

10

AAA87339.1 L41869 Hordeum vulgare

DESCRIPTION: beta-glucosidase. BGQ60. expression specific to starchy
endosperm of seed.

15

AAC49177.1 U33817 Sorghum bicolor

DESCRIPTION: beta-glucosidase, catalyzes the hydrolysis of the cyanogenic
beta-glucoside dhurrin. dhurrinase.

20

CAA64442.1 X94986 Manihot esculenta

DESCRIPTION: beta glucosidase. bglA.

25

AAD02839.1 AF082991 Avena sativa

DESCRIPTION: beta-D-glucosidase beta subunit precursor. P60b.
avenacosidase.

30

AAD09850.1 U44087 Zea mays

DESCRIPTION: beta-D-glucosidase precursor. glu2. product subunit
structure: autodimer of 58.4 kDa monomers Allele: glu2-B73.

35

AAD10503.1 U33816 Zea mays

DESCRIPTION: functions in defense of young plant parts against pests via
the production of hydroxamic acids from hydroxamic acid glucosides.
beta-D-glucosidase.

40

AAB03266.1 U44773 Zea mays

DESCRIPTION: beta-D-glucosidase. glu1. autodimer of 58.4 kD monomers.

45

AAF34651.1 AF221527 *Prunus serotina*
DESCRIPTION: putative prunasin hydrolase precursor. beta-glucosidase;
glycosyl hydrolase family 1 member.

5

AAA84906.1 U28047 *Oryza sativa*
DESCRIPTION: catalyzes the release of either giberellin or cyanogenic
substances from their glucoconjugates. beta glucosidase. beta-D-glucoside
glucohydrolase; dimer of 60 kDa monomers; localized in the plastid.

10

CAC08209.1 AJ005950 *Cicer arietinum*
DESCRIPTION: beta-glucosidase.

15 718

AAF61647.1 AF190634 *Nicotiana tabacum*
DESCRIPTION: UDP-glucose:salicylic acid glucosyltransferase. SA-GTase.

20

BAA89009.1 AB027455 *Petunia x hybrida*
DESCRIPTION: anthocyanin 5-O-glucosyltransferase. PH1.

25

BAA93039.1 AB033758 *Citrus unshiu*
DESCRIPTION: limonoid UDP-glucosyltransferase. LGTase.

30

BAA36423.1 AB013598 *Verbena x hybrida*
DESCRIPTION: UDP-glucose:anthocyanin 5-O-glucosyltransferase. HGT8.

35

BAA36421.1 AB013596 *Perilla frutescens*
DESCRIPTION: UDP-glucose:anthocyanin 5-O-glucosyltransferase. PF3R4.

40

AAF98390.1 AF287143 *Brassica napus*
DESCRIPTION: catalyzes the transfer of glucose from UDP-glucose to
sinapate and some other hydroxycinnamates (4-coumarate, caffeate,
ferulate). UDP-glucose:sinapate glucosyltransferase. SGT1. SGT.

45

BAA36422.1 AB013597 *Perilla frutescens*
DESCRIPTION: UDP-glucose:anthocyanin 5-O-glucosyltransferase homologue.
PF3R6.

- 5 BAB07962.1 AP002524 *Oryza sativa*
DESCRIPTION: putative anthocyanin 5-O-glucosyltransferase. P0406H10.16.
contains ESTs AU067881(C10481),AU067882(C10481).
- 10 AAD21086.1 AF127218 *Forsythia x intermedia*
DESCRIPTION: adds glucose residue to position 3 of flavonoid compounds.
flavonoid 3-O-glucosyltransferase. UFGT.
- 15 AAK16178.1 AC079887 *Oryza sativa*
DESCRIPTION: putative glucosyltransferase. OSJNBa0040E01.5.
- 20 BAA12737.1 D85186 *Gentiana triflora*
DESCRIPTION: UDP-glucose:flavonoid-3-glucosyltransferase.
- 25 AAK16181.1 AC079887 *Oryza sativa*
DESCRIPTION: putative glucosyltransferase. OSJNBa0040E01.16.
- 30 AAK16175.1 AC079887 *Oryza sativa*
DESCRIPTION: putative glucosyltransferase. OSJNBa0040E01.15.
- AAK16172.1 AC079887 *Oryza sativa*
DESCRIPTION: putative glucosyltransferase. OSJNBa0040E01.14.
- 35 CAA59450.1 X85138 *Lycopersicon esculentum*
DESCRIPTION: twi1. homologous to glucosyltransferases.
- 40 AAF17077.1 AF199453 *Sorghum bicolor*
DESCRIPTION: UDP-glucose glucosyltransferase.
UDP-glucose:p-hydroxymandelonitrile-o- glucosyltransferase.
- 45 BAA89008.1 AB027454 *Petunia x hybrida*
DESCRIPTION: anthocyanidin 3-O-glucosyltransferase. PGT8.
- AAB81683.1 AF000372 *Vitis vinifera*
DESCRIPTION: UDP glucose:flavonoid 3-o-glucosyltransferase.

BAB41017.1 AB047090 Vitis labrusca x Vitis vinifera
DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. KyUFGT1.

The
gene was derived from one of the parents V. labruscana cv. Ishiharawase.

AAB81682.1 AF000371 Vitis vinifera
DESCRIPTION: UDP glucose:flavonoid 3-o-glucosyltransferase.

BAB41022.1 AB047095 Vitis vinifera
DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. RuUFGT2.

BAB41020.1 AB047093 Vitis vinifera
DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. ItUFGT2.

BAB41021.1 AB047094 Vitis vinifera
DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. RuUFGT1.

BAB41019.1 AB047092 Vitis vinifera
DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. ItUFGT1.

BAA83484.1 AB031274 Scutellaria baicalensis
DESCRIPTION: UDP-glucose: flavonoid 7-O-glucosyltransferase. ufgt.

BAB41025.1 AB047098 Vitis vinifera
DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. FIUFGT1.

BAB41023.1 AB047096 Vitis vinifera
DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. AIUFGT1.

BAA90787.1 AB038248 Ipomoea batatas
DESCRIPTION: UDP glucose: flavonoid 3-O-glucosyltransferase. uf3gt.

BAA19659.1 AB002818 Perilla frutescens
DESCRIPTION: flavonoid 3-O-glucosyltransferase. UDP glucose.

- BAB41018.1 AB047091 *Vitis labrusca* x *Vitis vinifera*
 DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. KyUFGT2.
 5 The
 gene originated in one of the parents *V. vinifera* cv. Centennial.
- AAB36652.1 U32643 *Nicotiana tabacum*
 10 DESCRIPTION: immediate-early salicylate-induced glucosyltransferase.
 IS10a.
- AAK28304.1 AF346432 *Nicotiana tabacum*
 15 DESCRIPTION: phenylpropanoid:glucosyltransferase 2. togt2.
 glucosyltransferase.
- BAB41024.1 AB047097 *Vitis vinifera*
 20 DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. AlUFGT2.
- BAB41026.1 AB047099 *Vitis vinifera*
 25 DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. FIUFGT2.
- CAA31855.1 X13500 *Zea mays*
 DESCRIPTION: UDP-glucose:flavonol 3-O-glucosyltransferase.
- 30 AAB86473.1 AF028237 *Ipomoea purpurea*
 DESCRIPTION: UDP glucose: flavonoid 3-O-glucosyltransferase. UF3GT-FL1.
- 35 CAA54614.1 X77464 *Manihot esculenta*
 DESCRIPTION: UTP-glucose glucosyltransferase. CGT7.
- 719

- 40 AAC24195.1 AF020425 *Nicotiana tabacum*
 DESCRIPTION: calmodulin binding protein. glutamate decarboxylase isozyme
 1. NtGAD1. calcium-calmodulin-dependent enzyme.
- 45 AAK18620.1 AF352732 *Nicotiana tabacum*
 DESCRIPTION: converts glutamate to gamma-aminobutyric acid. glutamate

decarboxylase isozyme 3. GAD; GAD3; NtGAD3; calcium/calmodulin-dependent enzyme.

5

AAB40608.1 U54774 *Nicotiana tabacum*
DESCRIPTION: glutamate decarboxylase. NtGAD1. calmodulin regulated enzyme; calmodulin-binding protein.

10

AAA33710.1 L16977 *Petunia x hybrida*
DESCRIPTION: glutamate decarboxylase. gad.

15

AAA33709.1 L16797 *Petunia x hybrida*
DESCRIPTION: glutamate decarboxylase. gad.

20

AAC39483.1 AF020424 *Nicotiana tabacum*
DESCRIPTION: glutamate decarboxylase isozyme 2. NtGAD2. calcium-calmodulin-dependent enzyme.

25

BAB32870.1 AB056062 *Oryza sativa*
DESCRIPTION: glutamate decarboxylase. GAD.

30

BAB32868.1 AB056060 *Oryza sativa*
DESCRIPTION: glutamate decarboxylase. GAD.

35

CAA56812.1 X80840 *Lycopersicon esculentum*
DESCRIPTION: homology to pyroxidal-5'-phosphate-dependant glutamate decarboxylases; putative start codon.

40

BAB32871.1 AB056063 *Oryza sativa*
DESCRIPTION: glutamate decarboxylase. GAD.

BAB32869.1 AB056061 *Oryza sativa*
DESCRIPTION: glutamate decarboxylase. GAD.

45

CAA50719.1 X71900 *Lycopersicon esculentum*
DESCRIPTION: histidine decarboxylase. hdc. pyridoxal 5'-phosphate

dependant.

720

-
- 5 BAA92713.1 AP001389 *Oryza sativa*
DESCRIPTION: ESTs AU033035(S1515),D39871(S1515) correspond to a
region of
the predicted gene. Similar to *Arabidopsis thaliana* chromosome II BAC
F22D22 genomic sequence; putative glucan synthase (AC006223).

10

- AAD25952.1 AF085717 *Gossypium hirsutum*
DESCRIPTION: putative callose synthase catalytic subunit. CFL1. cotton
FKS1-like protein; similar to *Saccharomyces cerevisiae* beta-1,3-glucan
synthase subunit FKS1.

15

721

-
- 20 CAB55396.1 AL117264 *Oryza sativa*
DESCRIPTION: zwh12.1. similar to *Arabidopsis* putative
UDP-galactase-4-epimerase (AC007060); Method: conceptual translation with
partial peptide sequencing.

- 25 CAA06339.1 AJ005082 *Cyamopsis tetragonoloba*
DESCRIPTION: UDP-galactose 4-epimerase.

- 30 AAA86532.1 U31544 *Pisum sativum*
DESCRIPTION: catabolism of galactose to glucose in Leloir pathway, and in
galactose synthesis from glucose. UDP-galactose-4-epimerase. galE.
galactowaldenase.

- 35 CAA06338.1 AJ005081 *Cyamopsis tetragonoloba*
DESCRIPTION: UDP-galactose 4-epimerase.

- 40 BAB40967.1 AB059568 *Pisum sativum*
DESCRIPTION: biosynthesis of UDP-D-xylose. UDP-D-glucuronate
carboxy-lyase. uxs1.

726

-
- 45 BAA88198.1 AP000837 *Oryza sativa*

DESCRIPTION: Similar to human dimethylaniline monooxygenase (AC002376).

5 BAA35120.1 AB008845 *Oryza sativa*
DESCRIPTION: NADH dependent Glutamate Synthase.

AAB41904.1 L37606 *Medicago sativa*
10 DESCRIPTION: NADH-dependent glutamate synthase.

BAA88195.1 AP000837 *Oryza sativa*
15 DESCRIPTION: Similar to human dimethylaniline monooxygenase (AC002376).

AAB46617.1 L01660 *Medicago sativa*
20 DESCRIPTION: the 3 cysteine residues in this region (amino acid residues 1246-1257) may serve to coordinate the [3Fe-4S] cluster that is probably found in this protein. See Knaff et al. (1991) J. Biol. Chem.266:150.
NADH-glutamate synthase. NADH-GOGAT; activity increases dramatically during nodule development; the 3 cysteine residues in this region may serve to coordinate the [3Fe-4S] cluster that is probably found in this
25 protein. See Knaff et al. (1991) J. Biol. Chem.266:15080-15084.

728

AAG43550.1 AF211532 *Nicotiana tabacum*
30 DESCRIPTION: Avr9/Cf-9 rapidly elicited protein 132. ACRE132. similar to RING finger proteins.

BAA96875.1 AB045121 *Oryza sativa*
35 DESCRIPTION: RING finger 1. RRF1.

AAK00436.1 AC060755 *Oryza sativa*
40 DESCRIPTION: putative zinc finger protein. OSJNBa0003O19.23.

BAA78746.1 AB023482 *Oryza sativa*
45 DESCRIPTION: Similar to Arabidopsis thaliana RING-H2 finger protein RHX1a
mRNA, partial cds.(AF079184).

- CAA74911.1 Y14573 *Hordeum vulgare*
DESCRIPTION: ring finger protein. putative.
- 5
- AAG46117.1 AC073166 *Oryza sativa*
DESCRIPTION: putative ring finger protein. OSJNBb0064P21.7.
- 10
- BAA85438.1 AP000616 *Oryza sativa*
DESCRIPTION: similar to RING-H2 finger protein RHA1a (AF078683).
- 15
- BAA77204.1 AB026262 *Cicer arietinum*
DESCRIPTION: ring finger protein.
- 730
-
- 20
- AAA86424.1 U44386 *Lycopersicon esculentum*
DESCRIPTION: heat shock protein. TFHS1. similar to protein encoded by the
arg2 gene in mung bean, encoded by Genbank Accession Number D14411.
- 731
-
- 25
- CAA06756.1 AJ005899 *Nicotiana tabacum*
DESCRIPTION: G subunit. G subunit of Vacuolar-type H⁺-ATPase. vag1.
- 30
- CAA06757.1 AJ005900 *Nicotiana tabacum*
DESCRIPTION: Subunit G of vacuolar-type H⁺-ATPase. vag2. vag2.
- 35
- AAD56039.1 AF184068 *Citrus limon*
DESCRIPTION: vacuolar membrane ATPase subunit G. LVMA10. V-ATPase
VMA10.
- 737
-
- 40
- AAF69008.1 AF257779 *Oryza sativa*
DESCRIPTION: stress-inducible protein. OsSI1.
- 739
-
- 45
- CAC12996.1 AJ299398 *Medicago truncatula*
DESCRIPTION: putative auxin import. putative AUX1-like permease. lax2.

5 AAF21982.1 AF115543 *Populus tremula* x *Populus tremuloides*
 DESCRIPTION: AUX1-like protein. PAX1.

 AAG17171.1 AF190880 *Populus tremula* x *Populus tremuloides*
 DESCRIPTION: putative AUX1-like permease. pax5.

 10 CAC12995.1 AJ299397 *Medicago truncatula*
 DESCRIPTION: putative auxin import. putative AUX1-like permease. lax1.

 15 CAC12997.1 AJ299399 *Medicago truncatula*
 DESCRIPTION: putative auxin import. putative AUX1-like permease. lax3.

 20 CAB65535.1 AJ011794 *Zea mays*
 DESCRIPTION: AUX1 protein. aux1.

 740

 25 CAA65269.1 X96406 *Solanum tuberosum*
 DESCRIPTION: 13-lipoxygenase.

 30 AAB65767.1 U37840 *Lycopersicon esculentum*
 DESCRIPTION: lipoxygenase. loxD. wound, systemin and methyl-jasmonate
 induced.

 35 BAA03102.1 D14000 *Oryza sativa*
 DESCRIPTION: lipoxygenase. lox2osPil.

 AAC12951.1 U56406 *Hordeum vulgare*
 DESCRIPTION: methyljasmonate-inducible lipoxygenase 2.

 40 CAB94852.1 AJ404331 *Prunus dulcis*
 DESCRIPTION: hydroperoxydation of polyunsaturated fatty acids.
 lipoxygenase. lox.

 45 AAG21691.1 AY008278 *Lycopersicon esculentum*

DESCRIPTION: lipoxygenase. oxido-reductase.

5 AAA79186.1 U36339 Cucumis sativus
DESCRIPTION: lipoxygenase.

10 AAB67858.1 U60200 Solanum tuberosum
DESCRIPTION: lipoxygenase. POTLX-1. expressed during early tuberization.

CAA64765.1 X95512 Solanum tuberosum
DESCRIPTION: lipoxygenase.

15 CAB83038.1 AJ271161 Cucumis sativus
DESCRIPTION: oxygenase. lipoxygenase-9. lox9.

20 CAA58859.1 X84040 Nicotiana tabacum
DESCRIPTION: lipoxygenase. Lox1.

25 AAB67865.1 U60202 Solanum tuberosum
DESCRIPTION: lipoxygenase. POTLX-3. expressed in ABA-treated leaves.

30 CAA55724.1 X79107 Solanum tuberosum
DESCRIPTION: lipoxygenase. Lox1:St:1.

AAB67860.1 U60201 Solanum tuberosum
DESCRIPTION: lipoxygenase. POTLX-2. expressed during early tuberization.

35 CAB65460.1 Y18548 Solanum tuberosum
DESCRIPTION: lipoxygenase. lox1-St-2.

40 AAD04258.1 AF039651 Solanum tuberosum
DESCRIPTION: 5-lipoxygenase.

45 AAB81594.1 AF019613 Solanum tuberosum
DESCRIPTION: lipoxygenase. plox1.

- AAA33986.1 J02795 Glycine max
DESCRIPTION: lipoxygenase-1.
- 5 AAB67732.1 U50075 Glycine max
DESCRIPTION: lipoxygenase L-5. vlxB.
- 10 CAA47717.1 X67304 Glycine max
DESCRIPTION: lipoxygenase.
- 15 AAB81595.1 AF019614 Solanum tuberosum
DESCRIPTION: lipoxygenase. plox2.
- 20 CAA64766.1 X95513 Solanum tuberosum
DESCRIPTION: lipoxygenase.
- 25 AAB31252.1 S73865 Solanum tuberosum
DESCRIPTION: linoleate:oxygen oxidoreductase. linoleate:oxygen
oxidoreductase, lipoxygenase, LOX. This sequence comes from Fig. 1;
lipoxygenase; LOX.
- 30 AAA53184.1 U09026 Lycopersicon esculentum
DESCRIPTION: lipoxygenase. loxA.
- 35 AAB65766.1 U37839 Lycopersicon esculentum
DESCRIPTION: lipoxygenase. loxC. expressed during ripening fruit.
- 40 CAA65268.1 X96405 Solanum tuberosum
DESCRIPTION: 13-lipoxygenase.
- 45 AAF15296.2 AF204210 Phaseolus vulgaris
DESCRIPTION: lipoxygenase. LOX4.
- CAA55319.1 X78581 Pisum sativum
DESCRIPTION: lipoxygenase. Lox1:Ps:3.

AAA03728.1 U04526 Glycine max

DESCRIPTION: lipoxygenase.

5

CAA34906.1 X17061 Pisum sativum

DESCRIPTION: lipoxygenase (AA 1-864).

10

CAA55318.1 X78580 Pisum sativum

DESCRIPTION: lipoxygenase. Lox1:Ps:2.

15

BAA03042.1 D13949 Glycine max

DESCRIPTION: lacking. lipoxygenase-2. lox2.

20

AAA33987.1 J03211 Glycine max

DESCRIPTION: lipoxygenase (EC 1.13.11.12).

25

AAB71759.1 U84198 Pisum sativum

DESCRIPTION: lipoxygenase. Lox1:Ps:1. expressed in root nodules.

30

AAB41272.1 U50081 Glycine max

DESCRIPTION: lipoxygenase-3.

35

CAA39604.1 X56139 Glycine max

DESCRIPTION: lipoxygenase. sc514.

AAA96817.1 U26457 Glycine max

DESCRIPTION: lipoxygenase. vlxC.

40

AAG42354.1 AF234983 Phaseolus vulgaris

DESCRIPTION: lipoxygenase.

45

AAG18376.1 AF283894 Zantedeschia aethiopica

DESCRIPTION: lipoxygenase. lox2.

AAD39093.1 AF095895 Oryza sativa

DESCRIPTION: rice EST AU030811, similar to rice Ca²⁺-ATPase (U82966).

5 AAD11618.1 AF050496 Lycopersicon esculentum
DESCRIPTION: Ca²⁺-ATPase. LCA1B; alternative transcript.

10 AAD11617.1 AF050495 Lycopersicon esculentum
DESCRIPTION: Ca²⁺-ATPase. LCA1A; alternative transcript.

15 AAA34138.1 M96324 Lycopersicon esculentum
DESCRIPTION: The calcium ATPase is a calcium ion pump. Ca²⁺-ATPase.
LCA1.

20 CAA63790.1 X93592 Dunaliella bioculata
DESCRIPTION: P-type ATPase. ca1. calcium pumping; CA1.

AAF73985.1 AF096871 Zea mays
DESCRIPTION: calcium pump. calcium ATPase. cap1.

25 AAB58910.1 U82966 Oryza sativa
DESCRIPTION: Ca²⁺-ATPase.

30 AAD46188.1 AF156691 Nicotiana plumbaginifolia
DESCRIPTION: plasma membrane proton ATPase. pma9.

35 AAB17186.1 U72148 Lycopersicon esculentum
DESCRIPTION: plasma membrane H⁺-ATPase. LHA4. plasma membrane
proton
pumping ATPase.

40 CAA47275.1 X66737 Nicotiana plumbaginifolia
DESCRIPTION: plasma membrane H⁺-ATPase. pma4.

45 CAA54045.1 X76535 Solanum tuberosum
DESCRIPTION: H⁽⁺⁾-transporting ATPase. PHA2.

AAD46186.1 AF156679 *Nicotiana plumbaginifolia*
DESCRIPTION: plasma membrane proton ATPase. pma6.

5 CAA59800.1 X85805 *Zea mays*
DESCRIPTION: H(+)-transporting ATPase. MHA-2.

10 BAA06629.1 D31843 *Oryza sativa*
DESCRIPTION: plasma membrane H⁺-ATPase. OSA2.

15 AAB35314.2 S79323 *Vicia faba*
DESCRIPTION: plasma membrane H(+)-ATPase precursor. plasma membrane
H(+)-ATPase. This sequence comes from Fig. 1; conceptual translation
presented here differs from translation in publication.

20 CAA59799.1 X85804 *Phaseolus vulgaris*
DESCRIPTION: H(+)-transporting ATPase. BHA-1.

25 AAB41898.1 U84891 *Mesembryanthemum crystallinum*
DESCRIPTION: plasma membrane proton pump. H⁺-transporting ATPase.
PMA.

30 AAA34094.1 M80489 *Nicotiana plumbaginifolia*
DESCRIPTION: plasma membrane H⁺ ATPase. pma1.

AAB84202.2 AF029256 *Kosteletzkya virginica*
DESCRIPTION: plasma membrane proton ATPase. ATP1.

35 AAA34052.1 M27888 *Nicotiana plumbaginifolia*
DESCRIPTION: H⁺-translocating ATPase.

40 AAA34173.1 M60166 *Lycopersicon esculentum*
DESCRIPTION: H⁺-ATPase. LHA1.

45 AAA34098.1 M80490 *Nicotiana plumbaginifolia*
DESCRIPTION: plasma membrane H⁺ ATPase. pma3.

- AAF98344.1 AF275745 *Lycopersicon esculentum*
DESCRIPTION: plasma membrane H⁺-ATPase. LHA2. P-type ion pump.
- 5 AAD55399.1 AF179442 *Lycopersicon esculentum*
DESCRIPTION: plasma membrane H⁺-ATPase isoform LHA2. LHA2.
- 10 CAC29436.1 AJ310524 *Vicia faba*
DESCRIPTION: P-type H⁺-ATPase. ha5. predominantly expressed in guard cells and flowers.
- 15 BAA08134.1 D45189 *Zostera marina*
DESCRIPTION: plasma membrane H⁺-ATPase. zha1.
- 20 BAA01058.1 D10207 *Oryza sativa*
DESCRIPTION: H-ATPase. OSA1.
- 25 CAB69824.1 AJ271439 *Prunus persica*
DESCRIPTION: plasma membrane H⁺ ATPase. PPA1.
- CAA54046.1 X76536 *Solanum tuberosum*
DESCRIPTION: H(+)-transporting ATPase. PHA1.
- 30 AAB60276.1 U09989 *Zea mays*
DESCRIPTION: H(+)-transporting ATPase. Mha1.
- 35 CAB69823.1 AJ271438 *Prunus persica*
DESCRIPTION: plasma membrane H⁺ ATPase. PPA2.
- 40 AAK31799.1 AY029190 *Lilium longiflorum*
DESCRIPTION: plasma membrane H⁺ ATPase. LILHA1.
- 45 BAA37150.1 AB022442 *Vicia faba*
DESCRIPTION: p-type H⁺-ATPase. VHA2.

- CAC29435.1 AJ310523 *Vicia faba*
DESCRIPTION: P-type H⁺-ATPase. vha4. predominantly expressed in flowers.
- 5 CAB85495.1 AJ132892 *Medicago truncatula*
DESCRIPTION: proton pump. H⁺-ATPase. ha1.
- 10 CAB85494.1 AJ132891 *Medicago truncatula*
DESCRIPTION: proton pump. H⁺-ATPase. ha1.
- 15 AAD46187.1 AF156683 *Nicotiana plumbaginifolia*
DESCRIPTION: plasma membrane proton ATPase. pma8.
- AAD29712.1 AF140499 *Oryza sativa*
DESCRIPTION: chloroplast envelope calcium ATPase precursor.
- 20 AAK32118.1 AF308816 *Hordeum vulgare*
DESCRIPTION: plasmalemma H⁺-ATPase 1.
- 25 AAG01028.1 AF289025 *Cucumis sativus*
DESCRIPTION: plasma membrane H⁺-ATPase.
- 30 AAF97591.1 AF263917 *Lycopersicon esculentum*
DESCRIPTION: plasma membrane proton ATPase. LHA8.
- 35 AAA81348.1 U38965 *Vicia faba*
DESCRIPTION: p-type H⁺-ATPase. VHA2.
- AAA20600.1 U08984 *Zea mays*
DESCRIPTION: plasma-membrane H⁺ ATPase. Zmpma1.
- 40 AAA20601.1 U08985 *Zea mays*
DESCRIPTION: plasma-membrane H⁺ ATPase. Zmpma1.
- 45 AAK32119.1 AF308817 *Hordeum vulgare*
DESCRIPTION: plasmalemma H⁺-ATPase 2.

742

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- 5 AAD02548.1 AF049922 *Petunia x hybrida*
DESCRIPTION: PGPS/D6. PGPS/D6. ER lumen protein retaining receptor homolog; putative HDEL receptor.

744

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- 10 AAG13424.1 AC051634 *Oryza sativa*
DESCRIPTION: putative mitochondrial inner membrane protein. OSJNBb0018B10.5.

- 15 AAG46068.1 AC079830 *Oryza sativa*
DESCRIPTION: putative inner mitochondrial membrane protein. OSJNBb0009F04.14.

746

-
- 20 BAA32557.1 AB017159 *Daucus carota*
DESCRIPTION: citrate synthase. DcCS.
- 25 AAA82743.1 U19481 *Citrus maxima*
DESCRIPTION: synthesis of citrate from oxaloacetate and acetylCoA. citrate synthase precursor. cit.
- 30 AAG28777.1 AF302906 *Oryza sativa*
DESCRIPTION: citrate synthase. similar to putative *Oryza sativa* citrate synthase in GenBank Accession Number AC004521.
- 35 CAA59008.1 X84226 *Nicotiana tabacum*
DESCRIPTION: citrate synthase. cit1.

- 40 CAA52976.1 X75082 *Solanum tuberosum*
DESCRIPTION: mitochondrial citrate-synthase. ethanolamine ammonia-lyase.

- BAA82390.1 AP000367 *Oryza sativa*
DESCRIPTION: ESTs C96653(C10531),C96654(C10531),C28571(C61641)
45 correspond
to a region of the predicted gene.; Similar to citrate synthetase.

(AC004521).

CAA59010.1 X84228 Beta vulgaris
5 DESCRIPTION: citrate (si)-synthase. cit1.

CAA59009.1 X84227 Populus x generosa
10 DESCRIPTION: citrate (si)-synthase. cit1.

BAA07328.1 D38132 Cucurbita sp.
DESCRIPTION: conversion of oxaloacetate to citrate in the glyoxylate
15 cycle. glyoxysomal citrate synthase.
750

AAA85365.1 L42466 Picea glauca
20 DESCRIPTION: ethylene-forming enzyme. EFE.

AAC95363.1 AF104925 Solanum chacoense
DESCRIPTION: 2-oxoglutarate-dependent dioxygenase. SPP2. pollination and
25 fertilization induced gene.

BAA75309.1 AB023790 Ipomoea batatas
DESCRIPTION: flavanone 3-hydroxylase. f3h III.

30 BAA75308.1 AB023789 Ipomoea batatas
DESCRIPTION: flavanone 3-hydroxylase. f3h II.

35 BAA75306.1 AB023787 Ipomoea batatas
DESCRIPTION: anthocyanidin synthase. ans II.

AAC48922.1 U06047 Vigna radiata
40 DESCRIPTION: 1-aminocyclopropane-1-carboxylate oxidase homolog.
751

BAB40010.1 AP003021 Oryza sativa
45 DESCRIPTION: putative wall-associated kinase 2. P0503E05.12.

DESCRIPTION: Similar to *Arabidopsis thaliana* wak4 gene; wall-associated kinase 4. (AJ009695).

10

DESCRIPTION: putative wall-associated kinase 1. P0503E05.18.

DESCRIPTION: Similar to *Arabidopsis thaliana* chromosome II BAC F12L6 genomic sequence, putative protein kinase. (AC004218).

15

DESCRIPTION: Similar to putative Ser/Thr protein kinase. (AC004218).

20

DESCRIPTION: putative wall-associated kinase 2. P0503E05.25. contains EST C24950(S16264).

25

DESCRIPTION: 11332.5. contains eukaryotic protein kinase domain PF.

30

DESCRIPTION: CRINKLY4 precursor. cr4. receptor kinase homolog.

35

DESCRIPTION: putative protein kinase. P0439B06.8. contains ESTs AU056701(S20808),AU056702(S20808).

40

DESCRIPTION: Pto-like protein kinase E. LhrrPtoE. confers resistance to bacterial speck disease.

45

DESCRIPTION: putative protein kinase. P0456F08.9. contains EST C23560(R0290).

- 5 BAB21240.1 AP002953 *Oryza sativa*
DESCRIPTION: Putative protein kinase. P0426D06.20. contains ESTs C22359(C11461),C22360(C11461).
- BAB40022.1 AP003021 *Oryza sativa*
DESCRIPTION: putative wall-associated kinase 1. P0503E05.26.
- 10 CAA97692.1 Z73295 *Catharanthus roseus*
DESCRIPTION: receptor-like protein kinase. CRPK1. Autophosphorylation predominantly on Thr, less on Ser. Mechanism: autophosphorylation in cis.
- 15 BAB16871.1 AP002537 *Oryza sativa*
DESCRIPTION: putative protein kinase APK1A*Arabidopsis thaliana*. P0001B06.24. contains ESTs C22608(R3192),D25110(R3192).
- 20 AAK11674.1 AF339747 *Lophopyrum elongatum*
DESCRIPTION: protein kinase. ESI47.
- 25 AAF43496.1 AF131222 *Lophopyrum elongatum*
DESCRIPTION: protein serine/threonine kinase. ESI47. induced in roots by salt stress, osmotic stress, and ABA treatment.
- 30 BAA90808.1 AP001168 *Oryza sativa*
DESCRIPTION: Similar to putative receptor-like protein kinase (AL035679).
- 35 AAF76313.1 AF220603 *Lycopersicon esculentum*
DESCRIPTION: Pto kinase. LescPth5.
- 40 AAB47421.1 U59316 *Lycopersicon esculentum*
DESCRIPTION: serine/threonine protein kinase Pto. pto. allele of Pto bacterial speck disease resistance gene in tomato.
- 45 AAB47423.1 U59315 *Lycopersicon pimpinellifolium*
DESCRIPTION: serine/threonine protein kinase Pto. Pto. bacterial speck disease resistance in tomato; disease resistance gene.

- AAC48914.1 U02271 *Lycopersicon pimpinellifolium*
DESCRIPTION: protein kinase.
- 5 AAF76306.1 AF220602 *Lycopersicon pimpinellifolium*
DESCRIPTION: Pto kinase.
- 10 AAG59657.1 AC084319 *Oryza sativa*
DESCRIPTION: putative protein kinase. OSJNBa0004B24.20.
- 15 AAK11567.1 AF318491 *Lycopersicon hirsutum*
DESCRIPTION: Pto-like protein kinase F. LhirPtoF.
- 20 AAK21965.1 AY028699 *Brassica napus*
DESCRIPTION: receptor protein kinase PERK1.
- 25 AAG25966.1 AF302082 *Nicotiana tabacum*
DESCRIPTION: cytokinin-regulated kinase 1. CRK1. protein kinase;
transcript abundance decreases rapidly after cytokinin treatment.
- 30 AAK11569.1 AF318493 *Lycopersicon hirsutum*
DESCRIPTION: Pto-like protein kinase D. LhirPtoD.
- 35 AAF66615.1 AF142596 *Nicotiana tabacum*
DESCRIPTION: LRR receptor-like protein kinase.
- 40 AAG03090.1 AC073405 *Oryza sativa*
DESCRIPTION: Similar to an Arabidopsis somatic embryogenesis
receptor-like kinase (AC007504).
- 45 BAA87853.1 AP000816 *Oryza sativa*
DESCRIPTION: EST AU030604(E51294) corresponds to a region of the
predicted gene. Similar to putative NAK-like Ser/Thr protein kinase.
(AF001308).

DESCRIPTION: ESTs C22657(S0014),C22656(S0014) correspond to a region
of
the predicted gene.; Similar to receptor protein kinase, ERECTA
(AC004484).

5

BAA84787.1 AP000559 Oryza sativa

DESCRIPTION: ESTs C22657(S0014),C22656(S0014) correspond to a region
of
the predicted gene.; Similar to receptor protein kinase, ERECTA
(AC004484).

10

CAA74662.1 Y14286 Brassica oleracea

DESCRIPTION: SFR3. extracellular S domain: 123-1346; transmembrane
domain: 1347-1412; intracellular kinase domain: from 1413.

15

CAA67145.1 X98520 Brassica oleracea

DESCRIPTION: receptor-like kinase. SFR2.

20

CAA73133.1 Y12530 Brassica oleracea

DESCRIPTION: serine /threonine kinase. ARLK.

25

AAK11568.1 AF318492 Lycopersicon hirsutum

DESCRIPTION: Pto-like protein kinase B. LhirPtoB.

30

BAA78764.1 AB023482 Oryza sativa

DESCRIPTION: ESTs C98382(C2985),D22444(C11129) correspond to a region
of
the predicted gene.; Similar to Arabidopsis thaliana APK1 gene for protein
tyrosine-serine-threonine kinase.(D12522).

35

AAK00425.1 AC069324 Oryza sativa

DESCRIPTION: Putative protein kinase. OSJNBa0071K19.11.

40

AAK31267.1 AC079890 Oryza sativa

DESCRIPTION: putative protein kinase. OSJNBb0089A17.2.

45

BAA94509.1 AB041503 Populus nigra

DESCRIPTION: protein kinase 1. PnPK1.

BAA94510.1 AB041504 Populus nigra

5 DESCRIPTION: protein kinase 2. PnPK2.

752

BAB39155.1 AB048713 Pisum sativum

10 DESCRIPTION: SCARECROW. PsSCR.

AAG13663.1 AF263457 Zea mays

15 DESCRIPTION: transcription factor. SCARECROW. SCR. ZmSCR.

BAA90816.1 AP001168 Oryza sativa

DESCRIPTION: Similar to SCARECROW (U62798).

20

AAC98090.1 AF067400 Zea mays

DESCRIPTION: Sc11 protein. Sc11. Scarecrow-like; similar to Zea mays
sequence presented in GenBank Accession Number T18310.

25

BAB39156.1 AB048714 Pisum sativum

DESCRIPTION: SCARECROW. PsSCR.

753

30

AAF21901.1 AF109392 Brassica napus

DESCRIPTION: ligand gated channel-like protein. glutamate receptor
homolog.

35 757

CAA92821.1 Z68504 Oryza sativa

DESCRIPTION: 3-hydroxy-3-methylglutaryl-CoA reductase.

40

AAA33360.1 M74800 Hevea brasiliensis

DESCRIPTION: 3-hydroxy-3-methylglutaryl-coenzyme A reductase. hmgr3.

45 CAA70440.1 Y09238 Zea mays

DESCRIPTION: 3-hydroxy-3-methylglutaryl coenzyme A reductase.

5 AAB69727.1 U72146 *Camptotheca acuminata*
DESCRIPTION: 3-hydroxy-3-methylglutaryl coenzyme A reductase. converts
HMGCoA in mevalonate precursor for isoprenoid compounds; HMGR; hmg2;
similar to protein encoded by GenBank Accession Number L10390.

10 AAD08820.1 U43961 *Oryza sativa*
DESCRIPTION: 3-hydroxy-3-methylglutaryl=CoA reductase. HMGR.

15 AAA68965.1 U14624 *Artemisia annua*
DESCRIPTION: 3-hydroxy-3-methylglutaryl coenzyme A reductase. AHM1.

20 AAD47596.1 AF142473 *Artemisia annua*
DESCRIPTION: HMG-CoA reductase. HMGR1.

AAD03789.1 U43711 *Morus alba*
DESCRIPTION: catalyzes the final step in mevalonate pathway.
3-hydroxy-3-methylglutaryl-coenzyme A reductase. HMGR.

25 AAA33108.1 M96068 *Catharanthus roseus*
DESCRIPTION: hydroxymethylglutaryl-CoA reductase. HMGR.

30 CAA48610.1 X68651 *Raphanus sativus*
DESCRIPTION: hydroxymethylglutaryl-CoA reductase (NADPH). HMGR1.

35 AAA93498.1 L01400 *Solanum tuberosum*
DESCRIPTION: convert HMG-CoA into mevalonate. hydroxymethylglutaryl
coenzyme A reductase. hmgr. putative.

40 AAA68966.1 U14625 *Artemisia annua*
DESCRIPTION: 3-hydroxy-3-methylglutaryl coenzyme A reductase. AHM4.

45 AAB52552.1 U51986 *Solanum tuberosum*
DESCRIPTION: HMG-CoA reductase.

- CAA48611.1 X68652 *Raphanus sativus*
DESCRIPTION: hydroxymethylglutaryl-CoA reductase (NADPH). HMG2.
- 5 BAA93631.1 AB022690 *Solanum tuberosum*
DESCRIPTION: 3-hydroxy-3-methylglutaryl coenzyme A reductase. HMG3.
- 10 AAB62581.1 U68072 *Lycopersicon esculentum*
DESCRIPTION: 3-hydroxy-3-methylglutaryl CoA reductase 2. HMG2.
- 15 AAA34169.1 M63642 *Lycopersicon esculentum*
DESCRIPTION: 3-hydroxy-3-methylglutaryl coenzyme A reductase. hmg2.
- 20 AAB69726.1 U72145 *Camptotheca acuminata*
DESCRIPTION: converts HMGC_oA to mevalonate. 3-hydroxy-3-methylglutaryl coenzyme a reductase. hmg3. HMGR.
- 25 AAB52551.1 U51985 *Solanum tuberosum*
DESCRIPTION: HMG-CoA reductase.
- 30 AAA33040.1 L10390 *Camptotheca acuminata*
DESCRIPTION: 3-hydroxy-3-methylglutaryl coA reductase.
- 35 AAD28179.1 AF110383 *Capsicum annuum*
DESCRIPTION: 3-hydroxy-3-methylglutaryl-coenzyme A reductase.
HMGR2M.
HMGR.
- 40 BAB20771.1 AB041031 *Solanum tuberosum*
DESCRIPTION: 3-hydroxy-3-methylglutaryl coenzyme A reductase. HMG2.
- 45 AAB53748.1 U95816 *Oryza sativa*
DESCRIPTION: 3-hydroxy-3-methylglutaryl-CoA reductase. HMGR.
- AAC05088.1 AF038045 *Gossypium hirsutum*
DESCRIPTION: catalyzes the synthesis of mevalonate from hmg-coA.
3-hydroxy-3-methylglutaryl-coenzyme A reductase 1. hmg1. hmg-coA reductase

1; HMGR1.

- CAA45181.1 X63649 *Nicotiana sylvestris*
5 DESCRIPTION: catalyses synthesis of mevalonate.
3-hydroxy-3-methylglutaryl-coenzyme A reductase. HMGR. endoplasmic
reticulum location.
- CAA38469.1 X54659 *Hevea brasiliensis*
10 DESCRIPTION: hydroxymethylglutaryl-CoA reductase. HMGR1.
- CAA38467.1 X54657 *Hevea brasiliensis*
15 DESCRIPTION: hydroxymethylglutaryl-CoA reductase. HMGR1.
- AAD38873.1 AF110382 *Oryza sativa*
20 DESCRIPTION: 3-hydroxy-3-methylglutaryl-coenzyme A reductase. HMGR3G.
HMG-CoA reductase.
- BAA36291.1 AB021862 *Cucumis melo*
25 DESCRIPTION: HMG-CoA reductase. Cm-HMGR. putative.
- AAB87727.1 U60452 *Nicotiana tabacum*
DESCRIPTION: hydroxy-methylglutaryl-coenzyme A reductase. HMGR1.
- 30 AAC05089.1 AF038046 *Gossypium hirsutum*
DESCRIPTION: catalyzes the synthesis of mevalonate from hmg-coA.
3-hydroxy-3-methylglutaryl-coenzyme A reductase 2. hmg2. hmg-coA reductase
2; HMGR2.
- 35 AAC15475.1 AF034760 *Tagetes erecta*
DESCRIPTION: 3-hydroxy-3-methylglutaryl coenzyme A reductase.
- 40 AAC15476.1 AF034761 *Tagetes erecta*
DESCRIPTION: 3-hydroxy-3-methylglutaryl coenzyme A reductase.
- 45 AAA21720.1 L28995 *Oryza sativa*
DESCRIPTION: conversion of hydroxymethylglutaryl coenzyme A to

mevalonate. 3-hydroxy-3-methylglutaryl coenzyme A reductase. putative.

- 5 AAA33358.1 M74798 Hevea brasiliensis
DESCRIPTION: 3-hydroxy-3-methylglutaryl-coenzyme A reductase. hmgr3.
- 10 AAC72378.1 AF096838 Solanum tuberosum
DESCRIPTION: 3-hydroxy-3-methylglutaryl coenzyme A reductase.
- 15 AAB04043.1 L40938 Lycopersicon esculentum
DESCRIPTION: HMGR CoA reductase. HMGR1.
- 20 CAA38468.1 X54658 Hevea brasiliensis
DESCRIPTION: hydroxymethylglutaryl-CoA reductase. HMGR2.
- 25 CAA52787.1 X74783 Lithospermum erythrorhizon
DESCRIPTION: 3-hydroxy-3-methyl glutaryl coenzyme A reductase. Lehmgr1.
- 30 AAD09278.1 U97683 Glycine max
DESCRIPTION: catalyzes the synthesis of mevalonate, the specific precursor of all isoprenoid compounds present in plants.
3-hydroxy-3-methylglutaryl-coenzyme A reductase. HMG-CoA reductase.
- 35 AAG43469.1 AF196964 Bixa orellana
DESCRIPTION: catalyzes mevalonate synthesis from hmg-CoA.
3-hydroxy-3-methylglutaryl-coenzyme A reductase.
- 40 BAA09705.1 D63389 Cucumis sativus
DESCRIPTION: 3-hydroxy-3-methylglutaryl CoA reductase.
- 45 AAB47161.1 S82272 Gossypium barbadense
DESCRIPTION: 3-hydroxy-3-methylglutaryl coenzyme A reductase.
/gene="3-hydroxy-3-methylglutaryl coenzyme A reductase,. This sequence comes from Fig. 2; 3-hydroxy-3-methylglutaryl CoA reductase; HMGR.

DESCRIPTION: 3-hydroxy-3-methylglutaryl-coenzyme A reductase. hmgr3.

5 AAC37434.1 L34827 Solanum tuberosum
DESCRIPTION: HMG-CoA reductase. hmg1 gene family.

10 AAC37432.1 L34825 Solanum tuberosum
DESCRIPTION: HMG-CoA reductase. hmg1 gene family.

AAC37435.1 L34828 Solanum tuberosum
DESCRIPTION: HMG-CoA reductase. hmg1 gene family.

15 AAC37433.1 L34826 Solanum tuberosum
DESCRIPTION: HMG-CoA reductase. hmg1 gene family.

20 AAC37431.1 L34823 Solanum tuberosum
DESCRIPTION: HMG-CoA reductase. hmg1 gene family.

761

25 CAA96512.1 Z71980 Malus x domestica
DESCRIPTION: knotted1-like homeobox protein.

30 BAA25921.1 AB004797 Nicotiana tabacum
DESCRIPTION: NTH23. homeobox gene.

35 AAD09582.1 U76409 Lycopersicon esculentum
DESCRIPTION: homeobox 1 protein. THox1. homeodomain protein.

AAC49918.1 AF000142 Lycopersicon esculentum
DESCRIPTION: class II knotted-like homeodomain protein. LeT12.

40 BAA08552.1 D49704 Oryza sativa
DESCRIPTION: OSH45. OSH44 transcript homeobox gene.

45 BAB18585.1 AB043957 Ceratopteris richardii
DESCRIPTION: CRKNOX3. crknnox3. knotted1-like homeodomain protein.

5 AAD00253.1 U76410 *Lycopersicon esculentum*
 DESCRIPTION: homeobox 2 protein. THox2. homeodomain protein.

CAA82314.1 Z29073 *Brassica napus*
 DESCRIPTION: homeodomain-containing protein. Bnhd1.

10 BAA77822.1 AB007628 *Oryza sativa*
 DESCRIPTION: HOS59. homeobox gene.

15 BAA77823.1 AB007629 *Oryza sativa*
 DESCRIPTION: HOS66. homeobox gene.

20 AAB81079.1 AF022390 *Hordeum vulgare*
 DESCRIPTION: knotted class 1 homeodomain protein. k. similar to the
 hooded gene product encoded by GenBank Accession Number X83518; similar
 to
 the maize knotted-1 gene product encoded by GenBank Accession Number
 X61308.

25 AAF32399.1 AF224499 *Triticum aestivum*
 DESCRIPTION: KNOTTED-1-like homeobox protein b. knox1b. KNOX1b.

30 BAA76750.1 AB025573 *Nicotiana tabacum*
 DESCRIPTION: KN1-type homeobox protein. NTH1.

35 AAF32400.1 AF224500 *Triticum aestivum*
 DESCRIPTION: KNOTTED-1-like homeobox protein d. knox1d. KNOX1d.

40 AAC49917.1 AF000141 *Lycopersicon esculentum*
 DESCRIPTION: class I knotted-like homeodomain protein. LeT6.

45 BAA25546.1 AB004785 *Nicotiana tabacum*
 DESCRIPTION: NTH15. homeobox gene.

- BAA79224.1 AB028883 *Oryza sativa*
DESCRIPTION: knotted1-type homeobox protein OSH6. OSH6.
- 5 BAA77818.1 AB007624 *Oryza sativa*
DESCRIPTION: HOS9. homeobox gene.
- 10 BAB19772.1 AP002881 *Oryza sativa*
DESCRIPTION: putative knotted1-type homeobox protein. P0035H10.13.
- 15 AAF23753.2 AF193813 *Brassica oleracea*
DESCRIPTION: shoot meristemless. Stm. homeodomain protein.
- 20 AAD00251.1 U76407 *Lycopersicon esculentum*
DESCRIPTION: knotted 2 protein. TKn2. homeodomain protein.
- CAA96510.1 Z71978 *Malus x domestica*
DESCRIPTION: kn1-like protein.
- 25 BAA31688.1 AB016071 *Oryza sativa*
DESCRIPTION: OSH15. homeobox gene.
- 30 BAA77817.1 AB007623 *Oryza sativa*
DESCRIPTION: HOS3. homeobox gene.
- 35 BAB18582.1 AB043954 *Ceratopteris richardii*
DESCRIPTION: CRKNOX1. crknx1. knotted1-like homeodomain protein.
- BAA76903.1 AB025713 *Nicotiana tabacum*
DESCRIPTION: homeobox 9. NTH9.
- 40 AAD00252.1 U76408 *Lycopersicon esculentum*
DESCRIPTION: knotted 3 protein. TKn3. homeodomain protein.
- 45 BAB18584.1 AB043956 *Ceratopteris richardii*

DESCRIPTION: CRKNOX2. crknx2. knotted1-like homeodomain protein.

CAA96511.1 Z71979 Malus x domestica
5 DESCRIPTION: kn1-like protein.

AAA20882.1 L13663 Glycine max
10 DESCRIPTION: SBH1. Sbh1. soybean homeobox-containing gene.

CAB88029.1 AJ276389 Dendrobium grex Madame Thong-In
DESCRIPTION: transcription factor. knotted1-like homeobox protein.

15 762

AAB65776.1 U97521 Vitis vinifera
DESCRIPTION: class IV endochitinase. VvChi4A.

20

AAB65777.1 U97522 Vitis vinifera
DESCRIPTION: class IV endochitinase. VvChi4B.

25 CAA53626.1 X76041 Triticum aestivum
DESCRIPTION: endochitinase. CHI.

AAG53609.1 AF280437 Secale cereale
30 DESCRIPTION: 31.7 kDa class I endochitinase-antifreeze protein precursor.
cht9.

BAA03750.1 D16222 Oryza sativa
35 DESCRIPTION: endochitinase. Cht-2.

AAA32986.1 M95835 Brassica napus
40 DESCRIPTION: endochitinase. Ch25.

BAA03749.1 D16221 Oryza sativa
DESCRIPTION: endochitinase. Cht-1.

45 AAB01895.1 U48687 Castanea sativa

DESCRIPTION: endochitinase.

763

5 AAA34065.1 M94135 *Nicotiana tabacum*
 DESCRIPTION: chloroplast carbonic anhydrase.

10 AAA34057.1 L19255 *Nicotiana tabacum*
 DESCRIPTION: carbonic anhydrase.

15 AAB65822.1 U55838 *Populus tremula* x *Populus tremuloides*
 DESCRIPTION: carbonic anhydrase. CA1b. EC 4.2.1.1.

20 AAC49785.1 U55837 *Populus tremula* x *Populus tremuloides*
 DESCRIPTION: carbonic anhydrase. CA1a. EC 4.2.1.1.

25 AAA34026.1 M27295 *Spinacia oleracea*
 DESCRIPTION: carbonic anhydrase precursor.

25 AAA34027.1 J05403 *Spinacia oleracea*
 DESCRIPTION: carbonic anhydrase (EC 4.2.1.1).

30 AAA86993.1 U19738 *Flaveria linearis*
 DESCRIPTION: reversible hydration of carbon dioxide. carbonic anhydrase
 1.

35 AAA86942.1 U08402 *Flaveria brownii*
 DESCRIPTION: carbonic anhydrase.

40 AAA86992.1 U19737 *Flaveria pringlei*
 DESCRIPTION: reversible hydration of carbon dioxide. carbonic anhydrase.

45 AAA86939.1 U08398 *Flaveria bidentis*
 DESCRIPTION: carbonic anhydrase.

45 AAD27876.2 AF139464 *Vigna radiata*

DESCRIPTION: carbonic anhydrase. CipCa1.

5 AAA33652.1 M63627 Pisum sativum
DESCRIPTION: carbonic anhydrase.

10 AAD29050.1 AF132855 Gossypium hirsutum
DESCRIPTION: interconversion of CO₂ and HCO₃⁻. carbonic anhydrase
isoform
2. CA2. zinc metalloenzyme; carbonate dehydratase.

15 AAD29049.1 AF132854 Gossypium hirsutum
DESCRIPTION: interconversion of CO₂ and HCO₃⁻. carbonic anhydrase
isoform
1. CA1. zinc metalloenzyme; carbonate dehydratase.

20 AAA86994.1 U19740 Flaveria linearis
DESCRIPTION: reversible hydration of carbon dioxide. carbonic anhydrase
2.

25 CAB43571.1 AJ239132 Glycine max
DESCRIPTION: hydration of carbon dioxide. carbonic anhydrase. ca1.

30 CAA63712.1 X93312 Medicago sativa
DESCRIPTION: Carbonic anhydrase. ca1.

35 AAA86945.1 U08403 Zea mays
DESCRIPTION: carbonic anhydrase.

AAA86944.1 U08401 Zea mays
DESCRIPTION: carbonic anhydrase.

40 AAC41656.1 L36959 Hordeum vulgare
DESCRIPTION: carbonic anhydrase. putative.

45 AAA86943.1 U08404 Oryza sativa
DESCRIPTION: carbonic anhydrase. nuclear encoded, localized to

chloroplast.

- 5 AAD56038.1 AF182806 *Oryza sativa*
DESCRIPTION: carbonic anhydrase 3. ca3.
- 10 BAA31953.1 AB016283 *Oryza sativa*
DESCRIPTION: carbonic anhydrase.
- 15 AAA69027.1 U19739 *Urochloa panicoides*
DESCRIPTION: reversible hydration of carbon dioxide. carbonic anhydrase
2.
- 20 AAA69028.1 U19741 *Urochloa panicoides*
DESCRIPTION: reversible hydration of carbon dioxide. carbonic anhydrase
1.
- 25 BAA95793.1 AB009887 *Nicotiana tabacum*
DESCRIPTION: carbonic anhydrase. carbonic anhydrase.
- 30 AAF78507.1 AF195204 *Pyrus pyrifolia*
DESCRIPTION: carbonic anhydrase isoform 1. CA1.
- 35 AAC33484.1 U49976 *Coccomyxa* sp. PA
DESCRIPTION: beta-type carbonic anhydrase beta-CA1.
- 40 AAA18560.1 M95073 *Zea mays*
DESCRIPTION: putative. silimar to carbonic anhydrases.
- 45 AAB19184.1 U41190 *Chlamydomonas reinhardtii*
DESCRIPTION: carbonic anhydrase precursor. beta-CA2.
- AAB19183.1 U41189 *Chlamydomonas reinhardtii*
DESCRIPTION: carbonic anhydrase precursor. beta-CA1.
- AAC49887.1 U80804 *Chlamydomonas reinhardtii*

DESCRIPTION: beta-carbonic anhydrase. ca1. beta-CA1.

5 AAC49888.1 U80805 Chlamydomonas reinhardtii
DESCRIPTION: beta-carbonic anhydrase. ca2. beta-CA2.

764

10 AAC06027.1 AF052058 Vigna unguiculata
DESCRIPTION: iron storage and mobilization in plants. ferritin subunit
cowpea2 precursor.

15 AAD50644.1 AF133814 Solanum tuberosum
DESCRIPTION: ferritin 1. F1.

20 AAB53099.1 U68217 Brassica napus
DESCRIPTION: iron binding protein. ferritin. LSC30.

25 AAA33959.1 M64337 Glycine max
DESCRIPTION: ferritin light chain. ferritin.

AAA34016.1 M72894 Glycine max
DESCRIPTION: ferritin light chain. SOF-H2.

30 CAA58146.1 X83076 Zea mays
DESCRIPTION: ferritin. Fer1.

35 AAB18928.1 U31648 Glycine max
DESCRIPTION: iron storage protein. ferritin.

40 CAA65771.1 X97059 Medicago sativa
DESCRIPTION: iron storage. ferritin. FER. abscisic acid regulated.

CAA43663.1 X61391 Zea mays
DESCRIPTION: ferritin.

45 CAA58147.1 X83077 Zea mays

DESCRIPTION: ferritin. Fer2.

5 AAC06026.1 AF052057 Vigna unguiculata
DESCRIPTION: iron storage and mobilization in plants. ferritin subunit
cowpea3 precursor.

10 CAA43664.1 X61392 Zea mays
DESCRIPTION: ferritin.

15 CAA51786.1 X73369 Pisum sativum
DESCRIPTION: ferritin.

CAA45763.1 X64417 Pisum sativum
DESCRIPTION: ferritin-precursor.

20 CAA41213.1 X58274 Phaseolus vulgaris
DESCRIPTION: ferritin. pfe.

25 AAA33958.1 M58336 Glycine max
DESCRIPTION: ferritin light chain. SOF-5L.

30 CAB42587.1 AJ238628 Chlorella protothecoides
DESCRIPTION: putative ferritin. dee188.

35 BAB17852.1 AB042612 Nicotiana tabacum
DESCRIPTION: ferritin 1. tob-fer-1. putative.

AAC15241.1 AF028072 Pinus taeda
DESCRIPTION: ferritin.

40 CAA47983.1 X67755 Vigna unguiculata
DESCRIPTION: ferritin 2. pfe2.

45 CAA47982.1 X67754 Vigna unguiculata
DESCRIPTION: ferritin 1. pfe1.

CAA47984.1 X67756 *Vigna unguiculata*
 DESCRIPTION: ferritin 5. pfe5.

5

AAC12282.1 AF052511 *Glycine max*
 DESCRIPTION: iron storage and mobilization. ferritin 2. soybean 2; cowpea
 2 homolog.

10

AAC12281.1 AF052513 *Glycine max*
 DESCRIPTION: iron storage and mobilization. ferritin 1. soybean 1; cowpea
 1 homolog.

15

765

AAC36697.1 AF075579 *Mesembryanthemum crystallinum*
 DESCRIPTION: protein phosphatase-2C. PP2C.

20

CAC10358.1 AJ277086 *Nicotiana tabacum*
 DESCRIPTION: protein phosphatase 2C. PP2C1.

25

CAB90633.1 AJ277743 *Fagus sylvatica*
 DESCRIPTION: protein phpsphatase 2C (PP2C). pp2C1. ABA-induced protein.

30

AAD17804.1 AF092431 *Lotus japonicus*
 DESCRIPTION: nodule-enhanced protein phosphatase type 2C. NPP2C1.

35

CAC10359.1 AJ277087 *Nicotiana tabacum*
 DESCRIPTION: protein phosphatase 2C. PP2C2.

40

CAC09575.1 AJ298987 *Fagus sylvatica*
 DESCRIPTION: protein phosphatase 2C (PP2C). pp2Cf1.

45

CAA72341.1 Y11607 *Medicago sativa*
 DESCRIPTION: protein phosphatase 2C. MP2C.

CAB61839.1 AJ242803 *Sporobolus stapfianus*

DESCRIPTION: putative serine/threonine phosphatase type 2c.

- 5 AAD17805.1 AF092432 Lotus japonicus
DESCRIPTION: protein phosphatase type 2C. PP2C2.
- 10 AAG43835.1 AF213455 Zea mays
DESCRIPTION: protein phosphatase type-2C. pp2c-1. PP2C-1.
- 15 AAG46118.1 AC073166 Oryza sativa
DESCRIPTION: putative protein phosphatase-2C. OSJNBb0064P21.12. tRNA-Lys.
- 20 AAG13599.1 AC051633 Oryza sativa
DESCRIPTION: putative protein phosphatase-2C. OSJNBb0015I11.26.
- 25 AAC36698.1 AF075580 Mesembryanthemum crystallinum
DESCRIPTION: protein phosphatase-2C. PP2C.
- 30 BAB12036.1 AP002820 Oryza sativa
DESCRIPTION: putative protein phosphatase. P0702D12.18.
- 35 AAC36700.1 AF075582 Mesembryanthemum crystallinum
DESCRIPTION: protein phosphatase-2C. PP2C.
- 40 AAC36699.1 AF075581 Mesembryanthemum crystallinum
DESCRIPTION: protein phosphatase-2C. PP2C.
- 45 AAK20060.1 AC025783 Oryza sativa
DESCRIPTION: putative protein phosphatase 2C. OSJNBa0001O14.1.
- AAD11430.1 AF097667 Mesembryanthemum crystallinum
DESCRIPTION: protein phosphatase 2C homolog. PP2C.
- CAB90634.1 AJ277744 Fagus sylvatica
DESCRIPTION: protein phosphatase 2C (PP2C). pp2C2. ABA and calcium

induced protein.

5 AAC35951.1 AF079355 Mesembryanthemum crystallinum
DESCRIPTION: protein phosphatase-2c. PP2C.

10 AAF19804.1 AF180355 Brassica oleracea
DESCRIPTION: ABI1 protein. ABI1. similar to Arabidopsis thaliana ABI1.

15 AAB93832.1 U81960 Zea mays
DESCRIPTION: kinase interaction domain mediates phosphorylation-dependent
binding to a subset of active receptor-like protein kinases; type 2C
protein phosphatase. kinase associated protein phosphatase. KAPP.

20 AAC26828.1 AF075603 Oryza sativa
DESCRIPTION: kinase interaction domain mediates phosphorylation-dependent
binding to a subset of active receptor-like protein kinases. kinase
associated protein phosphatase. kapp. type 2C protein phosphatase.

25 CAC09576.1 AJ298988 Fagus sylvatica
DESCRIPTION: protein phosphatase 2C (PP2C). pp2Cf2.

766

30 AAG08959.1 AF122051 Solanum tuberosum
DESCRIPTION: tuber-specific and sucrose-responsive element binding
factor. TSF. R2R3 MYB class transcription factor.

35 AAG08960.1 AF122052 Solanum tuberosum
DESCRIPTION: tuber-specific and sucrose-responsive element binding
factor. TSF. R2R3 MYB class transcription factor.

40 AAG08961.1 AF122053 Solanum tuberosum
DESCRIPTION: tuber-specific and sucrose-responsive element binding
factor. TSF. R2R3 MYB class transcription factor.

45 BAA88169.1 AP000836 Oryza sativa
DESCRIPTION: Similar to putative transcription factor (AF062890).

BAA88205.1 AP000837 *Oryza sativa*
DESCRIPTION: Similar to putative transcription factor (AF062890).

5

AAF34434.1 AF172282 *Oryza sativa*
DESCRIPTION: myb-like protein. DUPR11.29.

10 AAF78890.1 AF189788 *Hordeum vulgare*
DESCRIPTION: putative c-myb-like transcription factor. MYB3R-1.
HvMYB3R-1.

15 AAF78889.1 AF189787 *Hordeum vulgare*
DESCRIPTION: putative c-myb-like transcription factor. MYB3R-1.
HvMYB3R-1.

20 AAF67053.1 AF190304 *Adiantum raddianum*
DESCRIPTION: c-myb-like transcription factor. MYB3R-1. contains three
MYB
repeats.

25

AAF67052.1 AF190303 *Adiantum raddianum*
DESCRIPTION: c-myb-like transcription factor. MYB3R-1. contains three
MYB
repeats.

30

AAF78888.1 AF189786 *Physcomitrella patens*
DESCRIPTION: putative c-myb-like transcription factor. MYB3R-1.
PpMYB3R-1.

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AAF78887.1 AF189785 *Physcomitrella patens*
DESCRIPTION: putative c-myb-like transcription factor. MYB3R-1.
PpMYB3R-1.

40

AAF43043.1 AF236059 *Papaver rhoeas*
DESCRIPTION: putative Myb-related domain. pmr.

45

BAA94769.1 AP001859 *Oryza sativa*

DESCRIPTION: Similar to Arabidopsis thaliana chromosome 4, BAC clone F4D11; putative myb-protein. (AL022537).

- 5 AAF67050.1 AF190301 Secale cereale
 DESCRIPTION: c-myb-like transcription factor. MYB3R-1. contains three
 MYB
 repeats.
- 10 AAF67051.1 AF190302 Secale cereale
 DESCRIPTION: c-myb-like transcription factor. MYB3R-1. contains three
 MYB
 repeats.
- 15 CAA78388.1 Z13998 Petunia x hybrida
 DESCRIPTION: DNA-binding protein; transcriptional activator. protein 3.
 myb.Ph3. related to animal myb proto-oncoproteins.
- 20 BAB39987.1 AP003020 Oryza sativa
 DESCRIPTION: putative transcription factor (myb). P0498A12.16. contains
 ESTs AU097474(S5087),D40175(S1959).
- 25 BAB39972.1 AP003018 Oryza sativa
 DESCRIPTION: putative transcription factor (myb). OSJNBa0004B13.27.
 contains ESTs AU097474(S5087),D40175(S1959).
- 30 CAA72218.1 Y11415 Oryza sativa
 DESCRIPTION: myb.
- 35 BAA81731.1 AB029160 Glycine max
 DESCRIPTION: GmMYB29A1.
- 40 BAA81730.1 AB029159 Glycine max
 DESCRIPTION: GmMYB29A1.
- 45 CAA72217.1 Y11414 Oryza sativa
 DESCRIPTION: myb.

BAA81736.1 AB029165 Glycine max
DESCRIPTION: GmMYB29B2.

5

BAB12688.1 AP002746 Oryza sativa
DESCRIPTION: putative MYB family transcription factor. P0671B11.3.
contains ESTs AU082307(E0784),C72014(E0784).

10

BAA99440.1 AP002743 Oryza sativa
DESCRIPTION: putative MYB family transcription factor. P0710E05.27.
contains ESTs AU082307(E0784),C72014(E0784).

15

AAB41101.1 U72762 Nicotiana tabacum
DESCRIPTION: transcription factor Myb1. myb1. TMV-inducible Myb
homolog;
contains helix-turn-helix motif; contains redox-sensitive cysteine.

20

BAA88223.1 AB028651 Nicotiana tabacum
DESCRIPTION: myb-related transcription factor LBM3. lbm3.

25

BAA23340.1 D88620 Oryza sativa
DESCRIPTION: transfactor. OSMYB4. Osmyb4.

30

BAA93038.1 AP001552 Oryza sativa
DESCRIPTION: EST AU082058(C12976) corresponds to a region of the
predicted gene. Similar to Arabidopsis thaliana putative transcription
factor (AF062916).

35

AAA33067.1 L04497 Gossypium hirsutum
DESCRIPTION: MYB A; putative.

40

BAA81733.2 AB029162 Glycine max
DESCRIPTION: GmMYB29A2.

45

BAA88222.1 AB028650 Nicotiana tabacum
DESCRIPTION: myb-related transcription factor LBM2. lbm2.

- CAB43399.1 AJ006292 *Antirrhinum majus*
DESCRIPTION: Myb-related transcription factor mixta-like 1. mybml1.
- 5
- BAA81732.1 AB029161 *Glycine max*
DESCRIPTION: GmMYB29A2.
- 10
- AAG28525.1 AF198498 *Nicotiana tabacum*
DESCRIPTION: anther-specific myb-related protein 2. mybAS2. NtMYBAS2;
contains tandem R2, R3 myb domains similar to c-myb family.
- 15
- CAA50226.1 X70881 *Hordeum vulgare*
DESCRIPTION: MybHv33. myb3.
- 20
- CAA50223.1 X70878 *Hordeum vulgare*
DESCRIPTION: MybHv33. myb3.
- 25
- CAA78387.1 Z13997 *Petunia x hybrida*
DESCRIPTION: DNA-binding protein, transcriptional activator. protein 2.
myb.Ph2. related to animal myb proto-oncoproteins.
- 30
- CAA67000.1 X98355 *Oryza sativa*
DESCRIPTION: activator of alpha-amylase gene promoter. transcription
factor GAMyb. Gam1. Myb-like; expression is regulated by gibberellin.
- 35
- AAK19616.1 AF336283 *Gossypium hirsutum*
DESCRIPTION: GHMYB25. ghmyb25. similar to myb; contains an unspliced
intron.
- 40
- AAG28526.1 AF198499 *Nicotiana tabacum*
DESCRIPTION: anther-specific myb-related protein 1. mybAS1. NtMYBAS1;
contains N-terminal R2, R3 myb domain repeats similar to c-myb.
- 45
- CAA78386.1 Z13996 *Petunia x hybrida*
DESCRIPTION: DNA binding protein; transcriptional activator. protein 1.
myb.Ph3. Product related to animal myb proto-oncoproteins. Sequence from
nucleotide 992 is not included in clone cPF1 and has been obtained by PCR

amplification of cDNA.

5 CAA66952.1 X98308 Lycopersicon esculentum
DESCRIPTION: THM18. myb-related transcription factor.

10 BAA23341.1 D88621 Oryza sativa
DESCRIPTION: transfactor. OSMYB5. Osmyb5.

15 CAA50221.1 X70876 Hordeum vulgare
DESCRIPTION: MybHv5. myb2.

20 AAK19611.1 AF336278 Gossypium hirsutum
DESCRIPTION: BNLGHi233. bnlghi6233. similar to myb.

25 AAC04716.1 AF034130 Gossypium hirsutum
DESCRIPTION: putative MYB-like transcription factor. MYB-like DNA-
binding
domain protein. Cmy-D. similar to MYB A encoded by GenBank Accession
Number L04497.

30 CAA61021.1 X87690 Hordeum vulgare
DESCRIPTION: transcriptional activator of alpha-amylase gene promoter.
GAMyb protein. Gam1.

35 AAG22863.1 AY008692 Hordeum vulgare
DESCRIPTION: transcription factor GAMyb. Gamyb.

767

40 CAB08111.1 Z94180 Lycopersicon esculentum
DESCRIPTION: branched chain alpha-keto acid dehydrogenase E1-alpha
subunit.

45 CAA81558.1 Z26949 Solanum tuberosum
DESCRIPTION: subunit of the mitochondrial pyruvate dehydrogenase complex.
E1 alpha subunit of pyruvate dehydrogenase precursor.

AAC72195.1 AF069911 Zea mays
DESCRIPTION: pyruvate dehydrogenase E1 alpha subunit.

5 AAG43499.1 AF209924 Lycopersicon esculentum
DESCRIPTION: pyruvate dehydrogenase.

10 AAA97411.1 U51918 Pisum sativum
DESCRIPTION: pyruvate dehydrogenase E1 alpha subunit.

15 CAA10992.1 AJ222787 Hordeum vulgare
DESCRIPTION: alpha-keto acid dehydrogenase-like protein. homology to
branched chain alpha-keto acid dehydrogenase E1-alpha subunit.

768

20 AAF64450.1 AF239928 Euphorbia esula
DESCRIPTION: glutathione S-transferase. similar to auxin-inducible GST.

25 AAG16758.1 AY007560 Lycopersicon esculentum
DESCRIPTION: putative glutathione S-transferase T3.

AAG34803.1 AF243368 Glycine max
DESCRIPTION: glutathione S-transferase GST 13.

30 AAG16756.1 AY007558 Lycopersicon esculentum
DESCRIPTION: putative glutathione S-transferase T1.

35 AAG34796.1 AF243361 Glycine max
DESCRIPTION: glutathione S-transferase GST 6.

40 AAG34809.1 AF243374 Glycine max
DESCRIPTION: glutathione S-transferase GST 19.

45 AAG34797.1 AF243362 Glycine max
DESCRIPTION: glutathione S-transferase GST 7.

AAG34807.1 AF243372 Glycine max
DESCRIPTION: glutathione S-transferase GST 17.

5 AAG34798.1 AF243363 Glycine max
DESCRIPTION: glutathione S-transferase GST 8.

10 AAG34804.1 AF243369 Glycine max
DESCRIPTION: glutathione S-transferase GST 14.

15 AAG16759.1 AY007561 Lycopersicon esculentum
DESCRIPTION: putative glutathione S-transferase T4.

20 AAG34801.1 AF243366 Glycine max
DESCRIPTION: glutathione S-transferase GST 11.

AAG34810.1 AF243375 Glycine max
DESCRIPTION: glutathione S-transferase GST 20.

25 AAG16757.1 AY007559 Lycopersicon esculentum
DESCRIPTION: putative glutathione S-transferase T2.

30 AAC18566.1 AF048978 Glycine max
DESCRIPTION: 2,4-D inducible glutathione S-transferase. GSTa.

35 AAG34808.1 AF243373 Glycine max
DESCRIPTION: glutathione S-transferase GST 18.

AAG34800.1 AF243365 Glycine max
DESCRIPTION: glutathione S-transferase GST 10.

40 CAA71784.1 Y10820 Glycine max
DESCRIPTION: glutathione transferase.

45 AAG34844.1 AF244701 Zea mays
DESCRIPTION: glutathione S-transferase GST 36.

AAG32472.1 AF309379 *Oryza sativa* subsp. *japonica*
DESCRIPTION: putative glutathione S-transferase OsGSTU3.

5

AAA68430.1 J03679 *Solanum tuberosum*
DESCRIPTION: glutathione S-transferase. *gst1*. previously called
pathogenesis-related protein; *prp1-1*.

10

CAA04391.1 AJ000923 *Carica papaya*
DESCRIPTION: glutathione transferase. PGST1.

15

AAG34831.1 AF244688 *Zea mays*
DESCRIPTION: glutathione S-transferase GST 23.

20

CAA09187.1 AJ010448 *Alopecurus myosuroides*
DESCRIPTION: glutathione transferase. GST1a.

25

CAA09188.1 AJ010449 *Alopecurus myosuroides*
DESCRIPTION: glutathione transferase. GST1b.

AAG34802.1 AF243367 *Glycine max*
DESCRIPTION: glutathione S-transferase GST 12.

30

AAG34805.1 AF243370 *Glycine max*
DESCRIPTION: glutathione S-transferase GST 15.

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AAG34832.1 AF244689 *Zea mays*
DESCRIPTION: glutathione S-transferase GST 24.

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AAG34837.1 AF244694 *Zea mays*
DESCRIPTION: glutathione S-transferase GST 29.

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AAG34836.1 AF244693 *Zea mays*
DESCRIPTION: glutathione S-transferase GST 28.

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AAG32471.1 AF309378 *Oryza sativa* subsp. *japonica*
DESCRIPTION: putative glutathione S-transferase OsGSTU4.

5
AAG34849.1 AF244706 *Zea mays*
DESCRIPTION: glutathione S-transferase GST 41.

10 CAC24549.1 AJ296343 *Cichorium intybus* x *Cichorium endivia*
DESCRIPTION: glutathione S-transferase. chi-GST1. auxin-induced GST.

AAC32118.1 AF051214 *Picea mariana*
15 DESCRIPTION: probable glutathione S-transferase. Sb18. similar to
Nicotiana tabacum probable glutathione S-transferase encoded by GenBank
Accession Number X56266.

20 AAG34795.1 AF243360 *Glycine max*
DESCRIPTION: glutathione S-transferase GST 5.

AAG34841.1 AF244698 *Zea mays*
25 DESCRIPTION: glutathione S-transferase GST 33.

AAF29773.1 AF159229 *Gossypium hirsutum*
DESCRIPTION: glutathione S-transferase. GST.

30 769

AAG34797.1 AF243362 *Glycine max*
DESCRIPTION: glutathione S-transferase GST 7.

35

AAG34798.1 AF243363 *Glycine max*
DESCRIPTION: glutathione S-transferase GST 8.

40

AAG34803.1 AF243368 *Glycine max*
DESCRIPTION: glutathione S-transferase GST 13.

45 AAG16758.1 AY007560 *Lycopersicon esculentum*
DESCRIPTION: putative glutathione S-transferase T3.

- 5 AAF64450.1 AF239928 *Euphorbia esula*
DESCRIPTION: glutathione S-transferase. similar to auxin-inducible GST.
- 10 AAG34801.1 AF243366 *Glycine max*
DESCRIPTION: glutathione S-transferase GST 11.
- 15 AAG34804.1 AF243369 *Glycine max*
DESCRIPTION: glutathione S-transferase GST 14.
- 20 AAG34796.1 AF243361 *Glycine max*
DESCRIPTION: glutathione S-transferase GST 6.
- 25 AAG34809.1 AF243374 *Glycine max*
DESCRIPTION: glutathione S-transferase GST 19.
- 30 AAG16759.1 AY007561 *Lycopersicon esculentum*
DESCRIPTION: putative glutathione S-transferase T4.
- 35 AAG16757.1 AY007559 *Lycopersicon esculentum*
DESCRIPTION: putative glutathione S-transferase T2.
- 40 AAG16756.1 AY007558 *Lycopersicon esculentum*
DESCRIPTION: putative glutathione S-transferase T1.
- 45 AAG34807.1 AF243372 *Glycine max*
DESCRIPTION: glutathione S-transferase GST 17.
- AAG34810.1 AF243375 *Glycine max*
DESCRIPTION: glutathione S-transferase GST 20.
- AAG34844.1 AF244701 *Zea mays*
DESCRIPTION: glutathione S-transferase GST 36.

AAG34831.1 AF244688 Zea mays
DESCRIPTION: glutathione S-transferase GST 23.

5 AAC18566.1 AF048978 Glycine max
DESCRIPTION: 2,4-D inducible glutathione S-transferase. GSTa.

10 AAG34832.1 AF244689 Zea mays
DESCRIPTION: glutathione S-transferase GST 24.

15 AAG34808.1 AF243373 Glycine max
DESCRIPTION: glutathione S-transferase GST 18.

20 AAG34837.1 AF244694 Zea mays
DESCRIPTION: glutathione S-transferase GST 29.

AAG34800.1 AF243365 Glycine max
DESCRIPTION: glutathione S-transferase GST 10.

25 AAG34836.1 AF244693 Zea mays
DESCRIPTION: glutathione S-transferase GST 28.

30 CAA04391.1 AJ000923 Carica papaya
DESCRIPTION: glutathione transferase. PGST1.

35 CAA71784.1 Y10820 Glycine max
DESCRIPTION: glutathione transferase.

AAG34849.1 AF244706 Zea mays
DESCRIPTION: glutathione S-transferase GST 41.

40 AAA68430.1 J03679 Solanum tuberosum
DESCRIPTION: glutathione S-transferase. gst1. previously called
pathogenesis-related protein; prp1-1.

45 AAG34802.1 AF243367 Glycine max

DESCRIPTION: glutathione S-transferase GST 12.

5 CAC24549.1 AJ296343 Cichorium intybus x Cichorium endivia
DESCRIPTION: glutathione S-transferase. chi-GST1. auxin-induced GST.

10 CAA09187.1 AJ010448 Alopecurus myosuroides
DESCRIPTION: glutathione transferase. GST1a.

AAF22518.1 AF118925 Papaver somniferum
DESCRIPTION: glutathione S-transferase 2. GST2.

15 AAG32471.1 AF309378 Oryza sativa subsp. japonica
DESCRIPTION: putative glutathione S-transferase OsGSTU4.

20 CAA09188.1 AJ010449 Alopecurus myosuroides
DESCRIPTION: glutathione transferase. GST1b.

25 AAF22517.1 AF118924 Papaver somniferum
DESCRIPTION: glutathione S-transferase 1. GST1.

30 AAF22647.1 AF193439 Lycopersicon esculentum
DESCRIPTION: glutathione S-transferase/peroxidase. BI-GST/GPX.

AAG32473.1 AF309380 Oryza sativa subsp. japonica
DESCRIPTION: putative glutathione S-transferase OsGSTU2.

35 AAG32472.1 AF309379 Oryza sativa subsp. japonica
DESCRIPTION: putative glutathione S-transferase OsGSTU3.

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AAG46118.1 AC073166 Oryza sativa
DESCRIPTION: putative protein phosphatase-2C. OSJNBb0064P21.12. tRNA-
Lys.

45 AAG13599.1 AC051633 Oryza sativa

DESCRIPTION: putative protein phosphatase-2C. OSJNBb0015I11.26.

- 5 BAB12036.1 AP002820 *Oryza sativa*
DESCRIPTION: putative protein phosphatase. P0702D12.18.
- 10 AAC36698.1 AF075580 *Mesembryanthemum crystallinum*
DESCRIPTION: protein phosphatase-2C. PP2C.
- 15 CAA72341.1 Y11607 *Medicago sativa*
DESCRIPTION: protein phosphatase 2C. MP2C.
- 20 AAG43835.1 AF213455 *Zea mays*
DESCRIPTION: protein phosphatase type-2C. pp2c-1. PP2C-1.
- 25 CAB61839.1 AJ242803 *Sporobolus stapfianus*
DESCRIPTION: putative serine/threonine phosphatase type 2c.
- 30 AAD17804.1 AF092431 *Lotus japonicus*
DESCRIPTION: nodule-enhanced protein phosphatase type 2C. NPP2C1.
- AAD17805.1 AF092432 *Lotus japonicus*
DESCRIPTION: protein phosphatase type 2C. PP2C2.
- 35 AAC36697.1 AF075579 *Mesembryanthemum crystallinum*
DESCRIPTION: protein phosphatase-2C. PP2C.
- CAB90633.1 AJ277743 *Fagus sylvatica*
DESCRIPTION: protein phpsphatase 2C (PP2C). pp2C1. ABA-induced protein.
- 40 CAC10358.1 AJ277086 *Nicotiana tabacum*
DESCRIPTION: protein phosphatase 2C. PP2C1.
- 45 CAC10359.1 AJ277087 *Nicotiana tabacum*
DESCRIPTION: protein phosphatase 2C. PP2C2.

AAC36700.1 AF075582 Mesembryanthemum crystallinum
DESCRIPTION: protein phosphatase-2C. PP2C.

5

CAC09575.1 AJ298987 Fagus sylvatica
DESCRIPTION: protein phosphatase 2C (PP2C). pp2Cf1.

10 AAK20060.1 AC025783 Oryza sativa
DESCRIPTION: putative protein phosphatase 2C. OSJNBa0001O14.1.

15 CAB90634.1 AJ277744 Fagus sylvatica
DESCRIPTION: protein phosphatase 2C (PP2C). pp2C2. ABA and calcium
induced protein.

20 AAC35951.1 AF079355 Mesembryanthemum crystallinum
DESCRIPTION: protein phosphatase-2c. PP2C.

25 AAD11430.1 AF097667 Mesembryanthemum crystallinum
DESCRIPTION: protein phosphatase 2C homolog. PP2C.

30 AAB93832.1 U81960 Zea mays
DESCRIPTION: kinase interaction domain mediates phosphorylation-dependent
binding to a subset of active receptor-like protein kinases; type 2C
protein phosphatase. kinase associated protein phosphatase. KAPP.

35 AAC26828.1 AF075603 Oryza sativa
DESCRIPTION: kinase interaction domain mediates phosphorylation-dependent
binding to a subset of active receptor-like protein kinases. kinase
associated protein phosphatase. kapp. type 2C protein phosphatase.

40 AAC36699.1 AF075581 Mesembryanthemum crystallinum
DESCRIPTION: protein phosphatase-2C. PP2C.

45 CAC09576.1 AJ298988 Fagus sylvatica
DESCRIPTION: protein phosphatase 2C (PP2C). pp2Cf2.

777

AAD21872.1 AF078082 Phaseolus vulgaris
DESCRIPTION: receptor-like protein kinase homolog RK20-1.

5

AAB93834.1 U82481 Zea mays
DESCRIPTION: KI domain interacting kinase 1. KIK1. receptor-like protein
kinase; serine/threonine protein kinase.

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CAA74661.1 Y14285 Brassica oleracea
DESCRIPTION: SFR1. extracellular S domain: 8-1342; transmembrane domain:
1343-1411; intracellular kinase domain: 1412-2554.

15

AAD52097.1 AF088885 Nicotiana tabacum
DESCRIPTION: receptor-like kinase CHRK1. Chrk1.

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CAA73134.1 Y12531 Brassica oleracea
DESCRIPTION: serine/threonine kinase. BRLK.

25

CAB41879.1 Y18260 Brassica oleracea
DESCRIPTION: SRK15 protein. SRK15. receptor-like kinase.

30

CAB41878.1 Y18259 Brassica oleracea
DESCRIPTION: SRK5 protein. SRK5. receptor-like kinase.

35

CAB89179.1 AJ245479 Brassica napus subsp. napus
DESCRIPTION: ser /thr kinase. S-locus receptor kinase. srk.

40

CAA67145.1 X98520 Brassica oleracea
DESCRIPTION: receptor-like kinase. SFR2.

45

AAA33000.1 M76647 Brassica oleracea
DESCRIPTION: receptor protein kinase. SKR6.

CAA73133.1 Y12530 Brassica oleracea
DESCRIPTION: serine /threonine kinase. ARLK.

5

AAA62232.1 U00443 Brassica napus
DESCRIPTION: S-receptor kinase. protein contains an immunoglobulin-like domain.

10

AAC23542.1 U20948 Ipomoea trifida
DESCRIPTION: receptor protein kinase. IRK1.

15

CAA74662.1 Y14286 Brassica oleracea
DESCRIPTION: SFR3. extracellular S domain: 123-1346; transmembrane domain: 1347-1412; intracellular kinase domain: from 1413.

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BAA92837.1 AB032474 Brassica oleracea
DESCRIPTION: S60 S-locus receptor kinase. SRK60.

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BAA07577.2 D38564 Brassica rapa
DESCRIPTION: receptor protein kinase SRK12.

30

BAA23676.1 AB000970 Brassica rapa
DESCRIPTION: receptor kinase 1. BcRK1.

35

CAA79355.1 Z18921 Brassica oleracea
DESCRIPTION: S-receptor kinase-like protein.

40

BAB21001.1 AB054061 Brassica rapa
DESCRIPTION: S locus receptor kinase. SRK22.

45

BAA21132.1 D88193 Brassica rapa
DESCRIPTION: S-receptor kinase. SRK9 (B.c).

BAA06285.1 D30049 Brassica rapa
DESCRIPTION: S-receptor kinase SRK9.

BAA92836.1 AB032473 Brassica oleracea
DESCRIPTION: S18 S-locus receptor kinase. SRK18.

5 BAA07576.1 D38563 Brassica rapa
DESCRIPTION: receptor protein kinase SRK8.

10 BAB18292.1 AP002860 Oryza sativa
DESCRIPTION: putative receptor-like protein kinase. P0409B08.19.

15 AAK21965.1 AY028699 Brassica napus
DESCRIPTION: receptor protein kinase PERK1.

20 BAA92954.1 AP001551 Oryza sativa
DESCRIPTION: Similar to Oryza sativa protein kinase (OSPK10) mRNA.
(L27821).

25 BAB39873.1 AP002882 Oryza sativa
DESCRIPTION: putative protein kinase. P0439B06.8. contains ESTs
AU056701(S20808),AU056702(S20808).

30 AAK00425.1 AC069324 Oryza sativa
DESCRIPTION: Putative protein kinase. OSJNBa0071K19.11.

BAB39435.1 AP003338 Oryza sativa
DESCRIPTION: putative receptor kinase. OJ1212_B09.2.

35 BAB07904.1 AP002835 Oryza sativa
DESCRIPTION: putative S-receptor kinase. P0417G05.12.

40 BAA94518.1 AP001800 Oryza sativa
DESCRIPTION: Similar to Arabidopsis thaliana chromosome 2 section 111 of
255; putative receptor-like protein kinase (AC002392).

45 AAG16628.1 AY007545 Brassica napus
DESCRIPTION: protein serine/threonine kinase BNK1.

- 5 BAB39409.1 AP002901 *Oryza sativa*
DESCRIPTION: putative protein kinase. P0456F08.9. contains EST
C23560(R0290).
- 10 BAB16871.1 AP002537 *Oryza sativa*
DESCRIPTION: putative protein kinase APK1A *Arabidopsis thaliana*.
P0001B06.24. contains ESTs C22608(R3192),D25110(R3192).
- 15 AAF91324.1 AF244890 *Glycine max*
DESCRIPTION: receptor-like protein kinase 3. RLK3. GmRLK3.
- 20 BAA82556.1 AB030083 *Populus nigra*
DESCRIPTION: lectin-like protein kinase. PnLPK.
- 25 AAF91323.1 AF244889 *Glycine max*
DESCRIPTION: receptor-like protein kinase 2. RLK2. GmRLK2.
- 779

30 AAF91322.1 AF244888 *Glycine max*
DESCRIPTION: receptor-like protein kinase 1. RLK1. GmRLK1.
- 35 BAA78050.1 AB027757 *Cicer arietinum*
DESCRIPTION: NADPH oxidoreductase homolog.
- 40 BAA83082.1 AB030704 *Lithospermum erythrorhizon*
DESCRIPTION: LEDI-4 protein. LEDI-4. preferentially expressed in
darkness; putative NADPH quinone oxidoreductase; similar to
zeta-crystallin.
- 45 AAG53944.1 AF304461 *Triphysaria versicolor*
DESCRIPTION: quinone-oxidoreductase QR1. TvQR1.

780

AAK17067.1 AF254558 *Oryza sativa*
DESCRIPTION: NAC6. NAC6.

5

BAA89800.1 AB028185 *Oryza sativa*
DESCRIPTION: OsNAC6 protein. OsNAC6.

10

BAA89799.1 AB028184 *Oryza sativa*
DESCRIPTION: OsNAC5 protein. OsNAC5.

15

BAA89798.1 AB028183 *Oryza sativa*
DESCRIPTION: OsNAC4 protein. OsNAC4.

20

BAA89797.1 AB028182 *Oryza sativa*
DESCRIPTION: OsNAC3 protein. OsNAC3.

25

BAA89801.1 AB028186 *Oryza sativa*
DESCRIPTION: OsNAC7 protein. OsNAC7.

AAF68626.1 AF254124 *Medicago truncatula*
DESCRIPTION: NAC1. NAC1. NAC domain containing protein.

30

BAA89802.1 AB028187 *Oryza sativa*
DESCRIPTION: OsNAC8 protein. OsNAC8.

35

BAA78417.1 AB021178 *Nicotiana tabacum*
DESCRIPTION: NAC-domain protein. TERN. elicitor-responsive gene.

783

40

CAA54390.1 X77134 *Brassica napus*
DESCRIPTION: acyl-CoA binding protein.

45

CAA70200.1 Y08996 *Ricinus communis*
DESCRIPTION: acyl-CoA-binding protein.

- 5 CAB56693.1 AJ249833 *Digitalis lanata*
DESCRIPTION: binds medium- and long-chain acyl-coa esters. Acyl-CoA binding protein (ACBP). acbp3.
- 10 CAB56694.1 AJ249834 *Digitalis lanata*
DESCRIPTION: binds medium- and long-chain acyl-coa esters. Acyl-CoA binding protein (ACBP). acbp4.
- 15 AAB67736.1 U35015 *Gossypium hirsutum*
DESCRIPTION: acyl-CoA-binding protein.
- 784
20 -----
- CAA58994.1 X84208 *Sinapis alba*
DESCRIPTION: trypsin inhibitor 2. mti-2.
- 25 CAA76116.1 Y16190 *Sinapis alba*
DESCRIPTION: trypsin inhibitor 2. mti-2.
- 785
30 -----
- AAF66242.1 AF243180 *Lycopersicon esculentum*
DESCRIPTION: dicyanin. binuclear blue copper protein; contains two stellacyanins linked together.
- 35 AAC32421.1 U65511 *Cucumis sativus*
DESCRIPTION: putative oxygen activation and/or lignin formation. stellacyanin. member of a strictly plant-specific family of mononuclear blue copper proteins known as phytoeyanins, which are further classified into three distinct subfamilies: Uclacyanins, Stellacyanins, and
40 Plantacyanins; member of the subfamily of Stellacyanins; similar to *Rhus vernicifera* stellacyanin: SwissProt Accession Number P00302; similar to umecyanin: SwissProt Accession Number P42849; similar to mavicyanin; SwissProt Accession Number P80728; similar to BCB encoded by GenBank Accession Number Z15058; similar to F18A8.9, encoded by GenBank Accession
45 Number AC003105; similar to F7F1.27 encoded by GenBank Accession Number AC004669; similar to F9D12.16 encoded by GenBank Accession Number

AF077407; glycoprotein.

5 CAA80963.1 Z25471 Pisum sativum
DESCRIPTION: blue copper protein.

10 AAD10251.1 AF031195 Triticum aestivum
DESCRIPTION: blue copper-binding protein homolog. S85.

15 AAC64163.1 AF093537 Zea mays
DESCRIPTION: blue copper protein. similar to pea blue copper protein in
GenBank Accession Number Z25471.

20 CAA10134.1 AJ012693 Cicer arietinum
DESCRIPTION: basic blue copper protein.

25 AAF66243.1 AF243181 Lycopersicon esculentum
DESCRIPTION: plantacyanin. naturally occurring cupredoxin with a Val
residue in the position of the axial ligand Met; member of the
plantacyanin subfamily of a strictly plant-specific family of mononuclear
blue copper proteins known as phytoeyanins.

30 CAB65280.1 AJ248323 Medicago sativa subsp. x varia
DESCRIPTION: basic blue protein. babl.

35 AAC32448.1 U76296 Spinacia oleracea
DESCRIPTION: plantacyanin. member of a strictly plant-specific family of
mononuclear blue copper proteins known as phytoeyanins, which are further
classified into three distinct subfamilies: Uclacyanins, Stellacyanins,
and Plantacyanins; member of the subfamily of Plantacyanins;
non-glycosylated.

40 793

BAA81862.1 AB026295 Oryza sativa
DESCRIPTION: Similar to leucoanthocyanidin dioxygenase.(AI440611).

45 AAB39995.1 U82432 Dianthus caryophyllus
DESCRIPTION: anthocyanidin synthase. allele: S; 2-oxoglutarat-dependent

dioxygenase.

5 BAA36554.1 AB011796 Citrus unshiu
DESCRIPTION: flavonol synthase. CitFLS.

10 AAD56580.1 AF184273 Daucus carota
DESCRIPTION: leucoanthocyanidin dioxygenase 1. LDOX1. 2-oxoglutarate
dependent dioxygenase.

15 AAD56581.1 AF184274 Daucus carota
DESCRIPTION: leucoanthocyanidin dioxygenase 2. LDOX. 2-oxoglutarate
dependent dioxygenase.

20 CAA50498.1 X71360 Malus sp.
DESCRIPTION: anthocyanidin hydroxylase. apple equivalent to 'Candi' from
Antirrhinum majus.

25 AAD26205.1 AF117269 Malus x domestica
DESCRIPTION: anthocyanidin synthase. ANS.

30 AAB82287.1 AF026058 Matthiola incana
DESCRIPTION: anthocyanidin synthase.

CAA80264.1 Z22543 Petunia x hybrida
DESCRIPTION: flavonol synthase.

35 AAF64168.1 AF240764 Eustoma grandiflorum
DESCRIPTION: flavonol synthase. fls.

40 BAA20143.1 AB003779 Perilla frutescens
DESCRIPTION: leucoanthocyanidin dioxygenase.

45 AAB66560.1 AF015885 Callistephus chinensis
DESCRIPTION: anthocyanidin synthase.

BAB21477.1 AB044091 *Torenia fournieri*
DESCRIPTION: anthocyanidin synthase. 2-oxoglutarate dependent oxygenase.

5 CAA63092.1 X92178 *Solanum tuberosum*
DESCRIPTION: flavonol synthase.

10 AAD26261.1 AF119095 *Malus x domestica*
DESCRIPTION: flavonol synthase. FLS.

15 CAA53580.1 X75966 *Vitis vinifera*
DESCRIPTION: leucoanthocyanidin dioxygenase. LDOX.

BAA75305.1 AB023786 *Ipomoea batatas*
DESCRIPTION: anthocyanidin synthase. ans I.

20 AAB84049.1 AF028602 *Ipomoea purpurea*
DESCRIPTION: anthocyanidin synthase. ANS-FL1.

25 BAA75306.1 AB023787 *Ipomoea batatas*
DESCRIPTION: anthocyanidin synthase. ans II.

30 CAA73094.1 Y12489 *Forsythia x intermedia*
DESCRIPTION: anthocyanidin synthase.

35 CAA69252.1 Y07955 *Oryza sativa*
DESCRIPTION: anthocyanidin synthase. ANS.

794

40 AAD10204.1 AF030260 *Vicia sativa*
DESCRIPTION: CYP94A1. vagh111. cytochrome P450 fatty acid hydroxylase;
Method: conceptual translation with partial peptide sequencing.

AAG33645.1 AF092917 *Vicia sativa*
DESCRIPTION: cytochrome P450-dependent fatty acid hydroxylase. CYP94A2.
45

AAG17470.1 AF123609 *Triticum aestivum*
DESCRIPTION: cytochrome P450.

5 BAA99523.1 AP002484 *Oryza sativa*
DESCRIPTION: putative cytochrome P450. P0489A01.14.

10 AAK31592.1 AY029178 *Brassica rapa* subsp. *pekinensis*
DESCRIPTION: cytochrome P450. mf-CYP450. possible relevance to
male-sterility.

15 BAA99522.1 AP002484 *Oryza sativa*
DESCRIPTION: putative cytochrome P450. P0489A01.13.

20 BAA83370.1 AP000391 *Oryza sativa*
DESCRIPTION: ESTs AU056036(S20239),C72753(E2173),
AU056035(S20239)
correspond to a region of the predicted gene.; Similar to putative
cytochrome P-450 (AC003680).

25 CAB41474.1 AJ238402 *Catharanthus roseus*
DESCRIPTION: cytochrome P450. CYP96C1.

30 AAB94586.1 AF022457 *Glycine max*
DESCRIPTION: CYP97B2p. CYP97B2. cytochrome P450 monooxygenase.

35 AAK20054.1 AC025783 *Oryza sativa*
DESCRIPTION: putative cytochrome P450 monooxygenase.
OSJNBa0001O14.16.

40 AAK38086.1 AF321862 *Lolium rigidum*
DESCRIPTION: putative cytochrome P450.

AAK38085.1 AF321861 *Lolium rigidum*
DESCRIPTION: putative cytochrome P450.

45 AAB94588.1 AF022459 *Glycine max*

DESCRIPTION: CYP71D10p. CYP71D10. cytochrome P450 monooxygenase.

5 CAA89260.1 Z49263 Pisum sativum
DESCRIPTION: cytochrome P450.

10 AAG09208.1 AF175278 Pisum sativum
DESCRIPTION: wound-inducible P450 hydroxylase. CYP82A1.

15 AAC49188.2 U29333 Pisum sativum
DESCRIPTION: cytochrome P450 monooxygenase. CYP82. new cytochrome
P450 family.

20 BAB19083.1 AP002744 Oryza sativa
DESCRIPTION: putative cytochrome P450. P0006C01.25. contains ESTs
AU081507(C12518),C26520(C12518).

25 BAB19104.1 AP002839 Oryza sativa
DESCRIPTION: putative cytochrome P450. P0688A04.10. contains ESTs
AU081507(C12518),C26520(C12518).

30 AAK38092.1 AF321868 Lolium rigidum
DESCRIPTION: putative cytochrome P450.

35 CAA04117.1 AJ000478 Helianthus tuberosus
DESCRIPTION: fatty acid in-chain hydroxylase. cytochrome P450. CYP81B11.
chimeric sequence (from 5'-race).

40 AAK38091.1 AF321867 Lolium rigidum
DESCRIPTION: putative cytochrome P450.

CAA04116.1 AJ000477 Helianthus tuberosus
DESCRIPTION: fatty acid in-chain hydroxylase. cytochrome P450. CYP81B1c.

45 BAA22423.1 AB001380 Glycyrrhiza echinata
DESCRIPTION: cytochrome P450. CYP93B1.

- CAA71876.1 Y10982 Glycine max
DESCRIPTION: putative cytochrome P450.
- 5
- BAB39252.1 AP002968 Oryza sativa
DESCRIPTION: putative cytochrome P450. P0416G11.1.
- 10
- AAA33106.1 L10081 Catharanthus roseus
DESCRIPTION: cytochrome P-450 protein. CYP72. putative; CYP72 protein.
- 15
- AAA17746.1 L19075 Catharanthus roseus
DESCRIPTION: cytochrome P450. CYP72C. putative.
- 20
- BAA74466.1 AB022733 Glycyrrhiza echinata
DESCRIPTION: cytochrome P450. CYP Ge-51.
- 25
- BAB19121.1 AP002839 Oryza sativa
DESCRIPTION: putative cytochrome P450. P0688A04.28.
- 30
- AAA17732.1 L19074 Catharanthus roseus
DESCRIPTION: cytochrome P450. CYP72B.
- 35
- BAA93634.1 AB025016 Lotus japonicus
DESCRIPTION: cytochrome P450.
- 40
- AAB05376.3 U35226 Nicotiana plumbaginifolia
DESCRIPTION: putative cytochrome P-450.
- 45
- AAB61965.1 U48435 Solanum chacoense
DESCRIPTION: putative cytochrome P450.
- AAF27282.1 AF122821 Capsicum annum
DESCRIPTION: cytochrome P450. PepCYP.

CAB50768.1 AJ243804 Cicer arietinum
DESCRIPTION: putative isoflavone synthase. cytochrome P450. cyp93C3.

5 AAC34853.1 AF082028 Hemerocallis hybrid cultivar
DESCRIPTION: putative cyt P450-containing fatty acid hydroxylase.
senescence-associated protein 3. SA3. mRNA accumulates in senescing
petals.

10 CAB43505.1 AJ239051 Cicer arietinum
DESCRIPTION: cytochrome P450. cyp81E2.

15 BAB21156.1 AP002899 Oryza sativa
DESCRIPTION: putative cytochrome P450. P0456A01.12.

20 CAA50648.1 X71657 Solanum melongena
DESCRIPTION: P450 hydroxylase.

25 BAB19112.1 AP002839 Oryza sativa
DESCRIPTION: putative cytochrome P450. P0688A04.18. contains ESTs
AU067870(C10320),AU067869(C10320).

30 BAB19091.1 AP002744 Oryza sativa
DESCRIPTION: putative cytochrome P450. P0006C01.33. contains ESTs
AU067870(C10320),AU067869(C10320).

35 BAA84072.1 AB028152 Torenia hybrida
DESCRIPTION: flavone synthase II. cytochrome P450. TFNS5.

BAA76380.1 AB023636 Glycyrrhiza echinata
DESCRIPTION: cytochrome P450. CYP Ge-8.

40 CAA72208.1 Y11404 Zea mays
DESCRIPTION: cytochrome p450. cyp71c2.

45 CAA57423.1 X81829 Zea mays

DESCRIPTION: adenylate kinase homolog.

AAAF23372.1 AF187063 *Oryza sativa*

5 DESCRIPTION: catalyzes the transfer of phosphate from ATP to UMP or CMP to form ADP and UDP or CDP. UMP/CMP kinase b. *ura6*.

AAAF23371.1 AF187062 *Oryza sativa*

10 DESCRIPTION: catalyzes the transfer of phosphate from ATP to UMP or CMP to form ADP and UDP or CDP. UMP/CMP kinase a. *ura6*.

AAD41679.1 AF086603 *Ceratopteris richardii*

15 DESCRIPTION: adenylate kinase. ADK1.

BAA85443.1 AP000616 *Oryza sativa*

20 DESCRIPTION: similar to UMP/CMP kinase (AF000147).

808

CAA41774.1 X59046 *Oryza sativa*

25 DESCRIPTION: sucrose-UDP glucosyltransferase (isoenzyme 2). RSs2.

BAA89049.1 AB029401 *Citrus unshiu*

DESCRIPTION: sucrose synthase. CitSUS1-2.

30

AAA34196.1 L19762 *Lycopersicon esculentum*

DESCRIPTION: sucrose synthase.

35 BAA88905.1 AB022092 *Citrus unshiu*

DESCRIPTION: sucrose synthase. CitSUS1.

AAD28641.1 U73588 *Gossypium hirsutum*

40 DESCRIPTION: sucrose synthase.

CAA49428.1 X69773 *Vicia faba*

45 DESCRIPTION: sucrose synthase. VfSucs.

AAC37346.1 M97551 *Vicia faba*
DESCRIPTION: cleavage of sucrose.
UDP-glucose:D-fructose-2-glucosyltransferase. putative.

5

CAA09681.1 AJ011535 *Lycopersicon esculentum*
DESCRIPTION: sucrose synthase. sus2.

10 AAA97572.1 U24088 *Solanum tuberosum*
DESCRIPTION: sucrose synthase.

15 CAA09593.1 AJ011319 *Lycopersicon esculentum*
DESCRIPTION: sucrose synthase. sus3.

20 CAB40794.1 AJ131943 *Medicago truncatula*
DESCRIPTION: sucrose synthase. sucS1.

AAC17867.1 AF049487 *Medicago sativa*
DESCRIPTION: sucrose hydrolysis. sucrose synthase.
25

CAB40795.1 AJ131964 *Medicago truncatula*
DESCRIPTION: sucrose synthase. sucS1.

30 CAA65640.1 X96939 *Tulipa gesneriana*
DESCRIPTION: sucrose-synthase 21.

35 AAA97571.1 U24087 *Solanum tuberosum*
DESCRIPTION: sucrose synthase.

40 CAA63122.1 X92378 *Alnus glutinosa*
DESCRIPTION: sucrose synthase. sus1.

AAA33514.1 L22296 *Zea mays*
DESCRIPTION: UDP-glucose:D-fructose 2-glucosyl-transferase. Sus1.

45 CAA65639.1 X96938 *Tulipa gesneriana*

DESCRIPTION: sucrose-synthase 1.

5 AAC41682.1 L03366 Oryza sativa
DESCRIPTION: sucrose synthase 3. RSs3.

10 CAA75793.1 Y15802 Hordeum vulgare
DESCRIPTION: sucrose synthase 2. Ss2.

CAA49551.1 X69931 Hordeum vulgare
DESCRIPTION: sucrose synthase. Ss2.

15 CAA76056.1 Y16090 Daucus carota
DESCRIPTION: sucrose synthase isoform I. Susy*Dc1.

20 CAA53081.1 X75332 Daucus carota
DESCRIPTION: sucrose synthase.

25 AAA33515.1 L33244 Zea mays
DESCRIPTION: sucrose synthase 2. Sus1.

30 BAB20799.1 AB045710 Pyrus pyrifolia
DESCRIPTION: sucrose synthase 1. PypSUS1.

CAA03935.1 AJ000153 Triticum aestivum
DESCRIPTION: sucrose synthase type 2.

35 AAC39323.1 AF030231 Glycine max
DESCRIPTION: sucrose synthase. SS. nodulin-100.

40 BAA01108.1 D10266 Vigna radiata
DESCRIPTION: sucrose synthase. vss1.

45 CAA09910.1 AJ012080 Pisum sativum
DESCRIPTION: sucrose synthase.

AAC28107.1 AF079851 *Pisum sativum*
DESCRIPTION: nodule-enhanced sucrose synthase. ness.

5 CAC32462.1 AJ311496 *Pisum sativum*
DESCRIPTION: sucrose metabolism. sucrose synthase isoform 3. sus3.

10 CAA57881.1 X82504 *Chenopodium rubrum*
DESCRIPTION: sucrose synthase. CSS1.

15 CAA26229.1 X02382 *Zea mays*
DESCRIPTION: sucrose synthase.

20 CAA26247.1 X02400 *Zea mays*
DESCRIPTION: sucrose synthase.

CAA46017.1 X64770 *Oryza sativa*
DESCRIPTION: sucrose synthase. RSs1.

25 CAB38022.1 AJ132000 *Craterostigma plantagineum*
DESCRIPTION: sucrose metabolism. sucrose synthase. Ss2.

30 CAA78747.1 Z15028 *Oryza sativa*
DESCRIPTION: sucrose synthase.

35 AAF85966.1 AF263384 *Saccharum officinarum*
DESCRIPTION: sucrose synthase-1.

40 CAA46701.1 X65871 *Hordeum vulgare*
DESCRIPTION: sucrose synthase.

CAA04543.1 AJ001117 *Triticum aestivum*
DESCRIPTION: sucrose synthase type I. Ss1.

45 BAA88904.1 AB022091 *Citrus unshiu*

DESCRIPTION: sucrose synthase. CitSUSA.

5 BAA88981.1 AB025778 Citrus unshiu
DESCRIPTION: sucrose synthase. CitSUSA-2.

10 CAA04512.1 AJ001071 Pisum sativum
DESCRIPTION: second sucrose synthase.

CAA76057.1 Y16091 Daucus carota
DESCRIPTION: sucrose synthase isoform II. Susy*Dc2.

15 CAB38021.1 AJ131999 Craterostigma plantagineum
DESCRIPTION: sucrose metabolism. sucrose synthase. Ss1.

20 CAA57499.1 X81974 Beta vulgaris
DESCRIPTION: sucrose synthase. SBSS1.

25 CAA47264.1 X66728 Hordeum vulgare
DESCRIPTION: sucrose synthase.

809

30 AAB69317.1 AF012861 Petroselinum crispum
DESCRIPTION: plastidic glucose-6-phosphate dehydrogenase. pG6PDH.

35 AAF87216.1 AF231351 Nicotiana tabacum
DESCRIPTION: plastidic glucose 6-phosphate dehydrogenase. G6PDHP2.

CAA67782.1 X99405 Nicotiana tabacum
DESCRIPTION: glucose-6-phosphate dehydrogenase. G6PD.

40 CAB52708.1 AJ010712 Solanum tuberosum
DESCRIPTION: glucose-6-phosphate 1-dehydrogenase. g6pd.

45 CAB52685.1 AJ132346 Dunaliella bioculata
DESCRIPTION: plastidic glucose-6-phosphate dehydrogenase. g6PD.

CAA04993.1 AJ001770 *Nicotiana tabacum*
DESCRIPTION: glucose-6-phosphate dehydrogenase. TCG9.

5 BAA97662.1 AB029454 *Triticum aestivum*
DESCRIPTION: glucose-6-phosphate dehydrogenase. g6pdh.

10 BAA97663.1 AB029455 *Triticum aestivum*
DESCRIPTION: glucose-6-phosphate dehydrogenase. g6pdh.

15 BAA97664.1 AB029456 *Triticum aestivum*
DESCRIPTION: glucose-6-phosphate dehydrogenase. g6pdh.

20 AAG23802.1 AF260736 *Cucurbita pepo*
DESCRIPTION: plastidic glucose-6-phosphate dehydrogenase.

CAB66330.1 AJ279688 *Betula pendula*
DESCRIPTION: glucose-6-phosphate dehydrogenase. g6pd.

25 BAA82155.1 AB011441 *Triticum aestivum*
DESCRIPTION: glucose-6-phosphate dehydrogenase. WESR5. salt-stress
responding gene.

30 CAA06200.1 AJ004900 *Glycine max*
DESCRIPTION: pentose phosphate pathway oxidoreductase generating
NADPH.
glucose-6-phosphate-dehydrogenase.

35 812

BAA08910.1 D50407 *Cucumis sativus*
DESCRIPTION: glutamyl-tRNA reductase. hema.

40 AAD16897.1 AF105221 *Glycine max*
DESCRIPTION: converts glutamyl-tRNA to glutamate 1-semialdehyde.
glutamyl-tRNA reductase precursor. gtr1.

45 BAA11091.1 D67088 *Cucumis sativus*

DESCRIPTION: glutamyl-tRNA reductase. hemA2.

5 BAA25003.1 AB011416 Oryza sativa
DESCRIPTION: glutamyl-tRNA reductase.

10 AAG13620.1 AC078840 Oryza sativa
DESCRIPTION: putative glutamyl-tRNA reductase. OSJNBb0073N24.1.

15 CAA60054.1 X86101 Hordeum vulgare
DESCRIPTION: aminolevulinate synthesis (chlorophyll synthesis). glutamyl
tRNA reductase. hemA 1. 1st isoform.

20 CAA63140.1 X92403 Hordeum vulgare
DESCRIPTION: glutamyl-tRNA reductase. hemA1. isoform I.

BAA25167.1 D88382 Hordeum vulgare
DESCRIPTION: glutamyl-tRNA reductase. hemA1. isoform 1.

25 CAA60055.1 X86102 Hordeum vulgare
DESCRIPTION: aminolevulinate synthesis (chlorophyll synthesis). glutamyl
tRNA reductase. hemA 2. 2nd isoform.

30 BAA25168.1 D88383 Hordeum vulgare
DESCRIPTION: glutamyl-tRNA reductase. hemA3. isoform 3.

35 AAG41962.1 AF305613 Chlamydomonas reinhardtii
DESCRIPTION: glutamyl-tRNA reductase precursor. HemA. pGtr.

40 AAG02480.1 AF294753 Hordeum vulgare
DESCRIPTION: converts glutamyl-tRNA to glutamate 1-semialdehyde in the
chlorophyll biosynthetic pathway. glutamyl-tRNA reductase. hemA2.

45 AAG02479.1 AF294752 Hordeum vulgare
DESCRIPTION: converts glutamyl-tRNA to glutamate 1-semialdehyde in the
chlorophyll biosynthetic pathway. glutamyl-tRNA reductase. hemA1.

 BAA82556.1 AB030083 *Populus nigra*
 DESCRIPTION: lectin-like protein kinase. PnLPK.

5

AAD21872.1 AF078082 *Phaseolus vulgaris*
 DESCRIPTION: receptor-like protein kinase homolog RK20-1.

10

AAF43408.1 AF230515 *Oryza sativa* subsp. *japonica*
 DESCRIPTION: serine/threonine protein kinase. YK35.

15

CAB51480.1 Y14600 *Sorghum bicolor*
 DESCRIPTION: putative protein serine /threonine kinase. RLK1. accumulates
 in mesophyll cells.

20

CAA73134.1 Y12531 *Brassica oleracea*
 DESCRIPTION: serine/threonine kinase. BRLK.

25

AAB93834.1 U82481 *Zea mays*
 DESCRIPTION: KI domain interacting kinase 1. KIK1. receptor-like protein
 kinase; serine/threonine protein kinase.

30

AAK00425.1 AC069324 *Oryza sativa*
 DESCRIPTION: Putative protein kinase. OSJNBa0071K19.11.

35

BAA92954.1 AP001551 *Oryza sativa*
 DESCRIPTION: Similar to *Oryza sativa* protein kinase (OSPK10) mRNA.
 (L27821).

40

BAB39873.1 AP002882 *Oryza sativa*
 DESCRIPTION: putative protein kinase. P0439B06.8. contains ESTs
 AU056701(S20808),AU056702(S20808).

45

BAB19337.1 AP003044 *Oryza sativa*
 DESCRIPTION: putative protein kinase. P0038C05.10. contains ESTs
 AU056335(S20481),AU056336(S20481).

AAK21965.1 AY028699 Brassica napus
DESCRIPTION: receptor protein kinase PERK1.

5 BAA92953.1 AP001551 Oryza sativa
DESCRIPTION: Similar to Arabidopsis thaliana chromosome 4 BAC clone
F10M6
; S-receptor kinase -like protein. (AL021811).

10 BAB07906.1 AP002835 Oryza sativa
DESCRIPTION: putative S-receptor kinase. P0417G05.14.

15 BAA94516.1 AP001800 Oryza sativa
DESCRIPTION: Similar to Zea mays S-domain receptor-like protein kinase
(AJ010166).

20 AAD52097.1 AF088885 Nicotiana tabacum
DESCRIPTION: receptor-like kinase CHRK1. Chrkl.

25 BAB21240.1 AP002953 Oryza sativa
DESCRIPTION: Putative protein kinase. P0426D06.20. contains ESTs
C22359(C11461),C22360(C11461).

30 AAC23542.1 U20948 Ipomoea trifida
DESCRIPTION: receptor protein kinase. IRK1.

35 BAB18292.1 AP002860 Oryza sativa
DESCRIPTION: putative receptor-like protein kinase. P0409B08.19.

AAG16628.1 AY007545 Brassica napus
DESCRIPTION: protein serine/threonine kinase BNK1.
40

AAA33915.1 L27821 Oryza sativa
DESCRIPTION: receptor type serine/threonine kinase. protein kinase.

45 BAB03429.1 AP002817 Oryza sativa

DESCRIPTION: EST C22619(S11214) corresponds to a region of the predicted gene. Similar to Arabidopsis thaliana chromosome 2, BAC clone T17D12; putative protein kinase (AC006587).

5

BAB07999.1 AP002525 Oryza sativa
DESCRIPTION: putative protein kinase. P0462H08.22. contains EST C22619(S11214).

10

BAA94509.1 AB041503 Populus nigra
DESCRIPTION: protein kinase 1. PnPK1.

15

AAD46420.1 AF100771 Hordeum vulgare
DESCRIPTION: receptor-like kinase. Hv3ARK. similar to wheat ARK1AS.

20

BAA23676.1 AB000970 Brassica rapa
DESCRIPTION: receptor kinase 1. BcRK1.

25

AAD38286.1 AC007789 Oryza sativa
DESCRIPTION: putative protein kinase. OSJNBa0049B20.13.

BAB40081.1 AP003074 Oryza sativa
DESCRIPTION: putative receptor protein kinase. OSJNBa0004G10.30.

30

BAB18321.1 AP002865 Oryza sativa
DESCRIPTION: putative receptor protein kinase. P0034C11.11.

35

BAA94517.1 AP001800 Oryza sativa
DESCRIPTION: Similar to Zea mays S-domain receptor-like protein kinase (AJ010166).

40

BAA21132.1 D88193 Brassica rapa
DESCRIPTION: S-receptor kinase. SRK9 (B.c).

45

BAA06285.1 D30049 Brassica rapa
DESCRIPTION: S-receptor kinase SRK9.

BAB07905.1 AP002835 *Oryza sativa*
DESCRIPTION: putative S-receptor kinase. P0417G05.13.

5 BAA94529.2 AP001800 *Oryza sativa*
DESCRIPTION: Similar to *Zea mays* S-domain receptor-like protein kinase
(AJ010166).

10 AAB61708.1 U93048 *Daucus carota*
DESCRIPTION: somatic embryogenesis receptor-like kinase. SERK.

15 CAA79355.1 Z18921 *Brassica oleracea*
DESCRIPTION: S-receptor kinase-like protein.

20 AAK11674.1 AF339747 *Lophopyrum elongatum*
DESCRIPTION: protein kinase. ESI47.

25 AAF43496.1 AF131222 *Lophopyrum elongatum*
DESCRIPTION: protein serine/threonine kinase. ESI47. induced in roots by
salt stress, osmotic stress, and ABA treatment.

30 BAA94528.1 AP001800 *Oryza sativa*
DESCRIPTION: Similar to *Arabidopsis thaliana* chromosome 2 BAC T20K24;
putative receptor-like protein kinase (AC002392).

35 BAA94510.1 AB041504 *Populus nigra*
DESCRIPTION: protein kinase 2. PnPK2.

AAA33000.1 M76647 *Brassica oleracea*
DESCRIPTION: receptor protein kinase. SKR6.

40 CAA67145.1 X98520 *Brassica oleracea*
DESCRIPTION: receptor-like kinase. SFR2.

45 AAB47421.1 U59316 *Lycopersicon esculentum*
DESCRIPTION: serine/threonine protein kinase Pto. pto. allele of Pto

bacterial speck disease resistance gene in tomato.

5 BAA07577.2 D38564 Brassica rapa
DESCRIPTION: receptor protein kinase SRK12.

10 AAA33008.1 M97667 Brassica napus
DESCRIPTION: serine/threonine kinase receptor.

CAB89179.1 AJ245479 Brassica napus subsp. napus
DESCRIPTION: ser /thr kinase. S-locus receptor kinase. srk.

15 BAA92837.1 AB032474 Brassica oleracea
DESCRIPTION: S60 S-locus receptor kinase. SRK60.

814
20 -----
AAF23903.1 AF194416 Oryza sativa
DESCRIPTION: MAP kinase homolog. MAPK2. RMAPK2.

25 AAD52659.1 AF177392 Oryza sativa
DESCRIPTION: blast and wounding induced mitogen-activated protein kinase.
BWMK1. BWMK1 MAP kinase.

30 AAF23902.1 AF194415 Oryza sativa
DESCRIPTION: MAP kinase homolog. MAPK1. RMAPK1.

35 AAD28617.1 AF129087 Medicago sativa
DESCRIPTION: mitogen-activated protein kinase homologue. TDY1.

CAB61750.1 AJ275316 Cicer arietinum
DESCRIPTION: MAP kinase protein.
40

AAB57843.1 U96716 Selaginella lepidophylla
DESCRIPTION: MAP kinase-like protein. sdhn-6r.

45 AAF65766.1 AF242308 Euphorbia esula

DESCRIPTION: mitogen-activated protein kinase. regulated by tyrosine and threonine phosphorylation.

5 BAB18271.1 AB035141 Chlamydomonas reinhardtii
DESCRIPTION: mitogen-activated protein kinase. CrMPK2.

10 CAA58761.1 X83880 Nicotiana tabacum
DESCRIPTION: p45Ntf4 serine/threonine protein kinase. ntf4.

15 CAA47099.1 X66469 Medicago sativa
DESCRIPTION: MAP Kinase. MSK7.

AAB41548.1 L07042 Medicago sativa
20 DESCRIPTION: autophosphorylating serine/threonine protein kinase. MAP
kinase. MsERK1.

AAB58396.1 U94192 Nicotiana tabacum
25 DESCRIPTION: salicylic acid-activated MAP kinase. NtSIPK.

CAA50036.1 X70703 Pisum sativum
DESCRIPTION: MAP kinase homologue. PSMAPKIN.

30 AAF73236.1 AF153061 Pisum sativum
DESCRIPTION: MAP kinase 3. Mapk3. PsMAPK3.

35 BAB32406.1 AB055515 Nicotiana tabacum
DESCRIPTION: NRK1 MAPK. nrk1. A tobacco MAPK that is phosphorylated
and
activated by NQK1.

40 CAA58760.1 X83879 Nicotiana tabacum
DESCRIPTION: p43Nft6 serine/threonine protein kinase. ntf6.

45 CAA57721.1 X82270 Medicago sativa
DESCRIPTION: protein kinase. MMK4.

- 5 AAF81420.1 AF247136 *Capsicum annuum*
DESCRIPTION: MAP kinase 2. MK2. CAMK2; wound, UV-C, and cold-inducible expression.
- 10 AAD37790.1 AF149424 *Ipomoea batatas*
DESCRIPTION: MAP kinase.
- 15 AAG40580.1 AF216316 *Oryza sativa*
DESCRIPTION: MAP kinase 2. protein kinase; MAP2.
- 20 CAB37188.1 AJ224336 *Medicago sativa*
DESCRIPTION: MAP kinase. MMK3.
- AAF61238.1 AF241166 *Oryza sativa*
DESCRIPTION: MAP kinase MAPK2.
- 25 AAG40581.1 AF216317 *Oryza sativa*
DESCRIPTION: MAP kinase 3. protein kinase; MAP3.
- 30 CAB61889.1 AJ251330 *Oryza sativa*
DESCRIPTION: protein kinase. MAPK4 protein. mapk4.
- 35 CAA73323.1 Y12785 *Petroselinum crispum*
DESCRIPTION: MAP kinase I.
- CAC13967.1 AJ250311 *Oryza sativa*
DESCRIPTION: protein kinase. MAPK2 protein. mapk2.
- 40 CAA56314.1 X79993 *Avena sativa*
DESCRIPTION: MAP KINASE. Asmap1.
- 45 CAA49592.1 X69971 *Nicotiana tabacum*
DESCRIPTION: serine/threonine protein kinase. NTF3.

CAA58466.1 X83440 Petunia x hybrida
 DESCRIPTION: MAP/ERK kinase 1. MEK1.

5

AAK01710.1 AF332873 Oryza sativa
 DESCRIPTION: MAP kinase BIMK1.

10

AAG40579.1 AF216315 Oryza sativa
 DESCRIPTION: MAP kinase 1. protein kinase; MAP1.

15

CAA57719.1 X82268 Medicago sativa
 DESCRIPTION: protein kinase. MMK2.

20

AAC28850.1 AF079318 Triticum aestivum
 DESCRIPTION: protein kinase. MAP kinase homolog. WCK-1.

25

AAD32204.1 AF134730 Prunus armeniaca
 DESCRIPTION: putative mitogen-activated protein kinase MAPK. MAP kinase.

30

BAA74734.1 AB016802 Zea mays
 DESCRIPTION: MAP kinase 5. ZmMPK5.

35

AAF73257.1 AF154329 Pisum sativum
 DESCRIPTION: MAP kinase PsMAPK2. Mapk2.

40

BAA09600.1 D61377 Nicotiana tabacum
 DESCRIPTION: WIPK. MAP (mitogen-activated protein) kinase.

45

AAF81419.1 AF247135 Capsicum annuum
 DESCRIPTION: MAP kinase 1. MK1. wound and UV-C inducible expression.

BAA74733.1 AB016801 Zea mays
 DESCRIPTION: MAP kinase 4. ZmMPK4.

CAA64173.1 X94400 *Solanum tuberosum*
DESCRIPTION: soluble-starch-synthase. SSSIII.

5 AAC14014.1 AF023159 *Zea mays*
DESCRIPTION: starch synthase DULL1. dull1. similar to potato starch
synthase SSIII; likely to be the maize starch synthase defined
biochemically as SSII.

10 CAB40374.1 AJ225088 *Vigna unguiculata*
DESCRIPTION: ADP-glucose-starch glucosyltransferase. Starch synthase
isoform SS III.

15 AAF88000.1 AF258609 *Aegilops tauschii*
DESCRIPTION: starch synthase III.

20 AAF87999.1 AF258608 *Triticum aestivum*
DESCRIPTION: starch synthase III. wSSIII.

25 CAB40375.1 AJ006752 *Vigna unguiculata*
DESCRIPTION: ADP-glucose starch glucosyltransferase. starch synthase,
isoform V.

30 AAC14015.1 AF023160 *Zea mays*
DESCRIPTION: starch synthase DULL1. dull1. similar to potato starch
synthase SSIII; like to be the maize starch synthase defined biochemically
as SSII.

35 AAC17971.2 AF026422 *Chlamydomonas reinhardtii*
DESCRIPTION: soluble starch synthase. ADP-glucose:alpha-1,
4-D-glucan-4-alpha-D-glucosyltransferase.

40 AAD13342.1 AF019297 *Zea mays*
DESCRIPTION: starch synthase isoform zSTSII-2. zSSIIb.

45 CAB86618.1 AJ269502 *Triticum aestivum*
DESCRIPTION: transfers the glucosyl unit of ADP glucose to the
non-reducing end of an alpha 1,4. starch synthase IIa-1. wSs2a-1.

AAD13341.1 AF019296 Zea mays
 DESCRIPTION: starch synthase isoform zSTSII-1. zSSIIa.
 5

AAC17969.2 AF026420 Chlamydomonas reinhardtii
 DESCRIPTION: ADP-Glucose:alpha-1,
 4-D-glucan-4-alpha-D-glucosyltransferase. granule-bound starch synthase I
 precursor. STA2. GBSSI.
 10

BAA82346.1 AB029546 Phaseolus vulgaris
 DESCRIPTION: granule-bound starch synthase I. GBSSI.
 15

CAA37732.1 X53694 Oryza sativa
 DESCRIPTION: starch synthase.
 20

CAA52273.1 X74160 Manihot esculenta
 DESCRIPTION: starch (bacterial glycogen) synthase. GBSS.
 25

AAF72561.1 AF141954 Oryza sativa
 DESCRIPTION: granule-bound starch synthase. Waxy.
 30

CAA46294.1 X65183 Oryza sativa
 DESCRIPTION: glycogen (starch) synthase. waxy gene. starch granule
 enzyme.
 35

AAF72562.1 AF141955 Oryza sativa
 DESCRIPTION: granule-bound starch synthase. Waxy.
 40

CAA44065.1 X62134 Oryza sativa
 DESCRIPTION: starch biosynthesis. starch (bacterial glycogen) synthase.
 Wx.
 45

AAB02197.1 U48227 Triticum aestivum
 DESCRIPTION: soluble starch synthase.
 45

- AAFI3168.1 AF173900 *Manihot esculenta*
DESCRIPTION: granule bound starch synthase II precursor. GBSSII.
MEGBSSII.
- 5 CAA45472.1 X64108 *Oryza sativa*
DESCRIPTION: starch granule-bound starch synthase. waxy.
- 10 AAC61675.2 AF031162 *Oryza sativa*
DESCRIPTION: granule-bound starch synthase. Waxy.
- 15 AAC70779.1 AF097922 *Astragalus membranaceus*
DESCRIPTION: granule-bound glycogen (starch) synthase. GBSS.
- 20 CAA06958.1 AJ006293 *Antirrhinum majus*
DESCRIPTION: granule-bound starch synthase. waxy.
- AAC19119.1 AF068834 *Ipomoea batatas*
DESCRIPTION: starch synthase.
- 25 AAD49850.1 AF165890 *Oryza sativa* subsp. *japonica*
DESCRIPTION: soluble starch synthase.
- 30 BAA81848.1 AB026295 *Oryza sativa*
DESCRIPTION: ESTs AU075322(C11109),D22430(C11109) correspond to a
region
of the predicted gene.; Rice gene for soluble starch synthase (SSS1),
complete cds (exon1-15).(D38221).
- 35 BAA03739.1 D16202 *Oryza sativa*
DESCRIPTION: soluble starch synthase precursor.
- 40 CAA61268.1 X88789 *Pisum sativum*
DESCRIPTION: glycogen (starch) synthase.
- 45 AAA86423.1 U44126 *Ipomoea batatas*
DESCRIPTION: starch synthase. SPSS67.

- 5 AAF14233.1 AF109395 *Triticum aestivum*
 DESCRIPTION: granule-bound starch synthase GBSSII.
- 10 CAA41359.1 X58453 *Solanum tuberosum*
 DESCRIPTION: glycogen (starch) synthase. amf. waxy protein, granule-bound
 starch synthase.
- 15 AAG43519.1 AF210699 *Perilla frutescens*
 DESCRIPTION: granule-bound starch synthase. GBSSI. waxy protein.
- 819

 BAA13032.1 D86180 *Pisum sativum*
 DESCRIPTION: phosphoribosylanthranilate transferase. PAT1.
- 20 822

 AAB86850.1 AF031540 *Fritillaria agrestis*
 DESCRIPTION: cytochrome C. cytC.
- 25 AAC84135.1 AF101422 *Cichorium intybus*
 DESCRIPTION: cytochrome.
- 30 BAA02159.1 D12634 *Oryza sativa*
 DESCRIPTION: 'cytochrome C'.
- 35 AAA63515.1 M63704 *Oryza sativa*
 DESCRIPTION: cytochrome c. Cc-1.
- 40 AAA92712.1 L77113 *Helianthus annuus*
 DESCRIPTION: cytochrome c. cytcl. putative.
- 45 AAB70265.1 AF017367 *Oryza sativa*
 DESCRIPTION: cytochrome C.
- AAA33084.1 M35173 *Chlamydomonas reinhardtii*

DESCRIPTION: apocytochrome c (cyc).

5 CAB16954.1 Z99829 Chlamydomonas reinhardtii
DESCRIPTION: cytochrome c. CYC1.

10 CAA79708.1 Z21499 Stellaria longipes
DESCRIPTION: mitochondrial cytochrome c.
823

15 BAA02159.1 D12634 Oryza sativa
DESCRIPTION: 'cytochrome C'.

AAA63515.1 M63704 Oryza sativa
DESCRIPTION: cytochrome c. Cc-1.

20 AAB86850.1 AF031540 Fritillaria agrestis
DESCRIPTION: cytochrome C. cytC.

25 AAC84135.1 AF101422 Cichorium intybus
DESCRIPTION: cytochrome.

30 AAA92712.1 L77113 Helianthus annuus
DESCRIPTION: cytochrome c. cytcl. putative.

35 AAB70265.1 AF017367 Oryza sativa
DESCRIPTION: cytochrome C.

AAA33084.1 M35173 Chlamydomonas reinhardtii
DESCRIPTION: apocytochrome c (cyc).

40 CAB16954.1 Z99829 Chlamydomonas reinhardtii
DESCRIPTION: cytochrome c. CYC1.

45 CAA79708.1 Z21499 Stellaria longipes
DESCRIPTION: mitochondrial cytochrome c.

-
- 5 BAB17113.1 AP002866 *Oryza sativa*
DESCRIPTION: putative white protein; ATP-binding cassette transporter.
P0410E01.34.
- 10 AAF43869.1 AF166114 Chloroplast *Mesostigma viride*
DESCRIPTION: probable transport protein. cysA.
- 15 BAA90508.1 AP001111 *Oryza sativa*
DESCRIPTION: similar to ABC transporter of *Arabidopsis thaliana*
(AC004697).
- 20 AAD54843.1 AF137379 Chloroplast *Nephroselmis olivacea*
DESCRIPTION: probable transport protein. cysA.
- 25 BAA57907.1 AB001684 *Chlorella vulgaris*
DESCRIPTION: sulfate transport system permease protein. cysA.
- 30 BAA90507.1 AP001111 *Oryza sativa*
DESCRIPTION: similar to ABC transporter of *Arabidopsis thaliana*
(AC004697).
- 35 BAB40032.1 AP003046 *Oryza sativa*
DESCRIPTION: putative ABC transporter. P0445D12.3.
- 40 AAG49003.1 AY013246 *Hordeum vulgare*
DESCRIPTION: putative ABC transporter. 635P2.4b; GC splice donor
confirmed by cDNA alignment and comparative sequence.
- 45 BAB21275.1 AP002844 *Oryza sativa*
DESCRIPTION: putative ABC transporter protein. P0410E03.6.
- AAG45492.1 AY013245 *Oryza sativa*
DESCRIPTION: 36I5.4. putative ABC transporter; GC splice donor confirmed
by cDNA alignment and comparative sequence.

- AAG49002.1 AY013246 *Hordeum vulgare*
 DESCRIPTION: putative ABC transporter. 635P2.4a; GC splice donor
 5 confirmed by cDNA and comparative sequencing.
- BAB21276.1 AP002844 *Oryza sativa*
 DESCRIPTION: putative ABC transporter protein. P0410E03.7. contains EST
 10 D22472(C1173).
- AAD10836.1 U52079 *Solanum tuberosum*
 DESCRIPTION: P-glycoprotein. pmdr1. binds ATP; ATPase; transporter;
 15 transmembrane protein.
- BAB21279.1 AP002844 *Oryza sativa*
 DESCRIPTION: putative ABC transporter protein. P0410E03.10. contains ESTs
 20 AU065360(R3463),AU101680(R3463).
- BAB21273.1 AP002844 *Oryza sativa*
 DESCRIPTION: putative ABC transporter protein. P0410E03.4.
 25
- BAA83352.1 AP000391 *Oryza sativa*
 DESCRIPTION: ESTs AU067992(C11433),AU077424(C11433) correspond to
 a
 30 region of the predicted gene.; Similar to ABC transporter-7 (U43892).
- BAA96612.1 AP002482 *Oryza sativa*
 DESCRIPTION: Similar to *Arabidopsis thaliana* chromosome 2, BAC F14M4 ;
 35 putative ABC transporter (AC004411).
- 827
-
- AAG34803.1 AF243368 *Glycine max*
 40 DESCRIPTION: glutathione S-transferase GST 13.
- AAG16758.1 AY007560 *Lycopersicon esculentum*
 DESCRIPTION: putative glutathione S-transferase T3.
 45

- AAG34798.1 AF243363 Glycine max
DESCRIPTION: glutathione S-transferase GST 8.
- 5 AAF64450.1 AF239928 Euphorbia esula
DESCRIPTION: glutathione S-transferase. similar to auxin-inducible GST.
- 10 AAG34807.1 AF243372 Glycine max
DESCRIPTION: glutathione S-transferase GST 17.
- 15 AAG34796.1 AF243361 Glycine max
DESCRIPTION: glutathione S-transferase GST 6.
- 20 AAG16759.1 AY007561 Lycopersicon esculentum
DESCRIPTION: putative glutathione S-transferase T4.
- AAG34797.1 AF243362 Glycine max
DESCRIPTION: glutathione S-transferase GST 7.
- 25 AAG34801.1 AF243366 Glycine max
DESCRIPTION: glutathione S-transferase GST 11.
- 30 AAG34804.1 AF243369 Glycine max
DESCRIPTION: glutathione S-transferase GST 14.
- 35 AAG34809.1 AF243374 Glycine max
DESCRIPTION: glutathione S-transferase GST 19.
- 40 AAG34808.1 AF243373 Glycine max
DESCRIPTION: glutathione S-transferase GST 18.
- AAG34810.1 AF243375 Glycine max
DESCRIPTION: glutathione S-transferase GST 20.
- 45 AAG16757.1 AY007559 Lycopersicon esculentum
DESCRIPTION: putative glutathione S-transferase T2.

5 AAG16756.1 AY007558 *Lycopersicon esculentum*
 DESCRIPTION: putative glutathione S-transferase T1.

AAG34844.1 AF244701 *Zea mays*
 DESCRIPTION: glutathione S-transferase GST 36.

10 AAG34805.1 AF243370 *Glycine max*
 DESCRIPTION: glutathione S-transferase GST 15.

15 AAG34831.1 AF244688 *Zea mays*
 DESCRIPTION: glutathione S-transferase GST 23.

20 AAG34832.1 AF244689 *Zea mays*
 DESCRIPTION: glutathione S-transferase GST 24.

25 AAG34849.1 AF244706 *Zea mays*
 DESCRIPTION: glutathione S-transferase GST 41.

AAG34802.1 AF243367 *Glycine max*
 DESCRIPTION: glutathione S-transferase GST 12.

30 CAA09187.1 AJ010448 *Alopecurus myosuroides*
 DESCRIPTION: glutathione transferase. GST1a.

35 AAG34829.1 AF244686 *Zea mays*
 DESCRIPTION: glutathione S-transferase GST 21.

40 CAA09188.1 AJ010449 *Alopecurus myosuroides*
 DESCRIPTION: glutathione transferase. GST1b.

45 AAA68430.1 J03679 *Solanum tuberosum*
 DESCRIPTION: glutathione S-transferase. gst1. previously called
 pathogenesis-related protein; prp1-1.

AAG34801.1 AF243366 Glycine max
DESCRIPTION: glutathione S-transferase GST 11.

5 AAG34804.1 AF243369 Glycine max
DESCRIPTION: glutathione S-transferase GST 14.

10 AAG34807.1 AF243372 Glycine max
DESCRIPTION: glutathione S-transferase GST 17.

15 AAG34809.1 AF243374 Glycine max
DESCRIPTION: glutathione S-transferase GST 19.

20 AAG34810.1 AF243375 Glycine max
DESCRIPTION: glutathione S-transferase GST 20.

AAG16757.1 AY007559 Lycopersicon esculentum
DESCRIPTION: putative glutathione S-transferase T2.

25 AAG16756.1 AY007558 Lycopersicon esculentum
DESCRIPTION: putative glutathione S-transferase T1.

30 AAG34802.1 AF243367 Glycine max
DESCRIPTION: glutathione S-transferase GST 12.

35 AAG34808.1 AF243373 Glycine max
DESCRIPTION: glutathione S-transferase GST 18.

AAG34844.1 AF244701 Zea mays
DESCRIPTION: glutathione S-transferase GST 36.

40 CAA09188.1 AJ010449 Alopecurus myosuroides
DESCRIPTION: glutathione transferase. GST1b.

45 CAA09187.1 AJ010448 Alopecurus myosuroides
DESCRIPTION: glutathione transferase. GST1a.

5 AAG32472.1 AF309379 *Oryza sativa* subsp. *japonica*
 DESCRIPTION: putative glutathione S-transferase OsGSTU3.

10 AAA68430.1 J03679 *Solanum tuberosum*
 DESCRIPTION: glutathione S-transferase. *gst1*. previously called
 pathogenesis-related protein; *prp1-1*.

15 AAG34837.1 AF244694 *Zea mays*
 DESCRIPTION: glutathione S-transferase GST 29.

20 AAG34800.1 AF243365 *Glycine max*
 DESCRIPTION: glutathione S-transferase GST 10.

25 AAG34831.1 AF244688 *Zea mays*
 DESCRIPTION: glutathione S-transferase GST 23.

30 AAC32118.1 AF051214 *Picea mariana*
 DESCRIPTION: probable glutathione S-transferase. Sb18. similar to
Nicotiana tabacum probable glutathione S-transferase encoded by GenBank
 Accession Number X56266.

35 AAG34805.1 AF243370 *Glycine max*
 DESCRIPTION: glutathione S-transferase GST 15.

AAC18566.1 AF048978 *Glycine max*
 DESCRIPTION: 2,4-D inducible glutathione S-transferase. GSTa.

40 AAG34829.1 AF244686 *Zea mays*
 DESCRIPTION: glutathione S-transferase GST 21.

45 CAA04391.1 AJ000923 *Carica papaya*
 DESCRIPTION: glutathione transferase. PGST1.

CAA71784.1 Y10820 *Glycine max*

DESCRIPTION: glutathione transferase.

5 AAG34795.1 AF243360 Glycine max
DESCRIPTION: glutathione S-transferase GST 5.

10 AAG34836.1 AF244693 Zea mays
DESCRIPTION: glutathione S-transferase GST 28.

AAG34832.1 AF244689 Zea mays
DESCRIPTION: glutathione S-transferase GST 24.

15 AAG34833.1 AF244690 Zea mays
DESCRIPTION: glutathione S-transferase GST 25.

20 AAG34849.1 AF244706 Zea mays
DESCRIPTION: glutathione S-transferase GST 41.

25 AAG34806.1 AF243371 Glycine max
DESCRIPTION: glutathione S-transferase GST 16.

30 CAA09189.1 AJ010450 Alopecurus myosuroides
DESCRIPTION: glutathione transferase. GST1c.
829

35 AAG34803.1 AF243368 Glycine max
DESCRIPTION: glutathione S-transferase GST 13.

AAF64450.1 AF239928 Euphorbia esula
DESCRIPTION: glutathione S-transferase. similar to auxin-inducible GST.

40 AAG16758.1 AY007560 Lycopersicon esculentum
DESCRIPTION: putative glutathione S-transferase T3.

45 AAG34798.1 AF243363 Glycine max
DESCRIPTION: glutathione S-transferase GST 8.

5 AAG34801.1 AF243366 Glycine max
 DESCRIPTION: glutathione S-transferase GST 11.

10 AAG34797.1 AF243362 Glycine max
 DESCRIPTION: glutathione S-transferase GST 7.

15 AAG34796.1 AF243361 Glycine max
 DESCRIPTION: glutathione S-transferase GST 6.

20 AAG34807.1 AF243372 Glycine max
 DESCRIPTION: glutathione S-transferase GST 17.

25 AAG16759.1 AY007561 Lycopersicon esculentum
 DESCRIPTION: putative glutathione S-transferase T4.

30 AAG34804.1 AF243369 Glycine max
 DESCRIPTION: glutathione S-transferase GST 14.

35 AAG34810.1 AF243375 Glycine max
 DESCRIPTION: glutathione S-transferase GST 20.

40 AAG34809.1 AF243374 Glycine max
 DESCRIPTION: glutathione S-transferase GST 19.

45 AAG16757.1 AY007559 Lycopersicon esculentum
 DESCRIPTION: putative glutathione S-transferase T2.

AAG16756.1 AY007558 Lycopersicon esculentum
 DESCRIPTION: putative glutathione S-transferase T1.

AAG34805.1 AF243370 Glycine max
 DESCRIPTION: glutathione S-transferase GST 15.

AAC18566.1 AF048978 Glycine max
DESCRIPTION: 2,4-D inducible glutathione S-transferase. GSTa.

5 AAG34808.1 AF243373 Glycine max
DESCRIPTION: glutathione S-transferase GST 18.

10 AAG34800.1 AF243365 Glycine max
DESCRIPTION: glutathione S-transferase GST 10.

15 AAG34829.1 AF244686 Zea mays
DESCRIPTION: glutathione S-transferase GST 21.

20 AAG34802.1 AF243367 Glycine max
DESCRIPTION: glutathione S-transferase GST 12.

AAG34837.1 AF244694 Zea mays
DESCRIPTION: glutathione S-transferase GST 29.

25 CAA09187.1 AJ010448 Alopecurus myosuroides
DESCRIPTION: glutathione transferase. GST1a.

30 CAA09188.1 AJ010449 Alopecurus myosuroides
DESCRIPTION: glutathione transferase. GST1b.

35 AAG34849.1 AF244706 Zea mays
DESCRIPTION: glutathione S-transferase GST 41.

40 AAG34844.1 AF244701 Zea mays
DESCRIPTION: glutathione S-transferase GST 36.

AAG34806.1 AF243371 Glycine max
DESCRIPTION: glutathione S-transferase GST 16.

45 CAA71784.1 Y10820 Glycine max
DESCRIPTION: glutathione transferase.

5 AAA68430.1 J03679 *Solanum tuberosum*
 DESCRIPTION: glutathione S-transferase. gst1. previously called
 pathogenesis-related protein; prp1-1.

10 CAA04391.1 AJ000923 *Carica papaya*
 DESCRIPTION: glutathione transferase. PGST1.

15 AAG34836.1 AF244693 *Zea mays*
 DESCRIPTION: glutathione S-transferase GST 28.

20 AAG34831.1 AF244688 *Zea mays*
 DESCRIPTION: glutathione S-transferase GST 23.

25 AAG34847.1 AF244704 *Zea mays*
 DESCRIPTION: glutathione S-transferase GST 39.

30 AAC32118.1 AF051214 *Picea mariana*
 DESCRIPTION: probable glutathione S-transferase. Sb18. similar to
 Nicotiana tabacum probable glutathione S-transferase encoded by GenBank
 Accession Number X56266.

35 AAF29773.1 AF159229 *Gossypium hirsutum*
 DESCRIPTION: glutathione S-transferase. GST.

40 AAG32472.1 AF309379 *Oryza sativa* subsp. *japonica*
 DESCRIPTION: putative glutathione S-transferase OsGSTU3.

45 AAG41204.1 AF321437 *Suaeda maritima*
 DESCRIPTION: glutathione transferase.

CAC24549.1 AJ296343 *Cichorium intybus* x *Cichorium endivia*
 DESCRIPTION: glutathione S-transferase. chi-GST1. auxin-induced GST.

830

BAA05624.1 D26575 Daucus carota
DESCRIPTION: transcriptional regulator. DNA-binding protein. homeodomain
at nt 520-699; leucine zipper at nt 700-805.

5

BAA93460.1 AB028072 Physcomitrella patens
DESCRIPTION: homeobox protein PpHB1. PpHB1. homeodomain-leucine
zipper
gene.

10

BAA93464.1 AB028076 Physcomitrella patens
DESCRIPTION: homeobox protein PpHB5. PpHB5. homeodomain-leucine
zipper
gene.

15

BAA93467.1 AB028079 Physcomitrella patens
DESCRIPTION: homeobox protein PpHB8. PpHB8. homeodomain-leucine
zipper
gene.

20

BAA93465.1 AB028077 Physcomitrella patens
DESCRIPTION: homeobox protein PpHB6. PpHB6. homeodomain-leucine
zipper
gene.

25

BAA05625.1 D26576 Daucus carota
DESCRIPTION: transcriptional regulator. DNA-binding protein. homeodomain
at nt 300-479; leucine zipper at nt 480-587.

30

BAA93468.1 AB028080 Physcomitrella patens
DESCRIPTION: homeobox protein PpHB9. PpHB9. homeodomain-leucine
zipper
gene.

35

40

BAA05623.1 D26574 Daucus carota
DESCRIPTION: transcriptional regulator. DNA-binding protein. homeodomain
at nt 498-677; leucine zipper at nt 678-785.

45

BAA05622.1 D26573 Daucus carota

DESCRIPTION: transcriptional regulator. DNA-binding protein. homeodomain at nt 585-764; leucine zipper at nt 765-851.

- 5 AAD37698.1 AF145729 *Oryza sativa*
DESCRIPTION: homeodomain leucine zipper protein. Oshox5. transcription factor.
- 10 CAA64221.1 X94449 *Pimpinella brachycarpa*
DESCRIPTION: transcription activator. homeobox-leucine zipper protein. PHZ4.
- 15 CAA64152.1 X94375 *Pimpinella brachycarpa*
DESCRIPTION: transcription activator. homeobox-leucine zipper protein.
- 20 CAA64491.1 X95193 *Pimpinella brachycarpa*
DESCRIPTION: transcription activator. homeobox-leucine zipper protein.
- 25 BAA93463.1 AB028075 *Physcomitrella patens*
DESCRIPTION: homeobox protein PpHB4. PpHB4. homeodomain-leucine zipper gene.
- 30 CAA06728.1 AJ005833 *Craterostigma plantagineum*
DESCRIPTION: transcription factor. homeodomain leucine zipper protein. hb-2.
- 35 AAD37695.1 AF145726 *Oryza sativa*
DESCRIPTION: homeodomain leucine zipper protein. Oshox2. transcription factor.
- 40 CAA65456.2 X96681 *Oryza sativa*
DESCRIPTION: transcription factor. DNA-binding protein. Oshox1. homeodomain leucine zipper gene.
- 45 AAF19980.1 AF211193 *Oryza sativa*
DESCRIPTION: homeodomain-leucine zipper transcription factor. Hox1. hox1.

AAK31270.1 AC079890 *Oryza sativa*

DESCRIPTION: homeodomain leucine zipper protein hox1.
OSJNBb0089A17.12.

5

CAA63222.1 X92489 *Glycine max*

DESCRIPTION: transcription activator. homeobox-leucine zipper protein.

10

CAA06717.1 AJ005820 *Craterostigma plantagineum*

DESCRIPTION: transcription factor. homeodomain leucine zipper protein.
hb-1.

15

AAA79778.1 L48485 *Helianthus annuus*

DESCRIPTION: homeodomain protein. putative.

831

20

CAA06334.1 AJ005077 *Lycopersicon esculentum*

DESCRIPTION: protein kinase. TCTR2 protein. TCTR2.

25

AAG31141.1 AF305911 *Oryza sativa*

DESCRIPTION: EDR1. EDR1. MAP kinase kinase kinase; similar to
Arabidopsis thaliana EDR1.

30

AAG31142.1 AF305912 *Hordeum vulgare*

DESCRIPTION: EDR1. EDR1. MAP kinase kinase kinase; similar to
Arabidopsis thaliana EDR1.

35

AAK30005.1 AY029067 *Rosa hybrid cultivar*

DESCRIPTION: CTR2 protein kinase.

40

AAD46406.1 AF096250 *Lycopersicon esculentum*

DESCRIPTION: ethylene-responsive protein kinase TCTR1. ER50.
serine/threonine kinase; similar to *Arabidopsis thaliana* negative
regulator of the ethylene response pathway encoded by GenBank Accession
Number L08789.

45

CAA73722.1 Y13273 *Lycopersicon esculentum*

DESCRIPTION: putative protein kinase.

5

AAD10057.1 AF110519 *Lycopersicon esculentum*

DESCRIPTION: ethylene-inducible CTR1-like protein kinase. protein kinase homolog; ethylene and fruit ripening inducible CTR1-like protein kinase; TCTR1v.

10

AAD10056.1 AF110518 *Lycopersicon esculentum*

DESCRIPTION: ethylene-inducible CTR1-like protein kinase. protein kinase homolog; ethylene and fruit ripening inducible CTR1-like protein kinase; TCTR1.

15

AAA34002.1 M67449 *Glycine max*

DESCRIPTION: protein kinase. PK6.

20

AAK11734.1 AY027437 *Arachis hypogaea*

DESCRIPTION: serine/threonine/tyrosine kinase.

25

BAB16918.1 AP002863 *Oryza sativa*

DESCRIPTION: putative protein kinase. P0005A05.22.

30

CAC09580.1 AJ298992 *Fagus sylvatica*

DESCRIPTION: Absciscic acid (ABA) and calcium induced protein kinase. protein kinase (PK). pk1.

35

CAA97692.1 Z73295 *Catharanthus roseus*

DESCRIPTION: receptor-like protein kinase. CRPK1. Autophosphorylation predominantly on Thr, less on Ser. Mechanism: autophosphorylation in cis.

40

AAF59906.1 AF197947 *Glycine max*

DESCRIPTION: receptor protein kinase-like protein. CLV1B.

45

AAF59905.1 AF197946 *Glycine max*

DESCRIPTION: receptor protein kinase-like protein. CLV1A.

AU056701(S20808),AU056702(S20808).

- 5 AAG25966.1 AF302082 *Nicotiana tabacum*
DESCRIPTION: cytokinin-regulated kinase 1. CRK1. protein kinase;
transcript abundance decreases rapidly after cytokinin treatment.
- 10 BAA06538.1 D31737 *Nicotiana tabacum*
DESCRIPTION: protein-serine/threonine kinase.
- 15 AAF76189.1 AF271206 *Rosa hybrid cultivar*
DESCRIPTION: CTR1-like protein kinase. Raf-like protein kinase.
- 20 BAA84787.1 AP000559 *Oryza sativa*
DESCRIPTION: ESTs C22657(S0014),C22656(S0014) correspond to a region
of
the predicted gene.; Similar to receptor protein kinase, ERECTA
(AC004484).
- 25 BAA83373.1 AP000391 *Oryza sativa*
DESCRIPTION: ESTs C22657(S0014),C22656(S0014) correspond to a region
of
the predicted gene.; Similar to receptor protein kinase, ERECTA
(AC004484).
- 30 AAF66615.1 AF142596 *Nicotiana tabacum*
DESCRIPTION: LRR receptor-like protein kinase.
- 35 AAF91322.1 AF244888 *Glycine max*
DESCRIPTION: receptor-like protein kinase 1. RLK1. GmRLK1.
- 40 AAD21872.1 AF078082 *Phaseolus vulgaris*
DESCRIPTION: receptor-like protein kinase homolog RK20-1.
- 45 CAA61510.1 X89226 *Oryza sativa*
DESCRIPTION: leucine-rich repeat/receptor protein kinase. lrk2.

- 5 BAA87853.1 AP000816 *Oryza sativa*
DESCRIPTION: EST AU030604(E51294) corresponds to a region of the
predicted gene. Similar to putative NAK-like Ser/Thr protein kinase.
(AF001308).
- 10 AAF91323.1 AF244889 *Glycine max*
DESCRIPTION: receptor-like protein kinase 2. RLK2. GmRLK2.
- 15 AAF91324.1 AF244890 *Glycine max*
DESCRIPTION: receptor-like protein kinase 3. RLK3. GmRLK3.
- 20 AAF43394.1 AF230501 *Oryza sativa* subsp. *japonica*
DESCRIPTION: serine/threonine protein kinase. YK1.
- 25 AAK16409.1 AF320086 *Zea mays*
DESCRIPTION: serine threonine kinase 1. stk1. expressed in mature tassel.
- 30 AAK21965.1 AY028699 *Brassica napus*
DESCRIPTION: receptor protein kinase PERK1.
- 35 BAB39437.1 AP003338 *Oryza sativa*
DESCRIPTION: receptor-like kinase. OJ1212_B09.6.
- 832
- 40 AAK11568.1 AF318492 *Lycopersicon hirsutum*
DESCRIPTION: Pto-like protein kinase B. LhirPtoB.
- 45 AAF35901.1 AF230332 *Zinnia elegans*
DESCRIPTION: expansin 2.
- CAC19184.1 AJ291817 *Cicer arietinum*
DESCRIPTION: expansin.
- AAG13982.1 AF297521 *Prunus avium*
DESCRIPTION: expansin 1. Expl. PruavExpl.

BAB19676.1 AB029083 *Prunus persica*
DESCRIPTION: expansin. PchExp1.

5

AAC33529.1 U93167 *Prunus armeniaca*
DESCRIPTION: expansin. PA-Exp1.

10 AAC33530.1 AF038815 *Prunus armeniaca*
DESCRIPTION: expansin. Exp2.

15 AAD47901.1 AF085330 *Pinus taeda*
DESCRIPTION: expansin.

20 AAB37746.1 U30382 *Cucumis sativus*
DESCRIPTION: expansin S1 precursor. Cs-EXP1. similar to pollen allergen
Lol pI, *Lolium perenne*, Swiss-Prot Accession Number P14946; former gene
name CuExS1; expansin-29 (Ex29) protein.

25 AAF21101.1 AF159563 *Fragaria x ananassa*
DESCRIPTION: expansin. Exp2. ripening regulated.

30 AAB40634.1 U64890 *Pinus taeda*
DESCRIPTION: expansin. similar to *Arabidopsis* expansin encoded by
GenBank
Accession Numbers U30476, U30478, U30480 and U30481, to *Cucumis sativus*
expansin encoded by GenBank Accession Numbers U30382 and U30460, and to
rice expansin encoded by GenBank Accession Numbers U30477 and U30479.

35

AAB40637.1 U64893 *Pinus taeda*
DESCRIPTION: expansin. similar to *Arabidopsis* expansin encoded by
GenBank
Accession Numbers U30476, U30478, U30480 and U30481, to *Cucumis sativus*
expansin encoded by GenBank Accession Numbers U30382 and U30460, and to
rice expansin encoded by GenBank Accession Numbers U30477 and U30479.

40

45 AAB40635.1 U64891 *Pinus taeda*
DESCRIPTION: expansin. similar to *Arabidopsis* expansin encoded by
GenBank

Accession Numbers U30476, U30478, U30480 and U30481, to *Cucumis sativus* expansin encoded by GenBank Accession Numbers U30382 and U30460, and to rice expansin encoded by GenBank Accession Numbers U30477 and U30479.

5

CAB43197.1 AJ239068 *Lycopersicon esculentum*
DESCRIPTION: cell wall loosening enzyme. expansin2. exp2.

10

AAB40636.1 U64892 *Pinus taeda*
DESCRIPTION: expansin. similar to *Arabidopsis* expansin encoded by GenBank
Accession Numbers U30476, U30478, U30480 and U30481, to *Cucumis sativus* expansin encoded by GenBank Accession Numbers U30382 and U30460, and to rice expansin encoded by GenBank Accession Numbers U30477 and U30479.

15

AAC64201.1 AF096776 *Lycopersicon esculentum*
DESCRIPTION: expansin. LeEXP2.

20

AAD49956.1 AF167360 *Rumex palustris*
DESCRIPTION: expansin. EXP1.

25

AAC96081.1 AF049354 *Nicotiana tabacum*
DESCRIPTION: involved in acid-growth response. alpha-expansin precursor. Nt-EXP5. cell wall protein.

30

AAC39512.1 AF043284 *Gossypium hirsutum*
DESCRIPTION: expansin. GhEX1. contains N-terminal signal peptide.

35

AAB81662.1 U85246 *Oryza sativa*
DESCRIPTION: expansin. Os-EXP4.

40

AAG13983.1 AF297522 *Prunus avium*
DESCRIPTION: expansin 2. Exp2. PruavExp2.

45

AAF32409.1 AF230276 *Triphysaria versicolor*
DESCRIPTION: alpha-expansin 3.

AAG32921.1 AF184233 *Lycopersicon esculentum*
DESCRIPTION: expansin. Exp10.

5 BAB32732.1 AB049406 *Eustoma grandiflorum*
DESCRIPTION: expansin. Eg Expansin.

10 AAF32411.1 AF230278 *Triphysaria versicolor*
DESCRIPTION: alpha-expansin 1.

15 AAF35902.1 AF230333 *Zinnia elegans*
DESCRIPTION: expansin 3.

20 AAB38074.1 U30477 *Oryza sativa*
DESCRIPTION: induces extension (creep) in plant cell walls. expansin
Os-EXP2. Os-EXP2. former gene name RiExB.

25 AAC96080.1 AF049353 *Nicotiana tabacum*
DESCRIPTION: involved in acid-growth response. alpha-expansin precursor.
Nt-EXP4. cell wall protein.

30 AAF17570.1 AF202119 *Marsilea quadrifolia*
DESCRIPTION: alpha-expansin. EXP1. Mq-EXP1.

CAC06433.1 AJ276007 *Festuca pratensis*
DESCRIPTION: expansin. exp2.

35 AAD13633.1 AF059489 *Lycopersicon esculentum*
DESCRIPTION: expansin precursor. Exp5.

40 CAC19183.1 AJ291816 *Cicer arietinum*
DESCRIPTION: expansin.

45 AAF62181.1 AF247163 *Oryza sativa*
DESCRIPTION: alpha-expansin OsEXP6. cell wall loosening factor; expressed
in internodes and leaves.

- AA62180.1 AF247162 *Oryza sativa*
DESCRIPTION: alpha-expansin OsEXP5. cell wall loosening factor; expressed in internodes, leaves, coleoptiles, and roots.
- 5
- CAB46492.1 AJ243340 *Lycopersicon esculentum*
DESCRIPTION: expansin9. exp9.
- 10
- BAA88200.1 AP000837 *Oryza sativa*
DESCRIPTION: EST AU078708(E60526) corresponds to a region of the predicted gene. Similar to expansin (U85246).
- 15
- AAF32410.1 AF230277 *Triphysaria versicolor*
DESCRIPTION: alpha-expansin 2.
- 20
- AAB37749.1 U30460 *Cucumis sativus*
DESCRIPTION: expansin S2 precursor. Cs-EXP2. similar to pollen allergen Lol pI, *Lolium perenne*, Swiss-Prot Accession Number P14946; former gene name CuExS2; expansin-30 (Ex30) protein.
- 25
- CAA04385.1 AJ000885 *Brassica napus*
DESCRIPTION: Cell wall extension in plants. Expansin.
- 30
- AAF17571.1 AF202120 *Regnellidium diphyllum*
DESCRIPTION: alpha-expansin. EXP1. Rd-EXP1.
- 35
- AAD13632.1 AF059488 *Lycopersicon esculentum*
DESCRIPTION: expansin precursor. Exp4.
- 40
- CAA06271.2 AJ004997 *Lycopersicon esculentum*
DESCRIPTION: expansin18. exp18.
- 45
- AAC63088.1 U82123 *Lycopersicon esculentum*
DESCRIPTION: expansin. LeEXP1. fruit ripening regulated expansin.
- AAC96077.1 AF049350 *Nicotiana tabacum*

DESCRIPTION: involved in acid-growth response. alpha-expansin precursor.
Nt-EXP1. cell wall protein.

5 AAF62182.1 AF247164 *Oryza sativa*
 DESCRIPTION: alpha-expansin OsEXP7. cell wall loosening factor; expressed
 in internodes and leaves.

10 CAC18802.1 AJ289154 *Glycine max*
 DESCRIPTION: expansion of cell walls. expansin. dd2/63.

15 AAC96078.1 AF049351 *Nicotiana tabacum*
 DESCRIPTION: involved in acid-growth response. alpha-expansin precursor.
 Nt-EXP2. cell wall protein.

20 AAG01875.1 AF291659 *Striga asiatica*
 DESCRIPTION: alpha-expansin 3. Exp3.

25 CAA69105.1 Y07782 *Oryza sativa*
 DESCRIPTION: expansin. RiExA.

30 AAC96079.1 AF049352 *Nicotiana tabacum*
 DESCRIPTION: involved in acid-growth response. alpha-expansin precursor.
 Nt-EXP3. cell wall protein.

833

35 AAA34030.1 J03492 *Spinacia oleracea*
 DESCRIPTION: glycolate oxidase (EC 1.1.3.15).

40 AAB40396.1 U80071 *Mesembryanthemum crystallinum*
 DESCRIPTION: glycolate oxidase. GOX.

45 BAA03131.1 D14044 *Cucurbita* sp.
 DESCRIPTION: glycolate oxidase.

45 AAB82143.1 AF022740 *Oryza sativa*
 DESCRIPTION: glycolate oxidase. GOX.

CAA63482.1 X92888 *Lycopersicon esculentum*
 DESCRIPTION: conversion of glycolate to glyoxylate + H₂O₂. glycolate
 5 oxidase.

AAC32392.1 AF082874 *Medicago sativa*
 DESCRIPTION: glycolate oxidase.
 10

AAC33509.1 U62485 *Nicotiana tabacum*
 DESCRIPTION: photorespiration. glycolate oxidase. GLO.
 15

AAF03097.1 AF162196 *Lactuca sativa*
 DESCRIPTION: glycolate oxidase.
 838
 20 -----

CAA06770.1 AJ005928 *Brassica napus*
 DESCRIPTION: squalene epoxidase homologue. Sqp1;2.
 25

CAA06773.1 AJ005931 *Brassica napus*
 DESCRIPTION: squalene epoxidase homologue. Sqp1;1.
 30

BAA24448.1 AB003516 *Panax ginseng*
 DESCRIPTION: squalene epoxidase.
 35

CAA06223.1 AJ004923 *Lycopersicon esculentum*
 DESCRIPTION: Squalene epoxidase. ERG.
 840

BAB12686.1 AP002746 *Oryza sativa*
 DESCRIPTION: putative pyrophosphate-dependent phosphofructo-1-kinase.
 40 P0671B11.1. contains ESTs
 AU068014(C11507),C28532(C61484),AU090544(C61415).

BAA99438.1 AP002743 *Oryza sativa*
 45 DESCRIPTION: putative pyrophosphate-dependent phosphofructo-1-kinase.
 P0710E05.25. contains ESTs

AU068014(C11507),C28532(C61484),AU090544(C61415).

- 5 AAB88875.1 U93272 *Prunus armeniaca*
DESCRIPTION: pyrophosphate-dependent phosphofructo-1-kinase.
- 10 CAA83683.1 Z32850 *Ricinus communis*
DESCRIPTION: pyrophosphate-dependent phosphofructokinase beta subunit.
- 15 AAC67587.1 AF095521 *Citrus x paradisi*
DESCRIPTION: pyrophosphate-dependent phosphofructokinase alpha subunit.
PPi-PFKa.
- 20 AAA63452.1 M55191 *Solanum tuberosum*
DESCRIPTION: pyrophosphate-fructose 6-phosphate 1-phosphotransferase
beta-subunit.
- 25 AAC67586.1 AF095520 *Citrus x paradisi*
DESCRIPTION: pyrophosphate-dependent phosphofructokinase beta subunit.
PPi-PFKb. PFP.
- 30 AAA63451.1 M55190 *Solanum tuberosum*
DESCRIPTION: pyrophosphate-fructose 6-phosphate 1-phosphotransferase
alpha-subunit.
- 35 CAA83682.1 Z32849 *Ricinus communis*
DESCRIPTION: pyrophosphate-dependent phosphofructokinase alpha subunit.
841
- 40 -----
AAG60182.1 AC084763 *Oryza sativa*
DESCRIPTION: putative ethylene-responsive element binding protein.
OSJNBa0027P10.12.
- 45 AAK31279.1 AC079890 *Oryza sativa*
DESCRIPTION: putative ethylene-responsive element binding protein.
OSJNBb0089A17.16.

AAG43545.1 AF211527 *Nicotiana tabacum*

DESCRIPTION: Avr9/Cf-9 rapidly elicited protein 1. ACRE1. similar to EREBP transcription factors.

5

AAF63205.1 AF245119 *Mesembryanthemum crystallinum*

DESCRIPTION: AP2-related transcription factor. CDBP. stress induced transcription factor.

10

BAA07321.1 D38123 *Nicotiana tabacum*

DESCRIPTION: ERF1. ethylene-responsive transcription factor.

15

BAA97122.1 AB016264 *Nicotiana sylvestris*

DESCRIPTION: ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf2.

20

CAB93940.1 AJ238740 *Catharanthus roseus*

DESCRIPTION: putative transcription factor. AP2-domain DNA-binding protein. orca2.

25

BAA87068.1 AB035270 *Matricaria chamomilla*

DESCRIPTION: ethylene-responsive element binding protein1 homolog. McEREBP1.

30

BAA97124.1 AB016266 *Nicotiana sylvestris*

DESCRIPTION: ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf4.

35

CAB96900.1 AJ251250 *Catharanthus roseus*

DESCRIPTION: transcription factor. AP2-domain DNA-binding protein. orca3.

40

CAB96899.1 AJ251249 *Catharanthus roseus*

DESCRIPTION: transcription factor. AP2-domain DNA-binding protein. orca3.

45

AAC62619.1 AF057373 *Nicotiana tabacum*

DESCRIPTION: transcription factor. ethylene response element binding

protein 1. EREBP1.

- 5 BAA97123.1 AB016265 *Nicotiana sylvestris*
DESCRIPTION: ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf3.
- 10 AAC24587.1 AF071893 *Prunus armeniaca*
DESCRIPTION: AP2 domain containing protein. AP2DCP.
- 15 CAC12822.1 AJ299252 *Nicotiana tabacum*
DESCRIPTION: AP2 domain-containing transcription factor. ap2.
- 20 AAF76898.1 AF274033 *Atriplex hortensis*
DESCRIPTION: apetala2 domain-containing protein.
- 25 BAA94514.2 AP001800 *Oryza sativa*
DESCRIPTION: Similar to *Arabidopsis thaliana* chromosome 4, BAC clone F9D16; putative Ap2 domain protein (AL035394).
- 30 AAC14323.1 AF058827 *Nicotiana tabacum*
DESCRIPTION: Tsi1. Tsi1. contains putative AP2 DNA-binding domain; similar to Pti6.
- 35 AAD00708.1 U91857 *Stylosanthes hamata*
DESCRIPTION: ethylene-responsive element binding protein homolog. similar to EREBP1, -2, -3 and -4 proteins encoded by GenBank Accession Numbers D38123, D38126, D38124, and D38125 respectively.
- 40 BAA76734.1 AB024575 *Nicotiana tabacum*
DESCRIPTION: ethylene responsive element binding factor.
- 45 BAB03248.1 AB037183 *Oryza sativa*
DESCRIPTION: ERF protein transcriptional repressor. ethylene responsive element binding factor3. osERF3.

BAB16083.1 AB036883 *Oryza sativa*
DESCRIPTION: transcriptional repressor. osERF3. osERF3. ERF protein family ERF3 associated repression domain.

5

AAF23899.1 AF193803 *Oryza sativa*
DESCRIPTION: transcription factor EREBP1. EREBP/AP2-like transcription factor.

10

AAF05606.1 AF190770 *Oryza sativa*
DESCRIPTION: EREBP-like protein. tsh1. TSH1; induced by ethylene.

15

CAB93939.1 AJ238739 *Catharanthus roseus*
DESCRIPTION: putative transcription factor. AP2-domain DNA-binding protein. orca1.

20

BAA78738.1 AB023482 *Oryza sativa*
DESCRIPTION: EST AU055776(S20048) corresponds to a region of the predicted gene.; Similar to *Arabidopsis thaliana* AP2 domain containing protein RAP2.10 mRNA, partial cds.(AF003103).

25

AAG43548.1 AF211530 *Nicotiana tabacum*
DESCRIPTION: Avr9/Cf-9 rapidly elicited protein 111A. ACRE111A. similar to EREBP transcription factors.

30

AAG43549.1 AF211531 *Nicotiana tabacum*
DESCRIPTION: Avr9/Cf-9 rapidly elicited protein 111B. ACRE111B. similar to EREBP transcription factors.

35

BAA99376.1 AP002526 *Oryza sativa*
DESCRIPTION: ESTs AU093391(E60370),AU091593(C60458), AU093392(E60370) correspond to a region of the predicted gene. Similar to *Arabidopsis thaliana* BAC F21J9; AP2 domain protein. (AC000103).

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AAK31271.1 AC079890 *Oryza sativa*
DESCRIPTION: putative transcriptional factor. OSJNBb0089A17.22.

45

transporters of nitrogenous compounds.

- 5 AAG46153.1 AC018727 *Oryza sativa*
DESCRIPTION: putative peptide transporter. OSJNBa0056G17.8.
- 10 CAC00544.1 AJ277084 *Nicotiana plumbaginifolia*
DESCRIPTION: ion transport. putative low-affinity nitrate transporter.
nrt1.1.
- 15 CAC00545.1 AJ277085 *Nicotiana plumbaginifolia*
DESCRIPTION: ion transport. putative low-affinity nitrate transporter.
nrt1.2.
- 20 AAA80582.1 U17987 *Brassica napus*
DESCRIPTION: putative nitrate transporter. RCH2 protein.
- 25 CAC07206.1 AJ278966 *Brassica napus*
DESCRIPTION: Low-affinity nitrate transporter. nitrate transporter. nrt1.
- 30 AAG21898.1 AC026815 *Oryza sativa*
DESCRIPTION: putative peptide transport protein. OSJNBa0079L16.13.
- 35 BAB19758.1 AB052786 *Glycine max*
DESCRIPTION: putative nitrate transporter NRT1-3. NRT1-3.
- 40 AAK15441.1 AC037426 *Oryza sativa*
DESCRIPTION: putative nitrate transporter. OSJNBb0014I11.9.
- 45 AAG21906.1 AC026815 *Oryza sativa*
DESCRIPTION: putative peptide transport protein. OSJNBa0079L16.9.
- BAB19760.1 AB052788 *Glycine max*
DESCRIPTION: nitrate transporter NRT1-5. NRT1-5.
- AAG46154.1 AC018727 *Oryza sativa*

DESCRIPTION: putative peptide transporter. OSJNBa0056G17.27.

5 BAB19757.1 AB052785 Glycine max
DESCRIPTION: nitrate transporter NRT1-2. NRT1-2.

10 BAB19756.1 AB052784 Glycine max
DESCRIPTION: nitrate transporter NRT1-1. NRT1-1.

15 BAB16322.1 AP002818 Oryza sativa
DESCRIPTION: putative peptide transporter-like protein. P0436E04.4.

AAB69642.1 AF000392 Lotus japonicus
DESCRIPTION: peptide transporter. LjNOD65.

20 CAA93316.1 Z69370 Cucumis sativus
DESCRIPTION: nitrite transporter. NiTR1.

25 AAD16016.1 AF080545 Nepenthes alata
DESCRIPTION: peptide transporter. PTR1.

30 BAB19759.1 AB052787 Glycine max
DESCRIPTION: putative nitrate transporter NRT1-4. NRT1-4.

AAD42860.1 AF154930 Prunus dulcis
DESCRIPTION: transporter-like protein. TLP1.

35 847

CAA61980.1 X89890 Bidens pilosa
DESCRIPTION: Calmodulin.

40 AAF73157.1 AF150059 Brassica napus
DESCRIPTION: calmodulin. CaM1. involved in seed germination.

45 BAA87825.1 AP000815 Oryza sativa

DESCRIPTION: ESTs AU030013(E50493),AU081341(E50493) correspond to
a region of the predicted gene. Similar to O.sativa gene encoding
calmodulin. (Z12828).

5

CAA67054.1 X98404 Capsicum annuum
DESCRIPTION: calmodulin-2.

10

AAA87347.1 M88307 Brassica juncea
DESCRIPTION: calmodulin.

15

AAA33397.1 L18912 Lilium longiflorum
DESCRIPTION: calcium binding protein, signal transduction. calmodulin.
putative.

20

AAG27432.1 AF295637 Elaeis guineensis
DESCRIPTION: calmodulin.

25

CAA42423.1 X59751 Daucus carota
DESCRIPTION: calmodulin. Ccam-1.

30

AAG11418.1 AF292108 Prunus avium
DESCRIPTION: calmodulin.

35

AAA92681.1 U13882 Pisum sativum
DESCRIPTION: calcium-binding protein. calmodulin.

35

AAB46588.1 U83402 Capsicum annuum
DESCRIPTION: calmodulin.

40

AAA33706.1 M80836 Petunia x hybrida
DESCRIPTION: calmodulin. CAM81.

45

AAF65511.1 AF108889 Capsicum annuum
DESCRIPTION: calmodulin.

CAA43143.1 X60738 Malus x domestica
DESCRIPTION: Calmodulin. CaM.

5

AAA19571.1 U10150 Brassica napus
DESCRIPTION: calcium binding. calmodulin. bcml.

10

CAA78301.1 Z12839 Lilium longiflorum
DESCRIPTION: calcium binding protein, signal transduction. calmodulin.

15

BAA88540.1 AP000969 Oryza sativa
DESCRIPTION: ESTs AU081349(E61253), D41425(S3918) correspond to a
region
of the predicted gene. Similar to calmodulin. (AF042840).

20

AAB36130.1 S81594 Vigna radiata
DESCRIPTION: auxin-regulated calmodulin. auxin-regulated calmodulin,
arCaM. This sequence comes from Fig. 1; arCaM.

25

AAC36059.1 AF042840 Oryza sativa
DESCRIPTION: calmodulin. CaM1.

30

AAA33901.1 L18913 Oryza sativa
DESCRIPTION: calcium binding protein, signal transduction. calmodulin.
putative.

35

AAA33900.1 L18914 Oryza sativa
DESCRIPTION: calcium binding protein, signal transduction. calmodulin.

40

AAA34237.1 L20691 Vigna radiata
DESCRIPTION: calmodulin.

45

CAA78288.1 Z12828 Oryza sativa
DESCRIPTION: calcium binding protein, signal transduction. calmodulin.

AAA32938.1 M27303 Hordeum vulgare

DESCRIPTION: calmodulin.

- CAA78287.1 Z12827 Oryza sativa
5 DESCRIPTION: calcium binding protein, signal transduction. calmodulin.
- AAC49587.1 U49105 Triticum aestivum
10 DESCRIPTION: calmodulin TaCaM4-1. calcium-binding protein.
- AAC49586.1 U49104 Triticum aestivum
DESCRIPTION: calmodulin TaCaM3-3. calcium-binding protein.
- 15 AAC49583.1 U48692 Triticum aestivum
DESCRIPTION: calmodulin TaCaM2-3. calcium-binding protein.
- 20 AAC49585.1 U49103 Triticum aestivum
DESCRIPTION: calmodulin TaCaM3-2. calcium-binding protein.
- 25 AAC49584.1 U48693 Triticum aestivum
DESCRIPTION: calmodulin TaCaM3-1. calcium-binding protein.
- AAC49582.1 U48691 Triticum aestivum
30 DESCRIPTION: calmodulin TaCaM2-2. calcium-binding protein.
- AAC49580.1 U48689 Triticum aestivum
DESCRIPTION: calmodulin TaCaM1-3. calcium-binding protein.
- 35 AAC49579.1 U48688 Triticum aestivum
DESCRIPTION: calmodulin TaCaM1-2. calcium binding protein.
- 40 AAC49578.1 U48242 Triticum aestivum
DESCRIPTION: calmodulin TaCaM1-1. calcium-binding.
- 45 AAA03580.1 L01431 Glycine max
DESCRIPTION: calcium-binding regulatory protein. calmodulin. SCaM-2.
putative.

DESCRIPTION: calcium-binding regulatory protein. calmodulin. SCaM-1.
putative.

5 AAA33705.1 M80831 Petunia x hybrida
DESCRIPTION: calmodulin-related protein. CAM53.

10 CAA74307.1 Y13974 Zea mays
DESCRIPTION: calmodulin.

15 CAA54583.1 X77397 Zea mays
DESCRIPTION: calmodulin. CaM2.

848

20 CAA06486.1 AJ005340 Linum usitatissimum
DESCRIPTION: IAA amidohydrolase. homolog.

850

25 BAB17350.1 AP002747 Oryza sativa
DESCRIPTION: putative nodulin. P0698G03.34. contains ESTs
D39891(S1543),D41717(S4395),AU033037(S1543).

30 BAA85440.1 AP000616 Oryza sativa
DESCRIPTION: ESTs AU055729(S20023),AU055730(S20023) correspond to a
region of the predicted gene.; similar to Medicago nodulin N21-like
protein (AC004218).

35 CAB53493.1 AJ245900 Oryza sativa
DESCRIPTION: CAA303720.1 protein. q3037.20. Similar to Medicago nodulin
N21 (MtN21).

852

40 AAD16018.1 AF081514 Taxus canadensis
DESCRIPTION: prenyltransferase. geranylgeranyl diphosphate synthase.
geranylgeranyl pyrophosphate synthase.

853

45 BAB32588.1 AB055807 Momordica charantia

DESCRIPTION: inhibitor against trypsin. bgit.

5 AAA34180.1 J05094 Lycopersicon peruvianum
DESCRIPTION: proteinase inhibitor I precursor.

10 AAA34198.1 M59427 Lycopersicon peruvianum
DESCRIPTION: proteinase inhibitor I. proteinase inhibitor I.

CAB61327.1 AJ132473 Amaranthus hypochondriacus
DESCRIPTION: Proteinase inhibition. trypsin inhibitor.

15 AAA60745.1 J04099 Lycopersicon esculentum
DESCRIPTION: proteinase inhibitor I. ER1.

20 CAA78269.1 Z12623 Nicotiana tabacum
DESCRIPTION: Putative precursor of serine proteinase inhibitor type I.
Pre-pro-proteinase inhibitor I.

25 CAA47461.1 X67076 Nicotiana tabacum
DESCRIPTION: inhibitor of microbial serine proteinases (major isoform).
TIMPa.

30 CAA78265.1 Z12619 Nicotiana tabacum
DESCRIPTION: precursor for serine proteinase inhibitor I.
Pre-pro-proteinase inhibitor I.

35 CAA47460.1 X67075 Nicotiana tabacum
DESCRIPTION: inhibitor of microbial serine proteinases (minor isoform).
TIMPb.

40 AAA34067.1 M74102 Nicotiana sylvestris
DESCRIPTION: pre-pro-proteinase inhibitor I.

45 AAC49603.1 U30861 Solanum tuberosum
DESCRIPTION: serine proteinase inhibitor. wound-inducible proteinase
inhibitor I.

- 5 BAA02823.1 D13662 *Nicotiana glauca* X *Nicotiana langsdorffii*
DESCRIPTION: genetic tumor-related proteinase inhibitor I precursor. GTI.
- 10 AAA34199.1 K03290 *Lycopersicon esculentum*
DESCRIPTION: wound-induced proteinase inhibitor I prepropeptide.
- 15 AAA34200.1 M13938 *Lycopersicon esculentum*
DESCRIPTION: proteinase inhibitor I. PIIF.
- 20 AAA69780.1 L06137 *Solanum tuberosum*
DESCRIPTION: proteinase inhibitor I. pin1. putative.
- 25 AAA72133.1 L06985 *Solanum tuberosum*
DESCRIPTION: proteinase inhibitor I. pin1. The 'a' of the first atg is missing.
- 30 CAA78259.1 Z12611 *Solanum tuberosum*
DESCRIPTION: proteinase inhibitor I.
- 35 AAA69781.1 L06606 *Solanum tuberosum*
DESCRIPTION: proteinase inhibitor I. precursor.
- 40 CAA48136.1 X67950 *Solanum tuberosum*
DESCRIPTION: protease inhibitor I. pin1.
- 45 CAA47907.1 X67675 *Solanum tuberosum*
DESCRIPTION: proteinase inhibitor I. pin1.
- 40 CAB71340.1 AJ250663 *Hordeum vulgare*
DESCRIPTION: putative proteinase inhibitor. bci-7. similarity to subtilisin/chymotrypsin inhibitor.
- 45 CAA57677.1 X82187 *Zea mays*
DESCRIPTION: serine proteinase inhibitor. substilin /chymotrypsin-like

inhibitor. pis7.

5 CAA55588.1 X78988 Zea mays
DESCRIPTION: proteinase inhibitor. MPI.

10 CAA49593.1 X69972 Zea mays
DESCRIPTION: proteinase inhibitor. MPI.

AAA33816.1 M17108 Solanum tuberosum
DESCRIPTION: proteinase inhibitor I. precursor.

15 CAA57307.1 X81647 Cucurbita maxima
DESCRIPTION: Pumpkin fruit trypsin inhibitor. pfiAF4.

20 CAA57203.1 X81447 Cucurbita maxima
DESCRIPTION: Pumpkin Fruit Chymotrypsin Inhibitor. pfiBM7.
859

25 AAC34855.1 AF082030 Hemerocallis hybrid cultivar
DESCRIPTION: senescence-associated protein 5. SA5. mRNA accumulates in
senescing petals and accumulation is induced by exogenous ABA.

30 AAG13616.1 AC078840 Oryza sativa
DESCRIPTION: putative senescence-associated protein. OSJNBb0073N24.21.
864

35 AAF62403.1 AF212183 Nicotiana tabacum
DESCRIPTION: harpin inducing protein. hin1. similar to hin1 protein.

40 CAA68848.1 Y07563 Nicotiana tabacum
DESCRIPTION: activated during hypersensitive response. hin1.

45 AAB97367.1 AF039532 Oryza sativa
DESCRIPTION: harpin induced gene 1 homolog. Hin1.
871

CAA11041.1 AJ223038 *Hevea brasiliensis*
DESCRIPTION: latex allergen. with sequence similarity to patatins.

5 AAC27724.1 U80598 *Hevea brasiliensis*
DESCRIPTION: latex patatin homolog. putative PLA2; latex protein
allergen; similar to *Solanum tubulin* patatin encoded by GenBank Accession
Number X03932.

10 AAK27797.1 AF318315 *Vigna unguiculata*
DESCRIPTION: patatin-like protein.

15 AAK18751.1 AF193067 *Vigna unguiculata*
DESCRIPTION: patatin-like protein.

20 AAB08428.1 U68484 *Nicotiana tabacum*
DESCRIPTION: patatin homolog.

25 AAD22170.1 AF061282 *Sorghum bicolor*
DESCRIPTION: patatin-like protein.

AAF98368.1 AF158027 *Nicotiana tabacum*
DESCRIPTION: patatin-like protein 1. PAT1. NtPat1.

30 AAD22169.1 AF061282 *Sorghum bicolor*
DESCRIPTION: patatin-like protein.

35 CAA81735.1 Z27221 *Solanum tuberosum*
DESCRIPTION: patatin.

40 CAA31575.1 X13178 *Solanum tuberosum*
DESCRIPTION: patatin B2 (AA 1 - 386).

45 AAA33819.1 M18880 *Solanum tuberosum*
DESCRIPTION: patatin.

-
- 5 BAA87853.1 AP000816 *Oryza sativa*
DESCRIPTION: EST AU030604(E51294) corresponds to a region of the
predicted gene. Similar to putative NAK-like Ser/Thr protein kinase.
(AF001308).
- 10 AAK21965.1 AY028699 *Brassica napus*
DESCRIPTION: receptor protein kinase PERK1.
- 15 AAD21872.1 AF078082 *Phaseolus vulgaris*
DESCRIPTION: receptor-like protein kinase homolog RK20-1.
- 20 AAK00425.1 AC069324 *Oryza sativa*
DESCRIPTION: Putative protein kinase. OSJNBa0071K19.11.
- 25 BAB39873.1 AP002882 *Oryza sativa*
DESCRIPTION: putative protein kinase. P0439B06.8. contains ESTs
AU056701(S20808),AU056702(S20808).
- 30 AAA33915.1 L27821 *Oryza sativa*
DESCRIPTION: receptor type serine/threonine kinase. protein kinase.
- 35 BAA82556.1 AB030083 *Populus nigra*
DESCRIPTION: lectin-like protein kinase. PnLPK.
- 40 AAK11674.1 AF339747 *Lophopyrum elongatum*
DESCRIPTION: protein kinase. ESI47.
- 45 AAF43496.1 AF131222 *Lophopyrum elongatum*
DESCRIPTION: protein serine/threonine kinase. ESI47. induced in roots by
salt stress, osmotic stress, and ABA treatment.
- AAG59657.1 AC084319 *Oryza sativa*
DESCRIPTION: putative protein kinase. OSJNBa0004B24.20.
- AAG03090.1 AC073405 *Oryza sativa*

DESCRIPTION: Similar to an Arabidopsis somatic embryogenesis receptor-like kinase (AC007504).

- 5 AAB93834.1 U82481 Zea mays
 DESCRIPTION: KI domain interacting kinase 1. KIK1. receptor-like protein kinase; serine/threonine protein kinase.
- 10 AAF66615.1 AF142596 Nicotiana tabacum
 DESCRIPTION: LRR receptor-like protein kinase.
- 15 AAG25966.1 AF302082 Nicotiana tabacum
 DESCRIPTION: cytokinin-regulated kinase 1. CRK1. protein kinase; transcript abundance decreases rapidly after cytokinin treatment.
- 20 AAB09771.1 U67422 Zea mays
 DESCRIPTION: CRINKLY4 precursor. cr4. receptor kinase homolog.
- 25 AAF34428.1 AF172282 Oryza sativa
 DESCRIPTION: receptor-like protein kinase. DUPR11.18.
- 30 BAB07906.1 AP002835 Oryza sativa
 DESCRIPTION: putative S-receptor kinase. P0417G05.14.
- 35 BAA94516.1 AP001800 Oryza sativa
 DESCRIPTION: Similar to Zea mays S-domain receptor-like protein kinase (AJ010166).
- 40 BAA87852.1 AP000816 Oryza sativa
 DESCRIPTION: Similar to putative Ser/Thr protein kinase. (AC004218).
- 45 BAA92221.1 AP001278 Oryza sativa
 DESCRIPTION: Similar to Arabidopsis thaliana chromosome II BAC F12L6 genomic sequence, putative protein kinase. (AC004218).

CAA73134.1 Y12531 Brassica oleracea
 DESCRIPTION: serine/threonine kinase. BRLK.
 5

BAA92954.1 AP001551 Oryza sativa
 DESCRIPTION: Similar to Oryza sativa protein kinase (OSPK10) mRNA.
 (L27821).
 10

AAG16628.1 AY007545 Brassica napus
 DESCRIPTION: protein serine/threonine kinase BNK1.
 15

CAB51834.1 00069 Oryza sativa
 DESCRIPTION: 11332.5. contains eukaryotic protein kinase domain PF.
 20

BAA06538.1 D31737 Nicotiana tabacum
 DESCRIPTION: protein-serine/threonine kinase.
 25

CAA73133.1 Y12530 Brassica oleracea
 DESCRIPTION: serine /threonine kinase. ARLK.
 30

CAB89179.1 AJ245479 Brassica napus subsp. napus
 DESCRIPTION: ser /thr kinase. S-locus receptor kinase. srk.
 35

AAA33008.1 M97667 Brassica napus
 DESCRIPTION: serine/threonine kinase receptor.
 40

BAA92837.1 AB032474 Brassica oleracea
 DESCRIPTION: S60 S-locus receptor kinase. SRK60.
 45

AAA33000.1 M76647 Brassica oleracea
 DESCRIPTION: receptor protein kinase. SKR6.

CAA79355.1 Z18921 Brassica oleracea
 DESCRIPTION: S-receptor kinase-like protein.

CAA67145.1 X98520 Brassica oleracea
DESCRIPTION: receptor-like kinase. SFR2.

5

CAA74661.1 Y14285 Brassica oleracea
DESCRIPTION: SFR1. extracellular S domain: 8-1342; transmembrane domain:
1343-1411; intracellular kinase domain: 1412-2554.

10

AAA62232.1 U00443 Brassica napus
DESCRIPTION: S-receptor kinase. protein contains an immunoglobulin-like
domain.

15

BAA23676.1 AB000970 Brassica rapa
DESCRIPTION: receptor kinase 1. BcRK1.

20

BAB07904.1 AP002835 Oryza sativa
DESCRIPTION: putative S-receptor kinase. P0417G05.12.

25

BAA94518.1 AP001800 Oryza sativa
DESCRIPTION: Similar to Arabidopsis thaliana chromosome 2 section 111 of
255; putative receptor-like protein kinase (AC002392).

30

BAA07577.2 D38564 Brassica rapa
DESCRIPTION: receptor protein kinase SRK12.

35

CAA74662.1 Y14286 Brassica oleracea
DESCRIPTION: SFR3. extracellular S domain: 123-1346; transmembrane
domain: 1347-1412; intracellular kinase domain: from 1413.

40

BAA07576.1 D38563 Brassica rapa
DESCRIPTION: receptor protein kinase SRK8.

45

BAB07999.1 AP002525 Oryza sativa
DESCRIPTION: putative protein kinase. P0462H08.22. contains EST
C22619(S11214).

BAB07905.1 AP002835 *Oryza sativa*
DESCRIPTION: putative S-receptor kinase. P0417G05.13.

- 5 BAB03429.1 AP002817 *Oryza sativa*
DESCRIPTION: EST C22619(S11214) corresponds to a region of the predicted gene. Similar to *Arabidopsis thaliana* chromosome 2, BAC clone T17D12; putative protein kinase (AC006587).

10 883

BAA90510.2 AP001111 *Oryza sativa*
DESCRIPTION: rice EST AU030811, similar to rice Ca²⁺-ATPase (U82966).

15

AAF73985.1 AF096871 *Zea mays*
DESCRIPTION: calcium pump. calcium ATPase. cap1.

20

CAA63790.1 X93592 *Dunaliella bioculata*
DESCRIPTION: P-type ATPase. cal. calcium pumping; CA1.

25

AAD11618.1 AF050496 *Lycopersicon esculentum*
DESCRIPTION: Ca²⁺-ATPase. LCA1B; alternative transcript.

30

AAA34138.1 M96324 *Lycopersicon esculentum*
DESCRIPTION: The calcium ATPase is a calcium ion pump. Ca²⁺-ATPase. LCA1.

35

AAB58910.1 U82966 *Oryza sativa*
DESCRIPTION: Ca²⁺-ATPase.

40

AAD11617.1 AF050495 *Lycopersicon esculentum*
DESCRIPTION: Ca²⁺-ATPase. LCA1A; alternative transcript.

45

AAG28435.1 AF195028 *Glycine max*
DESCRIPTION: plasma membrane Ca²⁺-ATPase. SCA1.

AAG28436.1 AF195029 *Glycine max*
DESCRIPTION: plasma membrane Ca²⁺-ATPase. SCA2.

- CAA68234.1 X99972 *Brassica oleracea*
 DESCRIPTION: calmodulin-stimulated calcium-ATPase.
- 5
- AAD31896.1 AF145478 *Mesembryanthemum crystallinum*
 DESCRIPTION: calcium ATPase.
- 10
- AAB60276.1 U09989 *Zea mays*
 DESCRIPTION: H(+)-transporting ATPase. Mha1.
- 15
- CAB69824.1 AJ271439 *Prunus persica*
 DESCRIPTION: plasma membrane H⁺ ATPase. PPA1.
- 20
- AAD46187.1 AF156683 *Nicotiana plumbaginifolia*
 DESCRIPTION: plasma membrane proton ATPase. pma8.
- 25
- BAA01058.1 D10207 *Oryza sativa*
 DESCRIPTION: H-ATPase. OSA1.
- 30
- AAB49042.1 U54690 *Dunaliella acidophila*
 DESCRIPTION: plasma membrane proton ATPase. dha1. DaDHA1; proton pump.
- 35
- AAA34173.1 M60166 *Lycopersicon esculentum*
 DESCRIPTION: H⁺-ATPase. LHA1.
- 40
- CAA52107.1 X73901 *Dunaliella bioculata*
 DESCRIPTION: plasma membrane ATPase. pma1.
- 45
- AAB35314.2 S79323 *Vicia faba*
 DESCRIPTION: plasma membrane H(+)-ATPase precursor. plasma membrane H(+)-ATPase. This sequence comes from Fig. 1; conceptual translation presented here differs from translation in publication.
- BAA06629.1 D31843 *Oryza sativa*

DESCRIPTION: plasma membrane H⁺-ATPase. OSA2.

5 AAA34094.1 M80489 *Nicotiana plumbaginifolia*
DESCRIPTION: plasma membrane H⁺ ATPase. pma1.

10 BAA08134.1 D45189 *Zostera marina*
DESCRIPTION: plasma membrane H⁺-ATPase. zha1.

CAB85494.1 AJ132891 *Medicago truncatula*
DESCRIPTION: proton pump. H⁺-ATPase. ha1.

15 CAB85495.1 AJ132892 *Medicago truncatula*
DESCRIPTION: proton pump. H⁺-ATPase. ha1.

20 AAB84202.2 AF029256 *Kosteletzkya virginica*
DESCRIPTION: plasma membrane proton ATPase. ATP1.

25 CAA47275.1 X66737 *Nicotiana plumbaginifolia*
DESCRIPTION: plasma membrane H⁺-ATPase. pma4.

30 CAA54045.1 X76535 *Solanum tuberosum*
DESCRIPTION: H(+)-transporting ATPase. PHA2.

AAD46186.1 AF156679 *Nicotiana plumbaginifolia*
DESCRIPTION: plasma membrane proton ATPase. pma6.

35 AAB17186.1 U72148 *Lycopersicon esculentum*
DESCRIPTION: plasma membrane H⁺-ATPase. LHA4. plasma membrane
proton
pumping ATPase.

40 CAB69823.1 AJ271438 *Prunus persica*
DESCRIPTION: plasma membrane H⁺ ATPase. PPA2.

45 AAB41898.1 U84891 *Mesembryanthemum crystallinum*

DESCRIPTION: plasma membrane proton pump. H⁺-transporting ATPase.
PMA.

5 CAC29436.1 AJ310524 *Vicia faba*
DESCRIPTION: P-type H⁺-ATPase. ha5. predominantly expressed in guard
cells and flowers.

10 BAA37150.1 AB022442 *Vicia faba*
DESCRIPTION: p-type H⁺-ATPase. VHA2.

CAA59800.1 X85805 *Zea mays*
15 DESCRIPTION: H(+)-transporting ATPase. MHA-2.

CAA59799.1 X85804 *Phaseolus vulgaris*
20 DESCRIPTION: H(+)-transporting ATPase. BHA-1.

CAC29435.1 AJ310523 *Vicia faba*
DESCRIPTION: P-type H⁺-ATPase. vha4. predominantly expressed in flowers.
25

AAD46188.1 AF156691 *Nicotiana plumbaginifolia*
DESCRIPTION: plasma membrane proton ATPase. pma9.

30 AAA34099.1 M80491 *Nicotiana plumbaginifolia*
DESCRIPTION: plasma membrane H⁺ ATPase. pma3.

AAA34052.1 M27888 *Nicotiana plumbaginifolia*
35 DESCRIPTION: H⁺-translocating ATPase.

CAA54046.1 X76536 *Solanum tuberosum*
40 DESCRIPTION: H(+)-transporting ATPase. PHA1.

AAA34098.1 M80490 *Nicotiana plumbaginifolia*
DESCRIPTION: plasma membrane H⁺ ATPase. pma3.

45 AAD55399.1 AF179442 *Lycopersicon esculentum*

DESCRIPTION: plasma membrane H⁺-ATPase isoform LHA2. LHA2.

AAAF98344.1 AF275745 *Lycopersicon esculentum*

5 DESCRIPTION: plasma membrane H⁺-ATPase. LHA2. P-type ion pump.

AAG01028.1 AF289025 *Cucumis sativus*

10 DESCRIPTION: plasma membrane H⁺-ATPase.

AAK31799.1 AY029190 *Lilium longiflorum*

DESCRIPTION: plasma membrane H⁺ ATPase. LILHA1.

15 AAA81348.1 U38965 *Vicia faba*

DESCRIPTION: p-type H⁺-ATPase. VHA2.

20 AAK32119.1 AF308817 *Hordeum vulgare*

DESCRIPTION: plasmalemma H⁺-ATPase 2.

AAK32118.1 AF308816 *Hordeum vulgare*

25 DESCRIPTION: plasmalemma H⁺-ATPase 1.

AAA20600.1 U08984 *Zea mays*

30 DESCRIPTION: plasma-membrane H⁺ ATPase. Zmpma1.

884

AAD21872.1 AF078082 *Phaseolus vulgaris*

35 DESCRIPTION: receptor-like protein kinase homolog RK20-1.

AAB93834.1 U82481 *Zea mays*

40 DESCRIPTION: KI domain interacting kinase 1. KIK1. receptor-like protein kinase; serine/threonine protein kinase.

CAA73134.1 Y12531 *Brassica oleracea*

DESCRIPTION: serine/threonine kinase. BRLK.

45

AAC23542.1 U20948 *Ipomoea trifida*

DESCRIPTION: receptor protein kinase. IRK1.

CAA67145.1 X98520 Brassica oleracea
5 DESCRIPTION: receptor-like kinase. SFR2.

CAA73133.1 Y12530 Brassica oleracea
10 DESCRIPTION: serine /threonine kinase. ARLK.

BAA23676.1 AB000970 Brassica rapa
DESCRIPTION: receptor kinase 1. BcRK1.

15 CAB41879.1 Y18260 Brassica oleracea
DESCRIPTION: SRK15 protein. SRK15. receptor-like kinase.

20 CAB41878.1 Y18259 Brassica oleracea
DESCRIPTION: SRK5 protein. SRK5. receptor-like kinase.

CAA74662.1 Y14286 Brassica oleracea
25 DESCRIPTION: SFR3. extracellular S domain: 123-1346; transmembrane
domain: 1347-1412; intracellular kinase domain: from 1413.

CAA74661.1 Y14285 Brassica oleracea
30 DESCRIPTION: SFR1. extracellular S domain: 8-1342; transmembrane domain:
1343-1411; intracellular kinase domain: 1412-2554.

BAA06285.1 D30049 Brassica rapa
35 DESCRIPTION: S-receptor kinase SRK9.

BAA21132.1 D88193 Brassica rapa
40 DESCRIPTION: S-receptor kinase. SRK9 (B.c).

BAA92836.1 AB032473 Brassica oleracea
DESCRIPTION: S18 S-locus receptor kinase. SRK18.

45 CAA79355.1 Z18921 Brassica oleracea

DESCRIPTION: S-receptor kinase-like protein.

5 AAA33000.1 M76647 Brassica oleracea
DESCRIPTION: receptor protein kinase. SKR6.

10 AAA62232.1 U00443 Brassica napus
DESCRIPTION: S-receptor kinase. protein contains an immunoglobulin-like domain.

15 AAA33008.1 M97667 Brassica napus
DESCRIPTION: serine/threonine kinase receptor.

20 CAB89179.1 AJ245479 Brassica napus subsp. napus
DESCRIPTION: ser /thr kinase. S-locus receptor kinase. srk.

BAB18292.1 AP002860 Oryza sativa
DESCRIPTION: putative receptor-like protein kinase. P0409B08.19.

25 AAD52097.1 AF088885 Nicotiana tabacum
DESCRIPTION: receptor-like kinase CHRK1. Chrk1.

30 BAA92837.1 AB032474 Brassica oleracea
DESCRIPTION: S60 S-locus receptor kinase. SRK60.

35 BAB21001.1 AB054061 Brassica rapa
DESCRIPTION: S locus receptor kinase. SRK22.

BAA07576.1 D38563 Brassica rapa
DESCRIPTION: receptor protein kinase SRK8.

40 BAA07577.2 D38564 Brassica rapa
DESCRIPTION: receptor protein kinase SRK12.

45 AAK02023.1 AC074283 Oryza sativa
DESCRIPTION: Putative protein kinase-like. OSJNBa0087H07.5.

- CAA79324.1 Z18884 Brassica oleracea
DESCRIPTION: S-receptor kinase related protein.
- 5
- BAB16871.1 AP002537 Oryza sativa
DESCRIPTION: putative protein kinase APK1A Arabidopsis thaliana.
P0001B06.24. contains ESTs C22608(R3192),D25110(R3192).
- 10
- BAB39873.1 AP002882 Oryza sativa
DESCRIPTION: putative protein kinase. P0439B06.8. contains ESTs
AU056701(S20808),AU056702(S20808).
- 15
- AAK21965.1 AY028699 Brassica napus
DESCRIPTION: receptor protein kinase PERK1.
- 20
- BAA87853.1 AP000816 Oryza sativa
DESCRIPTION: EST AU030604(E51294) corresponds to a region of the
predicted gene. Similar to putative NAK-like Ser/Thr protein kinase.
(AF001308).
- 25
- CAB51836.1 AJ243961 Oryza sativa
DESCRIPTION: Putative Ser/Thr protein kinase. 11332.7.
- 30
- AAA33915.1 L27821 Oryza sativa
DESCRIPTION: receptor type serine/threonine kinase. protein kinase.
- 35
- BAB21240.1 AP002953 Oryza sativa
DESCRIPTION: Putative protein kinase. P0426D06.20. contains ESTs
C22359(C11461),C22360(C11461).
- 40
- AAK00425.1 AC069324 Oryza sativa
DESCRIPTION: Putative protein kinase. OSJNBa0071K19.11.
- 45
- BAA92954.1 AP001551 Oryza sativa
DESCRIPTION: Similar to Oryza sativa protein kinase (OSPK10) mRNA.
(L27821).

- 5 AAF66615.1 AF142596 *Nicotiana tabacum*
 DESCRIPTION: LRR receptor-like protein kinase.
- 10 BAB17139.1 AP002867 *Oryza sativa*
 DESCRIPTION: putative receptor kinase. P0463F06.31.
- 15 885

 CAA80358.1 Z22645 *Solanum tuberosum*
 DESCRIPTION: cleavage of sucrose to glucose and fructose.
 beta-fructofuranosidase.
- 20 CAA79676.1 Z21486 *Solanum tuberosum*
 DESCRIPTION: cleavage of sucrose to glucose and fructose.
 beta-fructofuranosidase.
- 25 CAA57428.1 X81834 *Nicotiana tabacum*
 DESCRIPTION: beta-fructofuranosidase. Ntbfruc1. beta-fructosidase.
- 30 CAA49162.1 X69321 *Daucus carota*
 DESCRIPTION: beta-fructofuranosidase. Inva1*DC1.
- 35 CAA57389.1 X81792 *Chenopodium rubrum*
 DESCRIPTION: beta-fructofuranosidase. CIN1.
- 40 AAC17166.1 AF063246 *Pisum sativum*
 DESCRIPTION: hydrolyzes sucrose to glucose and fructose. cell wall
 invertase. bfruct1. isoform Pcl-2; the Pcl-1 isoform is in the file with
 GenBank Accession Number X85327; beta-fructofuranosidase.
- 45 CAA59677.1 X85327 *Pisum sativum*
 DESCRIPTION: hydrplyze sucrose into fructose and glucose. invertase.
 bfruct1. beta-fructofuranosidase.
- 50 AAD02263.1 AF043346 *Zea mays*
 DESCRIPTION: sucrose hydrolysis. cell wall invertase. incw3. Incw3;

beta-fructofuranosidase.

- CAA84526.1 Z35162 Vicia faba
5 DESCRIPTION: hydrolyze sucrose. beta-fructofuranosidase; cell wall
invertase I; fructosidase. VFCWINV1.
- AAC96065.1 AF030420 Triticum aestivum
10 DESCRIPTION: hydrolyzes sucrose. cell wall invertase. IVR1. hydrolase;
beta-fructofuranosidase; fructosidase.
- CAA53099.1 X75353 Daucus carota
15 DESCRIPTION: beta-fructofuranosidase.
- AAB68679.1 U92438 Phaseolus vulgaris
20 DESCRIPTION: soluble acid invertase. PVSAI; potential vacuolar targeted
enzyme; beta-fructofuranosidase.
- CAA89992.1 Z49831 Vicia faba
25 DESCRIPTION: hydrolyze sucrose. vacuolar invertase;
beta-fructofuranosidase. VFVCINV.
- CAA53097.1 X75351 Daucus carota
30 DESCRIPTION: beta-fructofuranosidase.
- CAA77267.1 Y18707 Daucus carota
35 DESCRIPTION: beta-fructofuranosidase, isoform I. Inv*Dc4. soluble acid
invertase.
- CAA53098.1 X75352 Daucus carota
40 DESCRIPTION: beta-fructofuranosidase.
- CAA77266.1 Y18706 Daucus carota
DESCRIPTION: beta-fructofuranosidase, isoform II. Inv*Dc5. soluble acid
invertase.
- 45 AAC96066.1 AF030421 Triticum aestivum

DESCRIPTION: hydrolyzes sucrose. cell wall invertase. IVR3. hydrolase;
beta-fructofuranosidase; fructosidase.

5 AAG36943.1 AF274299 Brassica oleracea

DESCRIPTION: cleaves sucrose into glucose and fructose at acid pH optima.
acid invertase AI7-3. sucrose hydrolysing enzyme; beta-fructofuranosidase.

887

10

AAD10836.1 U52079 Solanum tuberosum

DESCRIPTION: P-glycoprotein. pmdr1. binds ATP; ATPase; transporter;
transmembrane protein.

15

BAA96612.1 AP002482 Oryza sativa

DESCRIPTION: Similar to Arabidopsis thaliana chromosome 2, BAC F14M4 ;
putative ABC transporter (AC004411).

20

AAG49002.1 AY013246 Hordeum vulgare

DESCRIPTION: putative ABC transporter. 635P2.4a; GC splice donor
confirmed by cDNA and comparative sequencing.

25

AAG45492.1 AY013245 Oryza sativa

DESCRIPTION: 36I5.4. putative ABC transporter; GC splice donor confirmed
by cDNA alignment and comparative sequence.

30

BAA83352.1 AP000391 Oryza sativa

DESCRIPTION: ESTs AU067992(C11433),AU077424(C11433) correspond to
a
region of the predicted gene.; Similar to ABC transporter-7 (U43892).

35

AAG49003.1 AY013246 Hordeum vulgare

DESCRIPTION: putative ABC transporter. 635P2.4b; GC splice donor
confirmed by cDNA alignment and comparative sequence.

40

BAB17113.1 AP002866 Oryza sativa

DESCRIPTION: putative white protein; ATP-binding cassette transporter.
P0410E01.34.

45

BAA90508.1 AP001111 *Oryza sativa*
DESCRIPTION: similar to ABC transporter of *Arabidopsis thaliana*
(AC004697).

5

BAA90507.1 AP001111 *Oryza sativa*
DESCRIPTION: similar to ABC transporter of *Arabidopsis thaliana*
(AC004697).

10

BAB16495.1 AP002861 *Oryza sativa*
DESCRIPTION: putative ABC transporter ATP-binding protein. P0665D10.21.

15

BAB21276.1 AP002844 *Oryza sativa*
DESCRIPTION: putative ABC transporter protein. P0410E03.7. contains EST
D22472(C1173).

20

BAB21275.1 AP002844 *Oryza sativa*
DESCRIPTION: putative ABC transporter protein. P0410E03.6.

25

BAB21273.1 AP002844 *Oryza sativa*
DESCRIPTION: putative ABC transporter protein. P0410E03.4.

30

BAB40032.1 AP003046 *Oryza sativa*
DESCRIPTION: putative ABC transporter. P0445D12.3.

888

35

AAD21872.1 AF078082 *Phaseolus vulgaris*
DESCRIPTION: receptor-like protein kinase homolog RK20-1.

40

CAA73134.1 Y12531 *Brassica oleracea*
DESCRIPTION: serine/threonine kinase. BRLK.

45

AAB93834.1 U82481 *Zea mays*
DESCRIPTION: KI domain interacting kinase 1. KIK1. receptor-like protein
kinase; serine/threonine protein kinase.

45

AAC23542.1 U20948 *Ipomoea trifida*

DESCRIPTION: receptor protein kinase. IRK1.

AAA33000.1 M76647 Brassica oleracea

5 DESCRIPTION: receptor protein kinase. SKR6.

CAB89179.1 AJ245479 Brassica napus subsp. napus

10 DESCRIPTION: ser /thr kinase. S-locus receptor kinase. srk.

AAA33008.1 M97667 Brassica napus

DESCRIPTION: serine/threonine kinase receptor.

CAA74661.1 Y14285 Brassica oleracea

15 DESCRIPTION: SFR1. extracellular S domain: 8-1342; transmembrane domain: 1343-1411; intracellular kinase domain: 1412-2554.

CAA67145.1 X98520 Brassica oleracea

20 DESCRIPTION: receptor-like kinase. SFR2.

AAA62232.1 U00443 Brassica napus

25 DESCRIPTION: S-receptor kinase. protein contains an immunoglobulin-like domain.

CAA73133.1 Y12530 Brassica oleracea

30 DESCRIPTION: serine /threonine kinase. ARLK.

BAA23676.1 AB000970 Brassica rapa

35 DESCRIPTION: receptor kinase 1. BcRK1.

BAA92836.1 AB032473 Brassica oleracea

40 DESCRIPTION: S18 S-locus receptor kinase. SRK18.

CAA74662.1 Y14286 Brassica oleracea

45 DESCRIPTION: SFR3. extracellular S domain: 123-1346; transmembrane domain: 1347-1412; intracellular kinase domain: from 1413.

- CAA79355.1 Z18921 Brassica oleracea
DESCRIPTION: S-receptor kinase-like protein.
- 5 CAB41879.1 Y18260 Brassica oleracea
DESCRIPTION: SRK15 protein. SRK15. receptor-like kinase.
- 10 BAA06285.1 D30049 Brassica rapa
DESCRIPTION: S-receptor kinase SRK9.
- 15 BAA21132.1 D88193 Brassica rapa
DESCRIPTION: S-receptor kinase. SRK9 (B.c).
- 20 CAB41878.1 Y18259 Brassica oleracea
DESCRIPTION: SRK5 protein. SRK5. receptor-like kinase.
- BAA92837.1 AB032474 Brassica oleracea
DESCRIPTION: S60 S-locus receptor kinase. SRK60.
- 25 BAA07577.2 D38564 Brassica rapa
DESCRIPTION: receptor protein kinase SRK12.
- 30 BAB21001.1 AB054061 Brassica rapa
DESCRIPTION: S locus receptor kinase. SRK22.
- 35 BAA07576.1 D38563 Brassica rapa
DESCRIPTION: receptor protein kinase SRK8.
- 40 AAD52097.1 AF088885 Nicotiana tabacum
DESCRIPTION: receptor-like kinase CHRK1. Chrk1.
- AAK02023.1 AC074283 Oryza sativa
DESCRIPTION: Putative protein kinase-like. OSJNBa0087H07.5.
- 45 BAB18292.1 AP002860 Oryza sativa
DESCRIPTION: putative receptor-like protein kinase. P0409B08.19.

- 5 BAA87853.1 AP000816 *Oryza sativa*
DESCRIPTION: EST AU030604(E51294) corresponds to a region of the
predicted gene. Similar to putative NAK-like Ser/Thr protein kinase.
(AF001308).
- 10 AAK21965.1 AY028699 *Brassica napus*
DESCRIPTION: receptor protein kinase PERK1.
- 15 BAB21240.1 AP002953 *Oryza sativa*
DESCRIPTION: Putative protein kinase. P0426D06.20. contains ESTs
C22359(C11461),C22360(C11461).
- 20 BAB39873.1 AP002882 *Oryza sativa*
DESCRIPTION: putative protein kinase. P0439B06.8. contains ESTs
AU056701(S20808),AU056702(S20808).
- 25 BAB17331.1 AP002747 *Oryza sativa*
DESCRIPTION: putative receptor kinase. P0698G03.12.
- 30 BAB17139.1 AP002867 *Oryza sativa*
DESCRIPTION: putative receptor kinase. P0463F06.31.
- 35 AAK00425.1 AC069324 *Oryza sativa*
DESCRIPTION: Putative protein kinase. OSJNBa0071K19.11.
- 40 BAB16871.1 AP002537 *Oryza sativa*
DESCRIPTION: putative protein kinase APK1A*Arabidopsis thaliana*.
P0001B06.24. contains ESTs C22608(R3192),D25110(R3192).
- 45 BAA92954.1 AP001551 *Oryza sativa*
DESCRIPTION: Similar to *Oryza sativa* protein kinase (OSPK10) mRNA.
(L27821).
- 45 CAB51836.1 AJ243961 *Oryza sativa*
DESCRIPTION: Putative Ser/Thr protein kinase. I1332.7.

AAF78016.1 AF238472 Oryza sativa
DESCRIPTION: receptor-like kinase. RLG15. protein kinase.

BAB39451.1 AP003338 Oryza sativa
DESCRIPTION: putative receptor kinase. OJ1212_B09.24.

890

AAB47181.1 S82324 Zea mays
DESCRIPTION: /gene="calcium/calmodulin-dependent
protein kinase. This sequence comes from Fig. 1.

BAA22410.1 D38452 Zea mays
DESCRIPTION: calcium-dependent protein kinase-related kinase.

BAA12692.1 D84508 Zea mays
DESCRIPTION: CDPK-related protein kinase. Does not require calcium for
its activity.

AAG01179.1 AF289237 Zea mays
DESCRIPTION: calcium/calmodulin dependent protein kinase MCK2. MCK2.

CAA58750.1 X83869 Daucus carota
DESCRIPTION: CDPK-related protein kinase. CRK (or PK421).

BAA12691.1 D84507 Zea mays
DESCRIPTION: CDPK-related protein kinase. Does not require calcium for
its activity (by similarity).

AAC24961.1 AF009337 Tradescantia virginiana
DESCRIPTION: CDPK-related protein kinase. CRK1.

AAF23901.2 AF194414 Oryza sativa
DESCRIPTION: calcium-dependent protein kinase. CDPK5. OsCDPK5.

AAF23900.1 AF194413 *Oryza sativa*
DESCRIPTION: calcium-dependent protein kinase. CDPK1. OsCDPK1.

5 AAC78558.1 AF030879 *Solanum tuberosum*
DESCRIPTION: protein kinase CPK1.

10 AAD17800.1 AF090835 *Mesembryanthemum crystallinum*
DESCRIPTION: Ca²⁺-dependent protein kinase. CPK1. serine/threonine protein kinase.

15 AAB49984.1 U90262 *Cucurbita pepo*
DESCRIPTION: calcium-dependent calmodulin-independent protein kinase CDPK. cpCPK1. serine/threonine protein kinase that is activated by direct binding of calcium.

20 CAA07481.1 AJ007366 *Zea mays*
DESCRIPTION: calcium-dependent protein kinase.

25 BAB21081.1 AP002819 *Oryza sativa*
DESCRIPTION: putative calcium-dependent protein kinase. P0501G01.10.

30 BAA12715.1 D85039 *Zea mays*
DESCRIPTION: calcium-dependent protein kinase.

AAC25423.1 AF072908 *Nicotiana tabacum*
DESCRIPTION: calcium-dependent protein kinase. CDPK1.

35 CAA39936.1 X56599 *Daucus carota*
DESCRIPTION: calcium- dependent protein kinase. DcPK431.

40 CAA57157.1 X81394 *Oryza sativa*
DESCRIPTION: calcium-dependent protein kinase. OSCPK2.

45 AAF21062.1 AF216527 *Dunaliella tertiolecta*
DESCRIPTION: calcium-dependent protein kinase. CPK1; CDPK.

- 5 BAA81751.1 AB017517 *Marchantia polymorpha*
DESCRIPTION: calcium-dependent protein kinase. CDPK1. CDPK-B;
alternative
splicing.
- 10 BAA81749.1 AB017515 *Marchantia polymorpha*
DESCRIPTION: calcium-dependent protein kinase. CDPK1. CDPK-B;
alternative
splicing.
- 15 AAB88537.1 AF035944 *Fragaria x ananassa*
DESCRIPTION: calcium-dependent protein kinase. MAX17.
- 20 BAA81750.1 AB017516 *Marchantia polymorpha*
DESCRIPTION: calcium-dependent protein kinase. CDPK1. CDPK-A;
alternative
splicing.
- 25 BAA81748.1 AB017515 *Marchantia polymorpha*
DESCRIPTION: calcium-dependent protein kinase. CDPK1. CDPK-A;
alternative
splicing.
- 30 AAA69507.1 U28376 *Zea mays*
DESCRIPTION: calcium-dependent protein kinase. MZECDPK2.
- 35 AAA61682.1 L27484 *Zea mays*
DESCRIPTION: calcium-dependent protein kinase. CDPK.
- 40 AAB80693.1 U69174 *Glycine max*
DESCRIPTION: calmodulin-like domain protein kinase isoenzyme gamma.
CDPK
gamma.
- 45 BAA13232.1 D87042 *Zea mays*
DESCRIPTION: Calcium-dependent protein kinase.

BAA13440.1 D87707 Ipomoea batatas
DESCRIPTION: calcium dependent protein kinase. CDPK.

5

CAA89202.1 Z49233 Chlamydomonas eugametos
DESCRIPTION: calcium-stimulated protein kinase.

10 AAB70706.1 U82087 Tortula ruralis
DESCRIPTION: calmodulin-like domain protein kinase. TrCPK1.

AAD28192.2 AF115406 Solanum tuberosum
15 DESCRIPTION: calcium-dependent protein kinase. CDPK; catalytic domain.

AAC49405.1 U08140 Vigna radiata
20 DESCRIPTION: calcium dependent protein kinase. CDPK.

BAA12338.1 D84408 Zea mays
DESCRIPTION: calcium dependent protein kinase. ZmCDPK1.

25 CAA65500.1 X96723 Medicago sativa
DESCRIPTION: protein kinase. CDPK.

30 BAA85396.1 AP000615 Oryza sativa
DESCRIPTION: ESTs C22369(C12239),C22370(C12239),
AU057852(S21844),AU057853(S21844) correspond to a region of the predicted
gene.; similar to calcium dependent protein kinase. (AF048691).

35 AAA33443.1 L15390 Zea mays
DESCRIPTION: calcium-dependent protein kinase. CDPK.

40 AAB80692.1 U69173 Glycine max
DESCRIPTION: calmodulin-like domain protein kinase isoenzyme beta. CDPK
beta.

45 CAA57156.1 X81393 Oryza sativa
DESCRIPTION: calcium-dependent protein kinase. OSCPKII.

-
- 5 AAF20931.1 AF206721 *Brassica juncea*
DESCRIPTION: ascorbate oxidase.
- 10 BAA07734.1 D43624 *Nicotiana tabacum*
DESCRIPTION: ascorbate oxidase precursor.
- 15 AAA33119.1 J04494 *Cucumis sativus*
DESCRIPTION: ascorbate oxidase precursor (EC 1.10.3.3).
- 20 CAA75577.1 Y15295 *Medicago truncatula*
DESCRIPTION: L-ascorbate oxidase. MtN23.
- 25 AAF35911.2 AF233594 *Cucumis melo*
DESCRIPTION: ascorbate oxidase AO4. multicopper oxidase.
- 30 CAA39300.1 X55779 *Cucurbita* sp.
DESCRIPTION: ascorbate oxidase.
- 35 BAA09528.1 D55677 *Cucurbita maxima*
DESCRIPTION: ascorbate oxidase. AAO.
- 40 AAF35910.1 AF233593 *Cucumis melo*
DESCRIPTION: ascorbate oxidase AO1. multicopper oxidase.
- 45 CAA71275.1 Y10226 *Cucumis melo*
DESCRIPTION: L-ascorbate oxidase. ao3.
- 40 AAF20932.1 AF206722 *Brassica juncea*
DESCRIPTION: ascorbate oxidase.
- 45 AAF20933.1 AF206723 *Brassica juncea*
DESCRIPTION: ascorbate oxidase.

CAA71273.1 Y10224 Cucumis melo
DESCRIPTION: L-ascorbate oxidase. ao1.

5

CAA71274.1 Y10225 Cucumis melo
DESCRIPTION: L-ascorbate oxidase. ao1.

10 BAA20520.1 AB004799 Oryza sativa
DESCRIPTION: ascorbate oxidase.

15 AAF33751.1 AF202460 Capsicum annuum
DESCRIPTION: ascorbic acid oxidase.

20 AAB17193.1 U73105 Liriodendron tulipifera
DESCRIPTION: monolignol polymerization; lignin biosynthesis. laccase.
LAC2-3. diphenol oxidase; blue copper oxidase.

25 AAB17191.1 U73103 Liriodendron tulipifera
DESCRIPTION: monolignol polymerization; lignin biosynthesis. laccase.
LAC2-1. diphenol oxidase; blue copper oxidase.

30 AAC49536.1 U43542 Nicotiana tabacum
DESCRIPTION: diphenol oxidase. laccase.

35 AAB17194.1 U73106 Liriodendron tulipifera
DESCRIPTION: monolignol polymerization; lignin biosynthesis. laccase.
LAC2-4. diphenol oxidase; blue copper oxidase.

40 AAB17192.1 U73104 Liriodendron tulipifera
DESCRIPTION: monolignol polymerization; lignin biosynthesis. laccase.
LAC2-2. diphenol oxidase; blue copper oxidase.

AAC04576.1 AF047697 Oryza sativa
DESCRIPTION: p-diphenol oxidase. putative high-pI laccase.

45

AAB09228.1 U12757 Acer pseudoplatanus

DESCRIPTION: monolignol polymerization; lignin biosynthesis. laccase.
diphenol oxidase.

5 CAA45554.1 X64257 Brassica napus
DESCRIPTION: Bp10. protein homologous to ascorbate oxidase.

AAC49538.1 U45243 Nicotiana tabacum
10 DESCRIPTION: diphenol oxidase. laccase.

AAC49537.1 U43543 Nicotiana tabacum
15 DESCRIPTION: diphenol oxidase. laccase.

AAD02557.1 AF049931 Petunia x hybrida
DESCRIPTION: PGPS/NH15. PGPS/NH15. ascorbate oxidase homolog.
20 894

CAB43505.1 AJ239051 Cicer arietinum
DESCRIPTION: cytochrome P450. cyp81E2.

25 BAA74465.1 AB022732 Glycyrrhiza echinata
DESCRIPTION: cytochrome P450. CYP Ge-31.

30 BAA93634.1 AB025016 Lotus japonicus
DESCRIPTION: cytochrome P450.

BAA22422.1 AB001379 Glycyrrhiza echinata
35 DESCRIPTION: cytochrome P450. CYP81E1.

CAA04117.1 AJ000478 Helianthus tuberosus
DESCRIPTION: fatty acid in-chain hydroxylase. cytochrome P450. CYP81B11.
40 chimeric sequence (from 5'-race).

CAB41490.1 AJ238439 Cicer arietinum
45 DESCRIPTION: cytochrome P450 monooxygenase. cyp81E3v2.

- CAA04116.1 AJ000477 *Helianthus tuberosus*
DESCRIPTION: fatty acid in-chain hydroxylase. cytochrome P450. CYP81B1c.
- 5 CAA10067.1 AJ012581 *Cicer arietinum*
DESCRIPTION: cytochrome P450. cyp81E3.
- 10 AAK38079.1 AF321855 *Lolium rigidum*
DESCRIPTION: putative cytochrome P450.
- 15 AAK38080.1 AF321856 *Lolium rigidum*
DESCRIPTION: putative cytochrome P450.
- 20 AAK38081.1 AF321857 *Lolium rigidum*
DESCRIPTION: putative cytochrome P450.
- AAD56282.1 AF155332 *Petunia x hybrida*
DESCRIPTION: flavonoid 3'-hydroxylase. Ht1. cytochrome P450; CYP75B2.
- 25 AAC34853.1 AF082028 *Heimerocallis* hybrid cultivar
DESCRIPTION: putative cyt P450-containing fatty acid hydroxylase.
senescence-associated protein 3. SA3. mRNA accumulates in senescing
petals.
- 30 AAG09208.1 AF175278 *Pisum sativum*
DESCRIPTION: wound-inducible P450 hydroxylase. CYP82A1.
- 35 BAA12159.1 D83968 *Glycine max*
DESCRIPTION: Cytochrome P-450 (CYP93A1).
- 40 CAA71515.1 Y10491 *Glycine max*
DESCRIPTION: putative cytochrome P450.
- 45 CAA71876.1 Y10982 *Glycine max*
DESCRIPTION: putative cytochrome P450.

CAA65580.1 X96784 *Nicotiana tabacum*
DESCRIPTION: cytochrome P450. hsr515.

5 AAC49188.2 U29333 *Pisum sativum*
DESCRIPTION: cytochrome P450 monooxygenase. CYP82. new cytochrome
P450
family.

10 AAG44132.1 AF218296 *Pisum sativum*
DESCRIPTION: cytochrome P450. P450 isolog.

15 CAA71516.1 Y10492 *Glycine max*
DESCRIPTION: putative cytochrome P450.

20 CAA64635.1 X95342 *Nicotiana tabacum*
DESCRIPTION: cytochrome P450. hsr515. hypersensitivity-related gene.

25 AAC39454.1 AF014802 *Eschscholzia californica*
DESCRIPTION: (S)-N-methylcoclaurine 3'-hydroxylase. CYP82B1. cytochrome
P-450-dependent monooxygenase; methyl jasmonate-inducible cytochrome
P-450-dependent, homologous to wound-inducible CYP82A1 of *Pisum sativum*
GenBank Accession Number U29333.

30 AAB94590.1 AF022461 *Glycine max*
DESCRIPTION: CYP82C1p. CYP82C1. cytochrome P450 monooxygenase.

35 AAA32913.1 M32885 *Persea americana*
DESCRIPTION: cytochrome P-450LXXIA1 (cyp71A1).

40 CAA71877.1 Y10983 *Glycine max*
DESCRIPTION: putative cytochrome P450.

BAA84072.1 AB028152 *Torenia hybrida*
DESCRIPTION: flavone synthase II. cytochrome P450. TFNS5.

45 BAA13076.1 D86351 *Glycine max*

DESCRIPTION: cytochrome P-450 (CYP93A2).

AAG34695.1 AF313492 *Matthiola incana*

5 DESCRIPTION: putative cytochrome P450.

BAA84071.1 AB028151 *Antirrhinum majus*

10 DESCRIPTION: flavone synthase II. cytochrome P450. AFNS2.

AAC32274.1 AF081575 *Petunia x hybrida*

DESCRIPTION: flavonoid 3',5'-hydroxylase. Hfl. P450 enzyme.

15

BAA35080.1 AB015762 *Nicotiana tabacum*

DESCRIPTION: putative cytochrome P450. CYP82E1.

20

CAA50155.1 X70824 *Solanum melongena*

DESCRIPTION: flavonoid hydroxylase (P450). CYP75.

25

CAA70575.1 Y09423 *Nepeta racemosa*

DESCRIPTION: cytochrome P450. CYP71A5.

30

BAA92894.1 AB006790 *Petunia x hybrida*

DESCRIPTION: cytochrome P450. IMT-2.

35

CAA71513.1 Y10489 *Glycine max*

DESCRIPTION: putative cytochrome P450.

AAB94587.1 AF022458 *Glycine max*

DESCRIPTION: CYP98A2p. CYP98A2. cytochrome P450 monooxygenase.

40

895

BAA78764.1 AB023482 *Oryza sativa*

DESCRIPTION: ESTs C98382(C2985),D22444(C11129) correspond to a region of

45 the predicted gene.; Similar to *Arabidopsis thaliana* APK1 gene for protein tyrosine-serine-threonine kinase.(D12522).

AAF43496.1 AF131222 *Lophopyrum elongatum*

DESCRIPTION: protein serine/threonine kinase. ESI47. induced in roots by salt stress, osmotic stress, and ABA treatment.

5

AAK11674.1 AF339747 *Lophopyrum elongatum*

DESCRIPTION: protein kinase. ESI47.

10

AAG16628.1 AY007545 *Brassica napus*

DESCRIPTION: protein serine/threonine kinase BNK1.

15

BAA94510.1 AB041504 *Populus nigra*

DESCRIPTION: protein kinase 2. PnPK2.

20

BAA94509.1 AB041503 *Populus nigra*

DESCRIPTION: protein kinase 1. PnPK1.

25

BAA87853.1 AP000816 *Oryza sativa*

DESCRIPTION: EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative NAK-like Ser/Thr protein kinase. (AF001308).

30

BAB07999.1 AP002525 *Oryza sativa*

DESCRIPTION: putative protein kinase. P0462H08.22. contains EST C22619(S11214).

35

BAB03429.1 AP002817 *Oryza sativa*

DESCRIPTION: EST C22619(S11214) corresponds to a region of the predicted gene. Similar to *Arabidopsis thaliana* chromosome 2, BAC clone T17D12; putative protein kinase (AC006587).

40

BAB16871.1 AP002537 *Oryza sativa*

DESCRIPTION: putative protein kinase APK1A *Arabidopsis thaliana*. P0001B06.24. contains ESTs C22608(R3192), D25110(R3192).

45

BAB39873.1 AP002882 *Oryza sativa*

DESCRIPTION: putative protein kinase. P0439B06.8. contains ESTs

AU056701(S20808),AU056702(S20808).

- 5 BAB39409.1 AP002901 *Oryza sativa*
DESCRIPTION: putative protein kinase. P0456F08.9. contains EST
C23560(R0290).
- 10 AAK00425.1 AC069324 *Oryza sativa*
DESCRIPTION: Putative protein kinase. OSJNBa0071K19.11.
- 15 BAB21240.1 AP002953 *Oryza sativa*
DESCRIPTION: Putative protein kinase. P0426D06.20. contains ESTs
C22359(C11461),C22360(C11461).
- 20 AAK21965.1 AY028699 *Brassica napus*
DESCRIPTION: receptor protein kinase PERK1.
- 25 AAG59657.1 AC084319 *Oryza sativa*
DESCRIPTION: putative protein kinase. OSJNBa0004B24.20.
- 30 AAG03090.1 AC073405 *Oryza sativa*
DESCRIPTION: Similar to an Arabidopsis somatic embryogenesis
receptor-like kinase (AC007504).
- 35 CAB51834.1 00069 *Oryza sativa*
DESCRIPTION: 11332.5. contains eukaryotic protein kinase domain PF.
- 40 AAC61805.1 U28007 *Lycopersicon esculentum*
DESCRIPTION: serine/threonine protein kinase. Pto kinase interactor 1.
Pti1. Pti1 kinase.
- 45 AAF91336.1 AF249317 *Glycine max*
DESCRIPTION: Pti1 kinase-like protein. Pti1a. protein kinase.
- AAF91337.1 AF249318 *Glycine max*
DESCRIPTION: Pti1 kinase-like protein. Pti1b. protein kinase.

- 5 BAB21241.1 AP002953 *Oryza sativa*
DESCRIPTION: Putative Pto kinase interactor 1. P0426D06.21. contains ESTs AU108280(E0721),D48017(S13927).
- 10 AAB09771.1 U67422 *Zea mays*
DESCRIPTION: CRINKLY4 precursor. cr4. receptor kinase homolog.
- 15 CAA97692.1 Z73295 *Catharanthus roseus*
DESCRIPTION: receptor-like protein kinase. CRPK1. Autophosphorylation predominantly on Thr, less on Ser. Mechanism: autophosphorylation in cis.
- 20 BAA92221.1 AP001278 *Oryza sativa*
DESCRIPTION: Similar to Arabidopsis thaliana chromosome II BAC F12L6 genomic sequence, putative protein kinase. (AC004218).
- 25 BAA87852.1 AP000816 *Oryza sativa*
DESCRIPTION: Similar to putative Ser/Thr protein kinase. (AC004218).
- 30 AAB61708.1 U93048 *Daucus carota*
DESCRIPTION: somatic embryogenesis receptor-like kinase. SERK.
- 35 AAG25966.1 AF302082 *Nicotiana tabacum*
DESCRIPTION: cytokinin-regulated kinase 1. CRK1. protein kinase; transcript abundance decreases rapidly after cytokinin treatment.
- 40 BAA90808.1 AP001168 *Oryza sativa*
DESCRIPTION: Similar to putative receptor-like protein kinase (AL035679).
- 45 AAF76313.1 AF220603 *Lycopersicon esculentum*
DESCRIPTION: Pto kinase. LescPth5.
- 50 AAB47421.1 U59316 *Lycopersicon esculentum*
DESCRIPTION: serine/threonine protein kinase Pto. pto. allele of Pto bacterial speck disease resistance gene in tomato.

- AAC23542.1 U20948 *Ipomoea trifida*
DESCRIPTION: receptor protein kinase. IRK1.
- 5 BAB19337.1 AP003044 *Oryza sativa*
DESCRIPTION: putative protein kinase. P0038C05.10. contains ESTs
AU056335(S20481),AU056336(S20481).
- 10 AAC27894.1 AF023164 *Zea mays*
DESCRIPTION: leucine-rich repeat transmembrane protein kinase 1. ltk1.
- 15 AAF66615.1 AF142596 *Nicotiana tabacum*
DESCRIPTION: LRR receptor-like protein kinase.
- 20 CAB51480.1 Y14600 *Sorghum bicolor*
DESCRIPTION: putative protein serine /threonine kinase. RLK1. accumulates
in mesophyll cells.
- 25 BAA92954.1 AP001551 *Oryza sativa*
DESCRIPTION: Similar to *Oryza sativa* protein kinase (OSPK10) mRNA.
(L27821).
- 30 BAA92953.1 AP001551 *Oryza sativa*
DESCRIPTION: Similar to *Arabidopsis thaliana* chromosome 4 BAC clone
F10M6
; S-receptor kinase -like protein. (AL021811).
- 35 AAK11566.1 AF318490 *Lycopersicon hirsutum*
DESCRIPTION: Pto-like protein kinase E. LhirPtoE. confers resistance to
bacterial speck disease.
- 40 AAK11567.1 AF318491 *Lycopersicon hirsutum*
DESCRIPTION: Pto-like protein kinase F. LhirPtoF.
- 45 BAA82556.1 AB030083 *Populus nigra*
DESCRIPTION: lectin-like protein kinase. PnLPK.

CAA67145.1 X98520 Brassica oleracea
DESCRIPTION: receptor-like kinase. SFR2.

899

5

AAF61647.1 AF190634 Nicotiana tabacum
DESCRIPTION: UDP-glucose:salicylic acid glucosyltransferase. SA-GTase.

10 BAA89009.1 AB027455 Petunia x hybrida
DESCRIPTION: anthocyanin 5-O-glucosyltransferase. PH1.

15 AAA59054.1 L34847 Zea mays
DESCRIPTION: conjugation of the growth hormone indole-3-acetic acid
(IAA). IAA-glu synthetase. iaglu.

20 BAA93039.1 AB033758 Citrus unshiu
DESCRIPTION: limonoid UDP-glucosyltransferase. LGTase.

25 BAA36423.1 AB013598 Verbena x hybrida
DESCRIPTION: UDP-glucose:anthocyanin 5-O-glucosyltransferase. HGT8.

BAA36421.1 AB013596 Perilla frutescens
DESCRIPTION: UDP-glucose:anthocynin 5-O-glucosyltransferase. PF3R4.

30

AAF98390.1 AF287143 Brassica napus
DESCRIPTION: catalyzes the transfer of glucose from UDP-glucose to
sinapate and some other hydroxycinnamates (4-coumarate, caffeate,
ferulate). UDP-glucose:sinapate glucosyltransferase. SGT1. SGT.

35

BAA36422.1 AB013597 Perilla frutescens
DESCRIPTION: UDP-glucose:anthocyanin 5-O-glucosyltransferase homologue.
PF3R6.

40

BAB07962.1 AP002524 Oryza sativa
DESCRIPTION: putative anthocyanin 5-O-glucosyltransferase. P0406H10.16.
contains ESTs AU067881(C10481),AU067882(C10481).

45

- AAK16175.1 AC079887 *Oryza sativa*
DESCRIPTION: putative glucosyltransferase. OSJNBa0040E01.15.
- 5 AAK16181.1 AC079887 *Oryza sativa*
DESCRIPTION: putative glucosyltransferase. OSJNBa0040E01.16.
- 10 AAK16178.1 AC079887 *Oryza sativa*
DESCRIPTION: putative glucosyltransferase. OSJNBa0040E01.5.
- 15 AAG25643.1 AF303396 *Phaseolus vulgaris*
DESCRIPTION: UDP-glucosyltransferase HRA25. putative; defense associated.
- 20 AAK16172.1 AC079887 *Oryza sativa*
DESCRIPTION: putative glucosyltransferase. OSJNBa0040E01.14.
- BAA83484.1 AB031274 *Scutellaria baicalensis*
DESCRIPTION: UDP-glucose: flavonoid 7-O-glucosyltransferase. ufgt.
- 25 AAB36652.1 U32643 *Nicotiana tabacum*
DESCRIPTION: immediate-early salicylate-induced glucosyltransferase.
IS10a.
- 30 AAK28304.1 AF346432 *Nicotiana tabacum*
DESCRIPTION: phenylpropanoid:glucosyltransferase 2. togt2.
glucosyltransferase.
- 35 AAD21086.1 AF127218 *Forsythia x intermedia*
DESCRIPTION: adds glucose residue to position 3 of flavonoid compounds.
flavonoid 3-O-glucosyltransferase. UFGT.
- 40 AAB36653.1 U32644 *Nicotiana tabacum*
DESCRIPTION: immediate-early salicylate-induced glucosyltransferase.
IS5a.
- 45 BAA12737.1 D85186 *Gentiana triflora*
DESCRIPTION: UDP-glucose:flavonoid-3-glucosyltransferase.

AAK28303.1 AF346431 *Nicotiana tabacum*
 DESCRIPTION: phenylpropanoid:glucosyltransferase 1. togt1.
 5 glucosyltransferase.

AAF17077.1 AF199453 *Sorghum bicolor*
 DESCRIPTION: UDP-glucose glucosyltransferase.
 10 UDP-glucose:p-hydroxymandelonitrile-o- glucosyltransferase.

AAK16180.1 AC079887 *Oryza sativa*
 DESCRIPTION: putative glucosyltransferase. OSJNBa0040E01.21.
 15

CAA59450.1 X85138 *Lycopersicon esculentum*
 DESCRIPTION: twi1. homologous to glucosyltransferases.
 20

BAB41017.1 AB047090 *Vitis labrusca* x *Vitis vinifera*
 DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. KyUFGT1.
 The
 25 gene was derived from one of the parents *V. labruscana* cv. Ishiharawase.

BAB41026.1 AB047099 *Vitis vinifera*
 DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. FIUFGT2.
 30

BAB41024.1 AB047097 *Vitis vinifera*
 DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. AIUFGT2.
 35

BAB41022.1 AB047095 *Vitis vinifera*
 DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. RuUFGT2.
 40

BAB41020.1 AB047093 *Vitis vinifera*
 DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. ItUFGT2.
 45

BAA89008.1 AB027454 *Petunia x hybrida*
 DESCRIPTION: anthocyanidin 3-O-glucosyltransferase. PGT8.

- BAB41018.1 AB047091 *Vitis labrusca* x *Vitis vinifera*
 DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. KyUFGT2.
 The
 gene originated in one of the parents *V. vinifera* cv. Centennial.
- 5
- CAB56231.1 Y18871 *Dorotheanthus bellidiformis*
 DESCRIPTION: betanidin-5-O-glucosyltransferase.
- 10
- AAB81683.1 AF000372 *Vitis vinifera*
 DESCRIPTION: UDP glucose:flavonoid 3-o-glucosyltransferase.
- 15
- BAB41019.1 AB047092 *Vitis vinifera*
 DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. ItUFGT1.
- 20
- BAB41025.1 AB047098 *Vitis vinifera*
 DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. FIUFGT1.
- 25
- BAB41023.1 AB047096 *Vitis vinifera*
 DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. AlUFGT1.
- 30
- BAB41021.1 AB047094 *Vitis vinifera*
 DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. RuUFGT1.
- 35
- BAA19659.1 AB002818 *Perilla frutescens*
 DESCRIPTION: flavonoid 3-O-glucosyltransferase. UDP glucose.
- 40
- BAA90787.1 AB038248 *Ipomoea batatas*
 DESCRIPTION: UDP glucose: flavonoid 3-O-glucosyltransferase. uf3gt.
- 45
- AAD04166.1 AF101972 *Phaseolus lunatus*
 DESCRIPTION: catalyzes formation of O-glucosylzeatin from zeatin and
 UDPG; catalyzes formation of O-xylosylzeatin from zeatin and UDPX. zeatin
 O-glucosyltransferase. ZOG1. cytokinin O-glucosyltransferase.

- CAA39603.1 X56138 *Lycopersicon esculentum*
DESCRIPTION: small heat shock protein (class I).
- 5 AAD30453.1 AF123256 *Lycopersicon esculentum*
DESCRIPTION: 17.8 kD class I small heat shock protein. HSP17.8.
- 10 CAA37847.1 X53851 *Daucus carota*
DESCRIPTION: heat shock protein.
- 15 AAA33671.1 M33900 *Pisum sativum*
DESCRIPTION: 17.9 kDa heat shock protein (hsp17.9).
- 20 AAF34133.1 AF161179 *Malus x domestica*
DESCRIPTION: low molecular weight heat shock protein. Hsp1.
- 25 CAA41546.1 X58710 *Medicago sativa*
DESCRIPTION: heat shock protein.
- 30 AAB63310.1 U46544 *Helianthus annuus*
DESCRIPTION: 18.6 kDa heat-shock protein. Class I low-molecular-weight heat-shock protein.
- 35 AAB63311.1 U46545 *Helianthus annuus*
DESCRIPTION: 17.7 kDa heat shock protein. Class I low-molecular-weight heat-shock protein.
- 40 CAB08441.1 Z95153 *Helianthus annuus*
DESCRIPTION: 17.6 kD class I small heat-shock protein HSP17.6. Ha hsp17.6.
- 45 CAA42222.1 X59701 *Helianthus annuus*
DESCRIPTION: 17.6 kDa heat shock protein.
- 45 AAC39360.1 U63631 *Fragaria x ananassa*
DESCRIPTION: LMW heat shock protein.

- 5 AAA33910.1 M80939 Oryza sativa
DESCRIPTION: 16.9 kDa heat shock protein.
- CAA37848.1 X53852 Daucus carota
DESCRIPTION: heat shock protein.
- 10 AAA33909.1 M80938 Oryza sativa
DESCRIPTION: 16.9 kDa heat shock protein.
- 15 CAA43210.1 X60820 Oryza sativa
DESCRIPTION: 16.9 KD low molecular weight heat shock protein.
- 20 CAA37864.1 X53870 Chenopodium rubrum
DESCRIPTION: heat-shock protein.
- 25 AAD49336.1 AF166277 Nicotiana tabacum
DESCRIPTION: low molecular weight heat-shock protein. LHS-1. TLHS-1.
- AAA61632.1 U08601 Papaver somniferum
DESCRIPTION: low molecular weight heat-shock protein.
- 30 AAB72109.1 AF022217 Brassica rapa
DESCRIPTION: low molecular weight heat-shock protein. BcHSP17.6. 17.6 kDa; cytosolic class I.
- 35 CAA63902.1 X94192 Pennisetum glaucum
DESCRIPTION: heat shock protein 16.9. hsp16.9.
- 40 AAB39856.1 U81385 Oryza sativa
DESCRIPTION: heat shock protein. Oshsp16.9C. class I, low molecular mass.
- 45 CAA46641.1 X65725 Zea mays
DESCRIPTION: heat shock protein 17.2. Zmhsp 17.2. Class I low molecular weight heat shock protein.

- CAA08908.1 AJ009880 *Castanea sativa*
 DESCRIPTION: molecular chaperone. cytosolic class I small heat-shock
 protein HSP17.5. hsp17.5.
- CAB93512.1 AJ243565 *Brassica oleracea*
 DESCRIPTION: putative class I small heat shock protein. HSP17.7-a
 protein. hsp17.7-a.
- CAA63903.1 X94193 *Pennisetum glaucum*
 DESCRIPTION: heat shock protein 17.9. hsp17.9.
- CAB36910.1 AJ000691 *Quercus suber*
 DESCRIPTION: stress protein chaperone. heat shock protein 17.4. hsp17.
- CAA63901.1 X94191 *Pennisetum glaucum*
 DESCRIPTION: heat shock protein 17.0. hsp17.0.
- AAC78392.1 U83669 *Oryza sativa*
 DESCRIPTION: low molecular mass heat shock protein Oshsp17.3.
 OSHSP17.3.
 class I LMMHSP.
- BAA02160.1 D12635 *Oryza sativa*
 DESCRIPTION: 'low molecular weight heat shock protein'.
- AAC78393.1 U83670 *Oryza sativa*
 DESCRIPTION: low molecular mass heat shock protein Oshsp18.0.
 OSHSP18.0.
 class I LMMHSP.
- CAA31785.1 X13431 *Triticum aestivum*
 DESCRIPTION: put. heat shock protein (AA 1 -151).
- CAA63570.1 X92983 *Pseudotsuga menziesii*
 DESCRIPTION: low molecular weight heat-shock protein.

AAC78394.1 U83671 *Oryza sativa*
 DESCRIPTION: low molecular mass heat shock protein Oshsp17.7.
 5 OSHSP17.7.
 class I LMMHSP.

CAA63571.1 X92984 *Pseudotsuga menziesii*
 10 DESCRIPTION: low molecular weight heat-shock protein.

901

 AAG08959.1 AF122051 *Solanum tuberosum*
 15 DESCRIPTION: tuber-specific and sucrose-responsive element binding
 factor. TSF. R2R3 MYB class transcription factor.

AAG08960.1 AF122052 *Solanum tuberosum*
 20 DESCRIPTION: tuber-specific and sucrose-responsive element binding
 factor. TSF. R2R3 MYB class transcription factor.

AAG08961.1 AF122053 *Solanum tuberosum*
 25 DESCRIPTION: tuber-specific and sucrose-responsive element binding
 factor. TSF. R2R3 MYB class transcription factor.

AAF67053.1 AF190304 *Adiantum raddianum*
 30 DESCRIPTION: c-myb-like transcription factor. MYB3R-1. contains three
 MYB
 repeats.

AAF67052.1 AF190303 *Adiantum raddianum*
 35 DESCRIPTION: c-myb-like transcription factor. MYB3R-1. contains three
 MYB
 repeats.

40

AAF34434.1 AF172282 *Oryza sativa*
 DESCRIPTION: myb-like protein. DUPR11.29.

45 AAF78888.1 AF189786 *Physcomitrella patens*
 DESCRIPTION: putative c-myb-like transcription factor. MYB3R-1.

PpMYB3R-1.

AAF78887.1 AF189785 *Physcomitrella patens*

5 DESCRIPTION: putative c-myb-like transcription factor. MYB3R-1.
PpMYB3R-1.

AAF43043.1 AF236059 *Papaver rhoeas*

10 DESCRIPTION: putative Myb-related domain. pmr.

BAA94769.1 AP001859 *Oryza sativa*

15 DESCRIPTION: Similar to *Arabidopsis thaliana* chromosome 4, BAC clone
F4D11; putative myb-protein. (AL022537).

AAF78890.1 AF189788 *Hordeum vulgare*

20 DESCRIPTION: putative c-myb-like transcription factor. MYB3R-1.
HvMYB3R-1.

AAF78889.1 AF189787 *Hordeum vulgare*

25 DESCRIPTION: putative c-myb-like transcription factor. MYB3R-1.
HvMYB3R-1.

BAA88169.1 AP000836 *Oryza sativa*

30 DESCRIPTION: Similar to putative transcription factor (AF062890).

BAA88205.1 AP000837 *Oryza sativa*

35 DESCRIPTION: Similar to putative transcription factor (AF062890).

CAA78388.1 Z13998 *Petunia x hybrida*

40 DESCRIPTION: DNA-binding protein; transcriptional activator. protein 3.
myb.Ph3. related to animal myb proto-oncoproteins.

AAF67051.1 AF190302 *Secale cereale*

45 DESCRIPTION: c-myb-like transcription factor. MYB3R-1. contains three
MYB
repeats.

AAF67050.1 AF190301 Secale cereale
DESCRIPTION: c-myb-like transcription factor. MYB3R-1. contains three
MYB
repeats.

5

AAG28525.1 AF198498 Nicotiana tabacum
DESCRIPTION: anther-specific myb-related protein 2. mybAS2. NtMYBAS2;
contains tandem R2, R3 myb domains similar to c-myb family.

10

BAB12688.1 AP002746 Oryza sativa
DESCRIPTION: putative MYB family transcription factor. P0671B11.3.
contains ESTs AU082307(E0784),C72014(E0784).

15

BAA99440.1 AP002743 Oryza sativa
DESCRIPTION: putative MYB family transcription factor. P0710E05.27.
contains ESTs AU082307(E0784),C72014(E0784).

20

AAK19619.1 AF336286 Gossypium hirsutum
DESCRIPTION: GHMYB9. ghmyb9. similar to myb.

25

CAA64615.1 X95297 Lycopersicon esculentum
DESCRIPTION: transcription factor. THM1. myb-related.

30 BAA81730.1 AB029159 Glycine max
DESCRIPTION: GmMYB29A1.

35 CAA50224.1 X70879 Hordeum vulgare
DESCRIPTION: MybHv1. myb1.

40 CAA50222.1 X70877 Hordeum vulgare
DESCRIPTION: MybHv1. myb1.

CAB40189.1 AJ133638 Avena sativa
DESCRIPTION: transcriptional activator. myb protein. gamyb.

45

AAG28526.1 AF198499 Nicotiana tabacum

DESCRIPTION: anther-specific myb-related protein 1. mybAS1. NtMYBAS1;
contains N-terminal R2, R3 myb domain repeats similar to c-myb.

5 AAD31395.1 AF114162 *Lolium temulentum*

DESCRIPTION: gibberellin MYB transcription factor. GAMyb. R2/R3-MYB.

10 BAA81732.1 AB029161 *Glycine max*

DESCRIPTION: GmMYB29A2.

15 BAA81731.1 AB029160 *Glycine max*

DESCRIPTION: GmMYB29A1.

20 CAA61021.1 X87690 *Hordeum vulgare*

DESCRIPTION: transcriptional activator of alpha-amylase gene promoter.
GAMyb protein. Gam1.

25 AAG22863.1 AY008692 *Hordeum vulgare*

DESCRIPTION: transcription factor GAMyb. Gamyb.

30 BAA96421.1 AB044084 *Triticum aestivum*

DESCRIPTION: transcription activator for gibberellin response. GAMyb
protein. Ta-GAMyb.

35 BAA81733.2 AB029162 *Glycine max*

DESCRIPTION: GmMYB29A2.

40 BAA81736.1 AB029165 *Glycine max*

DESCRIPTION: GmMYB29B2.

45 AAA33067.1 L04497 *Gossypium hirsutum*

DESCRIPTION: MYB A; putative.

BAB39972.1 AP003018 *Oryza sativa*

DESCRIPTION: putative transcription factor (myb). OSJNBa0004B13.27.
contains ESTs AU097474(S5087),D40175(S1959).

- CAA72218.1 Y11415 *Oryza sativa*
DESCRIPTION: myb.
- 5 CAA67000.1 X98355 *Oryza sativa*
DESCRIPTION: activator of alpha-amylase gene promoter. transcription factor GAMyb. Gam1. Myb-like; expression is regulated by gibberellin.
- 10 BAB39987.1 AP003020 *Oryza sativa*
DESCRIPTION: putative transcription factor (myb). P0498A12.16. contains ESTs AU097474(S5087),D40175(S1959).
- 15 CAA78387.1 Z13997 *Petunia x hybrida*
DESCRIPTION: DNA-binding protein, transcriptional activator. protein 2. myb.Ph2. related to animal myb proto-oncoproteins.
- 20 CAA72217.1 Y11414 *Oryza sativa*
DESCRIPTION: myb.
- 25 BAA23341.1 D88621 *Oryza sativa*
DESCRIPTION: transfactor. OSMYB5. Osmyb5.
- 30 BAA93038.1 AP001552 *Oryza sativa*
DESCRIPTION: EST AU082058(C12976) corresponds to a region of the predicted gene. Similar to *Arabidopsis thaliana* putative transcription factor (AF062916).
- 35 CAA64614.1 X95296 *Lycopersicon esculentum*
DESCRIPTION: transcription factor. THM27. myb-related.
- 40 AAK19616.1 AF336283 *Gossypium hirsutum*
DESCRIPTION: GHMYB25. ghmyb25. similar to myb; contains an unspliced intron.
- 45 CAA78386.1 Z13996 *Petunia x hybrida*
DESCRIPTION: DNA binding protein; transcriptional activator. protein 1. myb.Ph3. Product related to animal myb proto-oncoproteins. Sequence from

nucleotide 992 is not included in clone cPF1 and has been obtained by PCR amplification of cDNA.

- 5 CAA67575.1 X99134 *Lycopersicon esculentum*
DESCRIPTION: transcription factor. THM6. myb-related.
- 10 BAA88222.1 AB028650 *Nicotiana tabacum*
DESCRIPTION: myb-related transcription factor LBM2. lbm2.
- 902
-
- 15 CAA57773.1 X82329 *Arachis hypogaea*
DESCRIPTION: chitinase (class II). chi2;1.
- 20 AAD54935.1 AF141373 *Petroselinum crispum*
DESCRIPTION: random hydrolysis of 1,4-beta-acetamido-2-deoxy-D-glucoside linkages in chitin. chitinase precursor. Chi2-1. class II.
- 25 AAD54936.1 AF141374 *Petroselinum crispum*
DESCRIPTION: random hydrolysis of 1,4-beta-acetamido-2-deoxy-D-glucoside linkages in chitin. chitinase precursor. Chi2-2. class II.
- 30 AAF00131.1 AF147091 *Fragaria x ananassa*
DESCRIPTION: chitin degradation. class II chitinase. Chi2-1.
- 35 AAC95376.1 AF105426 *Cynodon dactylon*
DESCRIPTION: chitinase. Cht2.
- 40 BAA95846.1 AP002070 *Oryza sativa*
DESCRIPTION: Similar to *Oryza sativa* clone RGCH7 chitinase. (AF013581).
- 45 AAA32986.1 M95835 *Brassica napus*
DESCRIPTION: endochitinase. Ch25.
- AAF69783.1 AF135143 *Arabis lemmonii*
DESCRIPTION: class I chitinase.

AAF69775.1 AF135135 *Arabis drummondii*
DESCRIPTION: class I chitinase.

5

AAF69792.1 AF135152 *Arabis parishii*
DESCRIPTION: class I chitinase.

10 AAC95375.1 AF105425 *Cynodon dactylon*
DESCRIPTION: chitinase. Cht1.

15 AAF69785.1 AF135145 *Arabis lignifera*
DESCRIPTION: class I chitinase.

20 AAF69770.1 AF135130 *Arabis holboellii*
DESCRIPTION: class I chitinase.

AAF69781.1 AF135141 *Arabis gunnisoniana*
DESCRIPTION: class I chitinase.

25 AAF69777.1 AF135137 *Arabis fecunda*
DESCRIPTION: class I chitinase.

30 AAF69790.1 AF135150 *Arabis microphylla*
DESCRIPTION: class I chitinase.

35 AAF69787.1 AF135147 *Arabis lignifera*
DESCRIPTION: class I chitinase.

40 AAF69772.1 AF135132 *Arabis gunnisoniana*
DESCRIPTION: class I chitinase.

AAF69782.1 AF135142 *Halimolobos perplexa* var. *perplexa*
DESCRIPTION: class I chitinase.

45 AAF69784.1 AF135144 *Arabis lemmonii*

DESCRIPTION: class I chitinase.

5 AAF69788.1 AF135148 *Arabis lyallii*
DESCRIPTION: class I chitinase.

10 BAA03750.1 D16222 *Oryza sativa*
DESCRIPTION: endochitinase. Cht-2.

15 AAF69776.1 AF135136 *Arabis fecunda*
DESCRIPTION: class I chitinase.

CAA40107.1 X56787 *Oryza sativa*
DESCRIPTION: chitinase.

20 BAB13369.1 AB048531 *Psophocarpus tetragonolobus*
DESCRIPTION: class I chitinase.

25 AAF69778.1 AF135138 *Arabis glabra*
DESCRIPTION: class I chitinase.

30 AAF69786.1 AF135146 *Arabis lignifera*
DESCRIPTION: class I chitinase.

BAA82826.1 AB023464 *Arabis gemmifera*
DESCRIPTION: basic endochitinase. ChiB.

35 AAF69773.1 AF135133 *Arabis blepharophylla*
DESCRIPTION: class I chitinase.

40 AAF69791.1 AF135151 *Arabis microphylla*
DESCRIPTION: class I chitinase.

45 AAF69793.1 AF135153 *Arabis parishii*
DESCRIPTION: class I chitinase.

- CAA39535.1 X56063 *Oryza sativa*
DESCRIPTION: chitinase.
- 5 BAA03749.1 D16221 *Oryza sativa*
DESCRIPTION: endochitinase. Cht-1.
- 10 AAF69789.1 AF135149 *Arabis microphylla*
DESCRIPTION: class I chitinase.
- 15 CAA71402.1 Y10373 *Medicago truncatula*
DESCRIPTION: chitinase.
- 20 AAC16010.1 AF061805 *Elaeagnus umbellata*
DESCRIPTION: acidic chitinase.
- CAA53626.1 X76041 *Triticum aestivum*
DESCRIPTION: endochitinase. CHI.
- 25 BAA33971.1 AB008892 *Nicotiana tabacum*
DESCRIPTION: chitinase 134. Chn134.
- 30 CAA47921.1 X67693 *Solanum tuberosum*
DESCRIPTION: chitinase. SK2. endochitinase.
- 35 AAF69780.1 AF135140 *Arabis glabra*
DESCRIPTION: class I chitinase.
- 40 BAB18519.1 AB051578 *Secale cereale*
DESCRIPTION: seed chitinase-a. rsca.
- AAA51377.1 L37289 *Oryza sativa*
DESCRIPTION: chitinolytic activity, antifungal activity. chitinase.
- 45 AAB41324.1 U83591 *Medicago sativa*

DESCRIPTION: protein kinase. ESI47.

5 AAG16628.1 AY007545 Brassica napus
DESCRIPTION: protein serine/threonine kinase BNK1.

10 BAA94509.1 AB041503 Populus nigra
DESCRIPTION: protein kinase 1. PnPK1.

15 BAA87853.1 AP000816 Oryza sativa
DESCRIPTION: EST AU030604(E51294) corresponds to a region of the
predicted gene. Similar to putative NAK-like Ser/Thr protein kinase.
(AF001308).

20 BAA94510.1 AB041504 Populus nigra
DESCRIPTION: protein kinase 2. PnPK2.

25 BAB16871.1 AP002537 Oryza sativa
DESCRIPTION: putative protein kinase APK1A Arabidopsis thaliana.
P0001B06.24. contains ESTs C22608(R3192),D25110(R3192).

30 BAB03429.1 AP002817 Oryza sativa
DESCRIPTION: EST C22619(S11214) corresponds to a region of the predicted
gene. Similar to Arabidopsis thaliana chromosome 2, BAC clone T17D12;
putative protein kinase (AC006587).

35 BAB07999.1 AP002525 Oryza sativa
DESCRIPTION: putative protein kinase. P0462H08.22. contains EST
C22619(S11214).

40 BAB39409.1 AP002901 Oryza sativa
DESCRIPTION: putative protein kinase. P0456F08.9. contains EST
C23560(R0290).

45 BAB21240.1 AP002953 Oryza sativa
DESCRIPTION: Putative protein kinase. P0426D06.20. contains ESTs
C22359(C11461),C22360(C11461).

AAK00425.1 AC069324 Oryza sativa
DESCRIPTION: Putative protein kinase. OSJNBa0071K19.11.

5

CAB51834.1 00069 Oryza sativa
DESCRIPTION: 11332.5. contains eukaryotic protein kinase domain PF.

10 BAB39873.1 AP002882 Oryza sativa
DESCRIPTION: putative protein kinase. P0439B06.8. contains ESTs
AU056701(S20808),AU056702(S20808).

15 AAK21965.1 AY028699 Brassica napus
DESCRIPTION: receptor protein kinase PERK1.

20 AAG03090.1 AC073405 Oryza sativa
DESCRIPTION: Similar to an Arabidopsis somatic embryogenesis
receptor-like kinase (AC007504).

25 BAB19337.1 AP003044 Oryza sativa
DESCRIPTION: putative protein kinase. P0038C05.10. contains ESTs
AU056335(S20481),AU056336(S20481).

30 BAA90808.1 AP001168 Oryza sativa
DESCRIPTION: Similar to putative receptor-like protein kinase (AL035679).

35 AAG59657.1 AC084319 Oryza sativa
DESCRIPTION: putative protein kinase. OSJNBa0004B24.20.

40 AAB47424.1 U59317 Lycopersicon pimpinellifolium
DESCRIPTION: serine/threonine protein kinase Fen. Fen. fenthion
sensitivity gene from tomato.

45 AAC48932.1 U13923 Lycopersicon pimpinellifolium
DESCRIPTION: Fen. putative serine/threonine protein kinase; similar to
product encoded by Lycopersicon pimpinellifolium Pto gene, GenBank
Accession Number U02271; Fen is a member of the Pto gene family.

AAF76307.1 AF220602 *Lycopersicon pimpinellifolium*
DESCRIPTION: Fen kinase.

5

BAA92221.1 AP001278 *Oryza sativa*
DESCRIPTION: Similar to *Arabidopsis thaliana* chromosome II BAC F12L6
genomic sequence, putative protein kinase. (AC004218).

10

BAA87852.1 AP000816 *Oryza sativa*
DESCRIPTION: Similar to putative Ser/Thr protein kinase. (AC004218).

15

AAB61708.1 U93048 *Daucus carota*
DESCRIPTION: somatic embryogenesis receptor-like kinase. SERK.

20

AAK11566.1 AF318490 *Lycopersicon hirsutum*
DESCRIPTION: Pto-like protein kinase E. LhirPtoE. confers resistance to
bacterial speck disease.

25

AAK11568.1 AF318492 *Lycopersicon hirsutum*
DESCRIPTION: Pto-like protein kinase B. LhirPtoB.

30

AAD21872.1 AF078082 *Phaseolus vulgaris*
DESCRIPTION: receptor-like protein kinase homolog RK20-1.

35

AAF66615.1 AF142596 *Nicotiana tabacum*
DESCRIPTION: LRR receptor-like protein kinase.

40

AAC23542.1 U20948 *Ipomoea trifida*
DESCRIPTION: receptor protein kinase. IRK1.

AAF91337.1 AF249318 *Glycine max*
DESCRIPTION: Pti1 kinase-like protein. Pti1b. protein kinase.

45

AAC27894.1 AF023164 *Zea mays*
DESCRIPTION: leucine-rich repeat transmembrane protein kinase 1. ltk1.

- AAF76314.1 AF220603 *Lycopersicon esculentum*
DESCRIPTION: Fen kinase. Lescfen.
- 5 AAB47422.1 U59318 *Lycopersicon esculentum*
DESCRIPTION: serine/threonine protein kinase Fen. fen. allele of Fen,
fenthion sensitivity gene from tomato.
- 10 AAF76313.1 AF220603 *Lycopersicon esculentum*
DESCRIPTION: Pto kinase. LescPth5.
- 15 AAB47421.1 U59316 *Lycopersicon esculentum*
DESCRIPTION: serine/threonine protein kinase Pto. pto. allele of Pto
bacterial speck disease resistance gene in tomato.
- 20 AAF91336.1 AF249317 *Glycine max*
DESCRIPTION: Pti1 kinase-like protein. Pti1a. protein kinase.
- 25 AAK11567.1 AF318491 *Lycopersicon hirsutum*
DESCRIPTION: Pto-like protein kinase F. LhirPtoF.
- 30 AAC61805.1 U28007 *Lycopersicon esculentum*
DESCRIPTION: serine/threonine protein kinase. Pto kinase interactor 1.
Pti1. Pti1 kinase.
- 35 AAB93834.1 U82481 *Zea mays*
DESCRIPTION: KI domain interacting kinase 1. KIK1. receptor-like protein
kinase; serine/threonine protein kinase.
- 40 CAA97692.1 Z73295 *Catharanthus roseus*
DESCRIPTION: receptor-like protein kinase. CRPK1. Autophosphorylation
predominantly on Thr, less on Ser. Mechanism: autophosphorylation in cis.
- 45 CAA73134.1 Y12531 *Brassica oleracea*
DESCRIPTION: serine/threonine kinase. BRLK.

AAF76306.1 AF220602 *Lycopersicon pimpinellifolium*

DESCRIPTION: Pto kinase.

5 AAB47423.1 U59315 *Lycopersicon pimpinellifolium*

DESCRIPTION: serine/threonine protein kinase Pto. Pto. bacterial speck
disease resistance in tomato; disease resistance gene.

10 BAB21241.1 AP002953 *Oryza sativa*

DESCRIPTION: Putative Pto kinase interactor 1. P0426D06.21. contains ESTs
AU108280(E0721),D48017(S13927).

15 AAC48914.1 U02271 *Lycopersicon pimpinellifolium*

DESCRIPTION: protein kinase.

904

20 AAF65545.1 AF233894 *Perilla citriodora*

DESCRIPTION: limonene synthase.

25 AAG31437.1 AF241792 *Perilla frutescens*

DESCRIPTION: limonene synthase.

30 AAK06663.1 AF317695 *Perilla frutescens* var. *frutescens*

DESCRIPTION: limonene synthase.

AAG31435.1 AF241790 *Perilla citriodora*

DESCRIPTION: limonene synthase.

35 BAA21629.1 AB005744 *Perilla frutescens*

DESCRIPTION: catalyzing the cyclization of geranyl pyrophosphate to
1-limonene. 1-limonene synthase. gPFLC. similar to perilla PFLC-1:DDBJ
Acc#D49368.

40

AAG31438.1 AF241793 *Perilla frutescens*

DESCRIPTION: limonene synthase.

45

BAA08367.1 D49368 *Perilla frutescens*

DESCRIPTION: limonene cyclase.

5 AAC37366.1 L13459 *Mentha spicata*
DESCRIPTION: 4S-limonene synthase.

10 AAD50304.1 AF175323 *Mentha longifolia*
DESCRIPTION: limonene synthase. monoterpene synthase.

AAG01140.1 AF282875 *Schizonepeta tenuifolia*
DESCRIPTION: (+)-4R-limonene synthase.

15 AAF21053.1 AF212433 *Capsicum annuum*
DESCRIPTION: UV-induced sesquiterpene cyclase. SC2.

20 BAA82141.1 AB023816 *Solanum tuberosum*
DESCRIPTION: vetispiradiene synthase. PVS4. potato sesquiterpene cyclase.

25 AAF74977.1 AF270425 *Gossypium hirsutum*
DESCRIPTION: (E,E)-farnesyl diphosphate cyclase. (+)-delta-cadinene
synthase. cdn2. sesquiterpene cyclase.

30 BAA82092.1 AB022598 *Solanum tuberosum*
DESCRIPTION: vetispiradiene synthase. PVS1. potato sesquiterpene cyclase.

35 BAA82109.1 AB022720 *Solanum tuberosum*
DESCRIPTION: vetispiradiene synthase. PVS3. potato sesquiterpene cyclase;
PVS3.

40 AAG09949.1 AF171216 *Lycopersicon esculentum*
DESCRIPTION: vetispiradiene synthase. LEVS2. sesquiterpene cyclase.

45 BAA82108.1 AB022719 *Solanum tuberosum*
DESCRIPTION: vetispiradiene synthase. PVS2. potato sesquiterpene cyclase;
PVS2.

- AAC12784.1 U88318 *Gossypium hirsutum*
DESCRIPTION: (E,E)-farnesyl diphosphate cyclizing. (+)-delta-cadinene synthase. cdn1. sesquiterpene cyclase; delta-cadinene synthase.
- 5 AAK15641.1 AF326117 *Capsicum annuum*
DESCRIPTION: sesquiterpene cyclase. PSC2.
- 10 AAC61260.1 AF061285 *Capsicum annuum*
DESCRIPTION: sesquiterpene cyclase. UV induced.
- 15 AAG24640.2 AF304444 *Artemisia annua*
DESCRIPTION: sesquiterpene cyclase.
- 20 CAC12731.1 AJ271792 *Artemisia annua*
DESCRIPTION: putative sesquiterpene cyclase. cASC125.
905
-
- 25 AAF64450.1 AF239928 *Euphorbia esula*
DESCRIPTION: glutathione S-transferase. similar to auxin-inducible GST.
- 30 AAG34803.1 AF243368 *Glycine max*
DESCRIPTION: glutathione S-transferase GST 13.
- AAG16759.1 AY007561 *Lycopersicon esculentum*
DESCRIPTION: putative glutathione S-transferase T4.
- 35 AAG34798.1 AF243363 *Glycine max*
DESCRIPTION: glutathione S-transferase GST 8.
- 40 AAG34797.1 AF243362 *Glycine max*
DESCRIPTION: glutathione S-transferase GST 7.
- 45 AAG16758.1 AY007560 *Lycopersicon esculentum*
DESCRIPTION: putative glutathione S-transferase T3.

- AAG34809.1 AF243374 Glycine max
DESCRIPTION: glutathione S-transferase GST 19.
- 5 AAG34801.1 AF243366 Glycine max
DESCRIPTION: glutathione S-transferase GST 11.
- 10 AAG34796.1 AF243361 Glycine max
DESCRIPTION: glutathione S-transferase GST 6.
- 15 AAG34807.1 AF243372 Glycine max
DESCRIPTION: glutathione S-transferase GST 17.
- 20 AAG16757.1 AY007559 Lycopersicon esculentum
DESCRIPTION: putative glutathione S-transferase T2.
- AAG16756.1 AY007558 Lycopersicon esculentum
DESCRIPTION: putative glutathione S-transferase T1.
- 25 AAG34804.1 AF243369 Glycine max
DESCRIPTION: glutathione S-transferase GST 14.
- 30 AAG34810.1 AF243375 Glycine max
DESCRIPTION: glutathione S-transferase GST 20.
- 35 AAG34808.1 AF243373 Glycine max
DESCRIPTION: glutathione S-transferase GST 18.
- 40 AAG34805.1 AF243370 Glycine max
DESCRIPTION: glutathione S-transferase GST 15.
- AAG34844.1 AF244701 Zea mays
DESCRIPTION: glutathione S-transferase GST 36.
- 45 AAG34829.1 AF244686 Zea mays
DESCRIPTION: glutathione S-transferase GST 21.

5 AAG34831.1 AF244688 Zea mays
 DESCRIPTION: glutathione S-transferase GST 23.

10 AAA68430.1 J03679 Solanum tuberosum
 DESCRIPTION: glutathione S-transferase. gst1. previously called
 pathogenesis-related protein; prp1-1.

15 AAC18566.1 AF048978 Glycine max
 DESCRIPTION: 2,4-D inducible glutathione S-transferase. GSTa.

20 AAG34832.1 AF244689 Zea mays
 DESCRIPTION: glutathione S-transferase GST 24.

25 AAG34800.1 AF243365 Glycine max
 DESCRIPTION: glutathione S-transferase GST 10.

30 AAG34849.1 AF244706 Zea mays
 DESCRIPTION: glutathione S-transferase GST 41.

35 AAG34837.1 AF244694 Zea mays
 DESCRIPTION: glutathione S-transferase GST 29.

AAC32118.1 AF051214 Picea mariana
 DESCRIPTION: probable glutathione S-transferase. Sb18. similar to
 Nicotiana tabacum probable glutathione S-transferase encoded by GenBank
 Accession Number X56266.

40 AAG41204.1 AF321437 Suaeda maritima
 DESCRIPTION: glutathione transferase.

45 AAG34802.1 AF243367 Glycine max
 DESCRIPTION: glutathione S-transferase GST 12.

AAF29773.1 AF159229 Gossypium hirsutum

DESCRIPTION: glutathione S-transferase. GST.

5 AAG32472.1 AF309379 Oryza sativa subsp. japonica
DESCRIPTION: putative glutathione S-transferase OsGSTU3.

10 AAG34836.1 AF244693 Zea mays
DESCRIPTION: glutathione S-transferase GST 28.

CAA04391.1 AJ000923 Carica papaya
DESCRIPTION: glutathione transferase. PGST1.

15 CAA71784.1 Y10820 Glycine max
DESCRIPTION: glutathione transferase.

20 CAA09187.1 AJ010448 Alopecurus myosuroides
DESCRIPTION: glutathione transferase. GST1a.

25 AAG34795.1 AF243360 Glycine max
DESCRIPTION: glutathione S-transferase GST 5.

30 CAA09188.1 AJ010449 Alopecurus myosuroides
DESCRIPTION: glutathione transferase. GST1b.

AAG34806.1 AF243371 Glycine max
DESCRIPTION: glutathione S-transferase GST 16.

35 CAC24549.1 AJ296343 Cichorium intybus x Cichorium endivia
DESCRIPTION: glutathione S-transferase. chi-GST1. auxin-induced GST.

40 AAC28101.1 AF079511 Mesembryanthemum crystallinum
DESCRIPTION: glutathione S-transferase.

907

45 -----
AAA33280.1 L20475 Datura stramonium
DESCRIPTION: 29kDa protein; high homology to aa sequence of tropinone

reductases.

- 5 AAA33281.1 L20473 *Datura stramonium*
DESCRIPTION: catalyses a stereospecific reduction of tropinone to
tropine. tropinone reductase-I.
- 10 CAC34420.1 AJ307584 *Solanum tuberosum*
DESCRIPTION: tropine forming tropinone reductase. tropinone reductase I.
TRI.
- 15 BAA85844.1 AB026544 *Hyoscyamus niger*
DESCRIPTION: tropinone reductase-I. tr1.
- 20 BAA13547.1 D88156 *Hyoscyamus niger*
DESCRIPTION: tropinone reductase-I.
- 25 AAA33282.1 L20474 *Datura stramonium*
DESCRIPTION: catalyses a stereospecific reduction of tropinone to
pseudotropine. tropinone reductase-II.
- 30 AAB09776.1 L20485 *Hyoscyamus niger*
DESCRIPTION: tropinone reductase-II.
- 35 CAB52307.1 AJ245634 *Solanum tuberosum*
DESCRIPTION: pseudotropine forming tropinone reductase. tropinone
reductase II. TRII.
- 40 CAC19810.1 AJ292343 *Solanum tuberosum*
DESCRIPTION: pseudotropine forming tropinone reductase. tropinone
reductase II. trII.
- 45 CAA45866.1 X64566 *Cuphea lanceolata*
DESCRIPTION: beta-ketoacyl-ACP reductase. Clkr27. 3-oxoacyl-[acyl-carrier

protein] reductase.

CAA45793.1 X64463 Brassica napus
5 DESCRIPTION: 3-oxoacyl-[acyl-carrier protein] reductase.

AAB82767.1 U89509 Zea mays
10 DESCRIPTION: cuticular wax biosynthesis. b-keto acyl reductase. glossy8.

AAB82766.1 U89510 Hordeum vulgare
DESCRIPTION: cuticular wax biosynthesis. b-keto acyl reductase. glossy8.

CAA74176.1 Y13861 Nicotiana tabacum
15 DESCRIPTION: enoyl-ACP reductase. enr-T2.

AAB20114.2 S60064 Brassica napus
20 DESCRIPTION: enoyl-acyl carrier protein reductase. This sequence comes from fig3; conceptual translation differs from published sequence.

CAA74177.1 Y13862 Nicotiana tabacum
25 DESCRIPTION: enoyl-ACP reductase. enr-T1.

AAC78100.1 AF093628 Oryza sativa
30 DESCRIPTION: protochlorophyllide reductase homolog.

CAA05879.1 AJ003124 Petunia x hybrida
35 DESCRIPTION: enoyl-ACP reductase. pte.

CAA64729.1 X95462 Brassica napus
DESCRIPTION: enoyl reductase.

CAA05816.1 AJ003025 Oryza sativa
40 DESCRIPTION: enoyl-ACP reductase.

BAA99570.1 AB036823 Chlorella vulgaris
45 DESCRIPTION: oxidoreductase. oxi.

909

-
- 5 BAA82107.1 AB022693 *Nicotiana tabacum*
DESCRIPTION: transcription factor. NtWRKY1.
- 10 AAC31956.1 AF080595 *Pimpinella brachycarpa*
DESCRIPTION: zinc finger protein. ZFP1. WRKY1.
- 15 AAD55974.1 AF121353 *Petroselinum crispum*
DESCRIPTION: zinc-finger type transcription factor WRKY1. WRKY1.
- 20 BAA77383.1 AB020590 *Nicotiana tabacum*
DESCRIPTION: transcription factor NtWRKY2.
- 25 AAC49527.1 U48831 *Petroselinum crispum*
DESCRIPTION: WRKY1. contains two WRKY domains; WRKY-type DNA-binding
protein; sequence-specific DNA-binding protein.
- 30 AAD32677.1 AF140554 *Avena sativa*
DESCRIPTION: DNA-binding protein WRKY1. wrky1. putative transcription
factor.
- 35 CAA88326.1 Z48429 *Avena fatua*
DESCRIPTION: binds conserved cis-element from cereal alpha-Amy2
promoters. DNA-binding protein.
- 40 AAD16139.1 AF096299 *Nicotiana tabacum*
DESCRIPTION: DNA-binding protein 2. WRKY2. transcription factor.
- 45 BAA86031.1 AB026890 *Nicotiana tabacum*
DESCRIPTION: transcription factor NtWRKY4.
- AAC37515.1 L44134 *Cucumis sativus*
DESCRIPTION: SPF1-like DNA-binding protein.

- AAK16171.1 AC079887 *Oryza sativa*
DESCRIPTION: putative DNA-binding protein. OSJNBa0040E01.10.
- 5
- AAF23898.1 AF193802 *Oryza sativa*
DESCRIPTION: zinc finger transcription factor WRKY1.
- 10
- AAD16138.1 AF096298 *Nicotiana tabacum*
DESCRIPTION: DNA-binding protein 1. WRKY1. transcription factor.
- 15
- AAC49529.1 U58540 *Petroselinum crispum*
DESCRIPTION: WRKY2. Contains two WRKY domains; WRKY-type DNA-binding protein.
- 20
- CAB97004.1 AJ278507 *Solanum tuberosum*
DESCRIPTION: putative transcription factor. WRKY DNA binding protein. WRKY1.
- 25
- BAB19075.1 AP002744 *Oryza sativa*
DESCRIPTION: putative DNA-binding protein homolog. P0006C01.17.
- 30
- BAB19096.1 AP002839 *Oryza sativa*
DESCRIPTION: putative DNA-binding protein homolog. P0688A04.2.
- 35
- AAK16170.1 AC079887 *Oryza sativa*
DESCRIPTION: putative DNA binding protein. OSJNBa0040E01.4.
- 40
- BAB40073.1 AP003074 *Oryza sativa*
DESCRIPTION: putative WRKY DNA binding protein. OSJNBa0004G10.20. contains EST C26525(C12525).
- 45
- AAD38283.1 AC007789 *Oryza sativa*
DESCRIPTION: putative WRKY DNA binding protein. OSJNBa0049B20.9.
- 50
- BAB18313.1 AP002865 *Oryza sativa*

DESCRIPTION: putative WRKY DNA binding protein. P0034C11.1. contains
EST
C26525(C12525).

5

CAA88331.1 Z48431 Avena fatua
DESCRIPTION: binds conserved cis-element from cereal alpha-Amy2
promoters. DNA-binding protein.

10

AAC49528.1 U56834 Petroselinum crispum
DESCRIPTION: DNA-binding. WRKY3. WRKY-type DNA-binding protein.

15

AAG35658.1 AF204925 Petroselinum crispum
DESCRIPTION: transcription factor WRKY4. WRKY4. binds to W box
(TTGACC)
elements.

20

BAB16432.1 AB041520 Nicotiana tabacum
DESCRIPTION: WRKY transcription factor Nt-SubD48. Nt-SubD48.

25

AAD32676.1 AF140553 Avena sativa
DESCRIPTION: DNA-binding protein WRKY3. wrky3. putative transcription
factor.

30

AAG46150.1 AC018727 Oryza sativa
DESCRIPTION: putative DNA-binding protein. OSJNBa0056G17.18.

35

BAA77358.1 AB020023 Nicotiana tabacum
DESCRIPTION: WRKY domain Zn-finger type DNA-binding protein. DNA-
binding
protein NtWRKY3.

40

AAG35659.1 AF204926 Petroselinum crispum
DESCRIPTION: transcription factor WRKY5. WRKY5. binds to W box
(TTGACC)
elements.

45

- AAD27591.1 AF121354 *Petroselinum crispum*
 DESCRIPTION: binds sequence specifically to W Boxes (TTGACC).
 transcription factor. WRKY3. sequence specific DNA-binding protein.
- 5 CAB66338.1 AJ279697 *Betula pendula*
 DESCRIPTION: wrky-type DNA binding protein. wrky.
- 10 AAF61864.1 AF193771 *Nicotiana tabacum*
 DESCRIPTION: DNA-binding protein 4. WRKY4. transcription factor.
- 15 BAA87069.1 AB035271 *Matricaria chamomilla*
 DESCRIPTION: elicitor-induced DNA-binding protein homolog. McWRKY1.
- 20 AAF61863.1 AF193770 *Nicotiana tabacum*
 DESCRIPTION: DNA-binding protein 3. WRKY3. transcription factor.
- 910

 AAC09420.1 M68929 Mitochondrion *Marchantia polymorpha*
 DESCRIPTION: rps14.
- 25 CAA33994.1 X15901 Plastid *Oryza sativa*
 DESCRIPTION: ribosomal protein S14. rps14.
- 30 911

 CAA55128.1 X78325 *Nicotiana tabacum*
 DESCRIPTION: chitinase/lysozyme. Pz.
- 35 CAA54373.1 X77110 *Nicotiana tabacum*
 DESCRIPTION: chitinase, class V. chi-V.
- 40 CAA54374.1 X77111 *Nicotiana tabacum*
 DESCRIPTION: chitinase, class V. chi-V.
- 912

 45 CAB55394.1 AL117264 *Oryza sativa*
 DESCRIPTION: zwh0010.1. similar to Arabidopsis germin-like protein 6

(AF032976); Method: conceptual translation with partial peptide sequencing.

5 BAA78563.1 AB024338 *Atriplex lentiformis*
DESCRIPTION: germin-like protein.

10 AAB97470.1 AF042489 *Oryza sativa*
DESCRIPTION: germin-like protein 16. glp16.

15 AAA33030.1 M93041 *Mesembryanthemum crystallinum*
DESCRIPTION: germin-like protein. germin-like protein.

CAB65371.1 AJ250834 *Pisum sativum*
DESCRIPTION: germin-like protein. ger2b. 2nd variant of the clone PsGER2.

20 CAB55559.1 AJ237943 *Triticum aestivum*
DESCRIPTION: germin-like protein. glp2b.

25 CAB65370.1 AJ250833 *Pisum sativum*
DESCRIPTION: germin-like protein. ger2a. 1st variant of this clone.

30 CAB55558.1 AJ237942 *Triticum aestivum*
DESCRIPTION: germin-like protein. glp2a.

35 AAD43971.1 AF141878 *Oryza sativa*
DESCRIPTION: germin-like protein 1 precursor. RGLP1. similar to barley epidermis/papilla-specific oxalate oxidase-like protein.

40 AAD43973.1 AF141880 *Oryza sativa*
DESCRIPTION: germin-like protein 1 precursor. RGLP1. similar to barley epidermis/papilla-specific oxalate oxidase-like protein.

45 AAC04837.1 AF032976 *Oryza sativa*
DESCRIPTION: germin-like protein 6. GER6. similar to wheat and barley oxalate oxidase.

AAG00425.1 AF250933 Hordeum vulgare
DESCRIPTION: germin A. GerA. apoplastic protein; contains prepeptide for
targeting into the cell wall.

5

AAD43972.1 AF141879 Oryza sativa
DESCRIPTION: germin-like protein 2 precursor. RGLP2. similar to barley
epidermis/papilla-specific oxalate oxidase-like protein.

10

CAA63659.1 X93171 Hordeum vulgare
DESCRIPTION: oxalate oxidase-like protein or germin-like protein.

15

AAC04833.1 AF032972 Oryza sativa
DESCRIPTION: germin-like protein 2. GER2. similar to wheat and barley
oxalate oxidase.

20

AAC04834.1 AF032973 Oryza sativa
DESCRIPTION: germin-like protein 3. GER3. similar to wheat and barley
oxalate oxidase.

25

AAC04832.1 AF032971 Oryza sativa
DESCRIPTION: germin-like protein 1. GER1. similar to wheat and barley
oxalate oxidase.

30

AAG00426.1 AF250934 Hordeum vulgare
DESCRIPTION: germin B. GerB. apoplastic protein; contains prepeptide for
targeting into the cell wall.

35

AAG00427.1 AF250935 Hordeum vulgare
DESCRIPTION: germin F. GerF. apoplastic protein; contains prepeptide for
targeting into the cell wall.

40

AAF34811.1 AF005084 Triticum aestivum
DESCRIPTION: oxalate oxidase. up-regulated by aluminum.

45

AAC04835.1 AF032974 Oryza sativa
DESCRIPTION: germin-like protein 4. GER4. similar to wheat and barley

oxalate oxidase.

- 5 BAB39965.1 AP003018 Oryza sativa
DESCRIPTION: probable germin protein 4. OSJNBa0004B13.19. contains ESTs
AU101991(S4037),AU070167(R0031).
- 10 BAB39980.1 AP003020 Oryza sativa
DESCRIPTION: probable germin protein 4. P0498A12.8. contains ESTs
AU101991(S4037),AU070167(R0031).
- 15 AAG00428.1 AF250936 Hordeum vulgare
DESCRIPTION: germin D. GerD. apoplastic protein; contains prepeptide for targeting into the cell wall.
- 20 AAA20245.1 U01963 Hordeum vulgare
DESCRIPTION: germin subunit.
- 25 CAC19429.1 AJ291825 Lolium perenne
DESCRIPTION: oxalate oxidase. oxO1.
- 30 AAA34270.1 M63223 Triticum aestivum
DESCRIPTION: germin. germin 9f-2.8.
- 35 AAA34268.1 M21962 Triticum aestivum
DESCRIPTION: germin protein precursor.
- CAA74595.1 Y14203 Hordeum vulgare
DESCRIPTION: oxalate oxidase.
- 40 AAG00429.1 AF250937 Hordeum vulgare
DESCRIPTION: germin E. GerE. apoplastic protein.
- 45 CAB65369.1 AJ250832 Pisum sativum
DESCRIPTION: germin-like protein. ger1.

oxalate oxidase.

5 AAC99473.1 AF039201 Pinus caribaea
DESCRIPTION: germin-like protein. PcGER1.

10 CAA71051.1 Y09916 Triticum aestivum
DESCRIPTION: germin homolog. pSBGer2.

AAC05146.1 AF049065 Pinus radiata
DESCRIPTION: germin-like protein. PRGer1.

15 CAC34417.1 AJ311624 Pisum sativum
DESCRIPTION: Germin-like protein. glp3.

915
20 -----
BAB19363.1 AP002542 Oryza sativa
DESCRIPTION: putative beta-1,3-glucanase. P0679C08.2.

25 AAD10386.1 U72255 Oryza sativa
DESCRIPTION: beta-1,3-glucanase precursor. Gns9.

30 CAB85903.1 AJ251646 Pisum sativum
DESCRIPTION: hydrolysis of beta-1,3 conjugated glucans. beta-1,3
glucanase. gns2.

35 AAA90953.1 U30323 Triticum aestivum
DESCRIPTION: beta 1,3-glucanase. Glc1.

40 BAA89481.1 AB029462 Salix gilgiana
DESCRIPTION: beta-1,3-glucanase. SgGN1.

BAB40807.1 AB052291 Pyrus pyrifolia
DESCRIPTION: catalyzing the hydrolysis of 1,3-beta-glucosyl linkages.
endo-1,3-beta-glucanase-like protein. bgn-1. Amino acid alignment of the
45 protein(BGN-1) encoded by pear pollen bgn-1 with barley
endo-1,3-beta-glucanase(GII. accession number: pdb/1GHS-B/2.3/2/306/N/)(40%

identity) and their hydrophobic cluster analysis(HCA)(a overall HCA
homology score of 87.1%) showed that it was most likely that the bgn-1
encoded a endo-1,3-beta-glucanase. A higher identity(59.3%) was found
between BGN-1 and a putative pea endo-1,3-beta-glucanase (accession
number:dad/AJ251646-1).

AAB82772.2 AF001523 Musa acuminata
DESCRIPTION: beta-1, 3-glucanase. similar to beta-1, 3-glucanase.

CAA49513.1 X69887 Brassica napus
DESCRIPTION: beta-1,3-glucanase homologue.

AAF08679.1 AF004838 Musa acuminata
DESCRIPTION: beta-1,3-glucanase.

CAA82271.1 Z28697 Nicotiana tabacum
DESCRIPTION: beta-1,3-glucanase.

AAD10384.1 U72253 Oryza sativa
DESCRIPTION: beta-1,3-glucanase precursor. Gns7.

CAB71021.1 AJ271598 Hieracium piloselloides
DESCRIPTION: putative role in callose degradation. putative
beta-1,3-glucanase. gluc.

CAA30261.1 X07280 Nicotiana plumbaginifolia
DESCRIPTION: beta-glucanase.

AAA51643.1 M23120 Nicotiana plumbaginifolia
DESCRIPTION: beta-glucanase precursor.

AAA87456.1 U22147 Hevea brasiliensis
DESCRIPTION: beta-1,3-glucanase. HGN1. hydrolytic enzyme.

AAA34078.1 M63634 Nicotiana plumbaginifolia
DESCRIPTION: regulator of beta(1,3)-glucanase. beta(1,3)-glucanase

regulator.

- 5 AAD10385.1 U72254 *Oryza sativa*
DESCRIPTION: beta-1,3-glucanase precursor. Gns8.
- 10 CAB38443.1 AJ133470 *Hevea brasiliensis*
DESCRIPTION: beta-1,3-glucanase. hgn1.
- AAB03501.1 U41323 *Glycine max*
DESCRIPTION: beta-1,3-glucanase. SGN1.
- 15 AAA32939.1 M62907 *Hordeum vulgare*
DESCRIPTION: hydrolysis of beta-(1-3)-glucan. (1-3)-beta-glucanase.
cBGL32.
- 20 AAD33881.1 AF141654 *Nicotiana tabacum*
DESCRIPTION: beta-1,3-glucanase. GGL4.
- 25 AAA03617.1 M80604 *Lycopersicon esculentum*
DESCRIPTION: beta-1,3-glucanase.
- 30 BAA77786.1 AB027431 *Oryza sativa*
DESCRIPTION: beta-1,3-glucanase.
- BAA77787.1 AB027432 *Oryza sativa*
DESCRIPTION: beta-1,3-glucanase.
- 35 CAB91554.1 AJ277900 *Vitis vinifera*
DESCRIPTION: beta 1-3 glucanase. gl.
- 40 AAC14399.1 AF030771 *Hordeum vulgare*
DESCRIPTION: beta-1,3-glucanase 2. BGL32.
- 45 CAA03908.1 AJ000081 *Citrus sinensis*
DESCRIPTION: glucan hydrolase. beta-1,3-glucanase. gns1.

AAG24921.1 AF311749 Hevea brasiliensis
 DESCRIPTION: beta-1,3-glucanase.
 5

AAA33946.1 M37753 Glycine max
 DESCRIPTION: beta-1,3-endoglucanase (EC 3.2.1.39).
 10

AAA63542.1 M59443 Nicotiana tabacum
 DESCRIPTION: acidic beta-1,3-glucanase. glucanase.
 15

AAD28732.1 AF112965 Triticum aestivum
 DESCRIPTION: beta-1,3-glucanase precursor. Glb3.
 20

AAD10381.1 U72250 Oryza sativa
 DESCRIPTION: beta-1,3-glucanase precursor. Gns4.
 25

CAA57255.1 X81560 Nicotiana tabacum
 DESCRIPTION: (1-)-beta-glucanase. Sp41a.
 30

AAD33880.1 AF141653 Nicotiana tabacum
 DESCRIPTION: beta-1,3-glucanase. GGL1.
 35

AAB86541.1 AF030166 Oryza sativa
 DESCRIPTION: glucanase. glul.
 40

AAA63539.1 M60402 Nicotiana tabacum
 DESCRIPTION: glucan beta-1,3-glucanase. glucanase GLA.
 45

AAA34053.1 M60464 Nicotiana tabacum
 DESCRIPTION: beta-1,3-glucanase.
 45

AAD10380.1 U72249 Oryza sativa
 DESCRIPTION: beta-1,3-glucanase precursor. Gns3.
 45

AAA63540.1 M60403 *Nicotiana tabacum*
DESCRIPTION: glucan-1,3-beta-glucosidase. glucanase GLB.

916

5

AAA85440.1 U32624 *Sorghum bicolor*
DESCRIPTION: cytochrome P-450. CYP79. P450TYR; N-hydroxylase.

10 AAF27289.1 AF140613 *Manihot esculenta*
DESCRIPTION: N-hydroxylating cytochrome P450. CYP79D1.

15 AAF27290.1 AF140614 *Manihot esculenta*
DESCRIPTION: N-hydroxylating cytochrome P450. CYP79D2.

AAD03415.1 AF069494 *Sinapis alba*
DESCRIPTION: converts tyrosine to para-hydrophenylacetaldoxime in
20 para-hydroxybenzylglucosinolate biosynthesis. cytochrome P450. CYP79B1.

AAG59648.1 AC084319 *Oryza sativa*
DESCRIPTION: putative cytochrome p450tyr. OSJNBa0004B24.15.
25

AAF66543.1 AF140609 *Triglochin maritimum*
DESCRIPTION: cytochrome P450 CYP79E1. CYP79E1.

30 AAF66544.1 AF140610 *Triglochin maritimum*
DESCRIPTION: cytochrome P450 CYP79E2. CYP79E2.

35 BAA92894.1 AB006790 *Petunia x hybrida*
DESCRIPTION: cytochrome P450. IMT-2.

AAB94587.1 AF022458 *Glycine max*
40 DESCRIPTION: CYP98A2p. CYP98A2. cytochrome P450 monooxygenase.

AAC32274.1 AF081575 *Petunia x hybrida*
DESCRIPTION: flavonoid 3',5'-hydroxylase. Hf1. P450 enzyme.
45

AAD56282.1 AF155332 *Petunia x hybrida*
DESCRIPTION: flavonoid 3'-hydroxylase. Ht1. cytochrome P450; CYP75B2.

5 CAA64635.1 X95342 *Nicotiana tabacum*
DESCRIPTION: cytochrome P450. hsr515. hypersensitivity-related gene.

10 CAA50155.1 X70824 *Solanum melongena*
DESCRIPTION: flavonoid hydroxylase (P450). CYP75.

15 AAG44132.1 AF218296 *Pisum sativum*
DESCRIPTION: cytochrome P450. P450 isolog.

20 AAA32913.1 M32885 *Persea americana*
DESCRIPTION: cytochrome P-450LXXIA1 (cyp71A1).

BAA84071.1 AB028151 *Antirrhinum majus*
DESCRIPTION: flavone synthase II. cytochrome P450. AFNS2.

25 AAD38930.1 AF135485 *Glycine max*
DESCRIPTION: cytochrome P450 monooxygenase CYP93D1. CYP93E1.

30 AAB17562.1 U72654 *Eustoma grandiflorum*
DESCRIPTION: flavonoid 3'5'-hydroxylase. F3'5'H. cytochrome P450; CYP75.

35 AAG34695.1 AF313492 *Matthiola incana*
DESCRIPTION: putative cytochrome P450.

CAA65580.1 X96784 *Nicotiana tabacum*
DESCRIPTION: cytochrome P450. hsr515.

40 BAA93634.1 AB025016 *Lotus japonicus*
DESCRIPTION: cytochrome P450.

45 CAA71513.1 Y10489 *Glycine max*
DESCRIPTION: putative cytochrome P450.

- 5 AAB94590.1 AF022461 Glycine max
DESCRIPTION: CYP82C1p. CYP82C1. cytochrome P450 monooxygenase.
- CAA71876.1 Y10982 Glycine max
DESCRIPTION: putative cytochrome P450.
- 10 BAA12159.1 D83968 Glycine max
DESCRIPTION: Cytochrome P-450 (CYP93A1).
- 15 AAG14962.1 AF214008 Brassica napus
DESCRIPTION: cytochrome p450-dependent monooxygenase. BNF5H2.
- 20 BAA74465.1 AB022732 Glycyrrhiza echinata
DESCRIPTION: cytochrome P450. CYP Ge-31.
- 25 BAA22422.1 AB001379 Glycyrrhiza echinata
DESCRIPTION: cytochrome P450. CYP81E1.
- AAG14961.1 AF214007 Brassica napus
DESCRIPTION: cytochrome p450-dependent monooxygenase. BNF5H1.
- 30 CAA04117.1 AJ000478 Helianthus tuberosus
DESCRIPTION: fatty acid in-chain hydroxylase. cytochrome P450. CYP81B1l.
chimeric sequence (from 5'-race).
- 35 CAA04116.1 AJ000477 Helianthus tuberosus
DESCRIPTION: fatty acid in-chain hydroxylase. cytochrome P450. CYP81B1c.
- 40 AAB94593.1 AF022464 Glycine max
DESCRIPTION: CYP77A3p. CYP77A3. cytochrome P450 monooxygenase.
- 45 BAA13076.1 D86351 Glycine max
DESCRIPTION: cytochrome P-450 (CYP93A2).

CAA50647.1 X71656 Solanum melongena
DESCRIPTION: P450 hydroxylase.

5 918

CAA06223.1 AJ004923 Lycopersicon esculentum
DESCRIPTION: Squalene epoxidase. ERG.

10 919

AAF71823.1 AF153276 Populus tremula x Populus tremuloides
DESCRIPTION: pumilio domain-containing protein PPD1. PPD1. similar to
Drosophila pumilio protein RNA-binding domain.

15

920

BAA82393.1 AP000367 Oryza sativa
DESCRIPTION: EST C96716(C10608) corresponds to a region of the predicted
gene.; Similar to putative receptor protein kinase. (AC002334).

20

CAC20842.1 AJ250467 Pinus sylvestris
DESCRIPTION: receptor protein kinase. upk.

25

AAB36558.1 U77888 Ipomoea nil
DESCRIPTION: receptor-like protein kinase INRPK1. inrpk1. leucine-rich
repeat.

30

AAF91324.1 AF244890 Glycine max
DESCRIPTION: receptor-like protein kinase 3. RLK3. GmRLK3.

35

BAB40094.1 AP003210 Oryza sativa
DESCRIPTION: putative receptor protein kinase. OSJNBa0010K01.7.

40 AAF91322.1 AF244888 Glycine max

DESCRIPTION: receptor-like protein kinase 1. RLK1. GmRLK1.

AAC36318.1 AF053127 Malus x domestica

45 DESCRIPTION: leucine-rich receptor-like protein kinase. LRPKm1.

- BAA84787.1 AP000559 *Oryza sativa*
 DESCRIPTION: ESTs C22657(S0014),C22656(S0014) correspond to a region
 of
 5 the predicted gene.; Similar to receptor protein kinase, ERECTA
 (AC004484).
- BAA83373.1 AP000391 *Oryza sativa*
 10 DESCRIPTION: ESTs C22657(S0014),C22656(S0014) correspond to a region
 of
 the predicted gene.; Similar to receptor protein kinase, ERECTA
 (AC004484).
- 15 AAF59905.1 AF197946 *Glycine max*
 DESCRIPTION: receptor protein kinase-like protein. CLV1A.
- 20 AAK27806.1 AC022457 *Oryza sativa*
 DESCRIPTION: putative protein kinase. OSJNBa0006L06.21.
- 25 AAF91323.1 AF244889 *Glycine max*
 DESCRIPTION: receptor-like protein kinase 2. RLK2. GmRLK2.
- 30 AAF34426.1 AF172282 *Oryza sativa*
 DESCRIPTION: leucine rich repeat containing protein kinase. DUPR11.16.
- 35 AAK27817.1 AC022457 *Oryza sativa*
 DESCRIPTION: putative protein kinase. OSJNBa0006L06.16.
- CAA61510.1 X89226 *Oryza sativa*
 DESCRIPTION: leucine-rich repeat/receptor protein kinase. Irk2.
- 40 BAB03621.1 AP002522 *Oryza sativa*
 DESCRIPTION: putative protein kinase Xa21. P0009G03.21.
- 45 AAB82755.1 U72725 *Oryza longistaminata*
 DESCRIPTION: receptor kinase-like protein. Xa21 gene family member A1;
 downstream of microsatellite region; disease resistance gene family

member.

5 BAB03629.1 AP002522 Oryza sativa
DESCRIPTION: putative protein kinase Xa21. P0009G03.30.

10 AAB61708.1 U93048 Daucus carota
DESCRIPTION: somatic embryogenesis receptor-like kinase. SERK.

15 AAF66615.1 AF142596 Nicotiana tabacum
DESCRIPTION: LRR receptor-like protein kinase.

AAB82756.1 U72724 Oryza sativa
DESCRIPTION: receptor kinase-like protein. Xa21 gene family member E.

20 CAB51480.1 Y14600 Sorghum bicolor
DESCRIPTION: putative protein serine /threonine kinase. RLK1. accumulates
in mesophyll cells.

25 BAB39873.1 AP002882 Oryza sativa
DESCRIPTION: putative protein kinase. P0439B06.8. contains ESTs
AU056701(S20808),AU056702(S20808).

30 BAB18321.1 AP002865 Oryza sativa
DESCRIPTION: putative receptor protein kinase. P0034C11.11.

35 BAB40081.1 AP003074 Oryza sativa
DESCRIPTION: putative receptor protein kinase. OSJNBa0004G10.30.

40 AAD38286.1 AC007789 Oryza sativa
DESCRIPTION: putative protein kinase. OSJNBa0049B20.13.

45 BAB21240.1 AP002953 Oryza sativa
DESCRIPTION: Putative protein kinase. P0426D06.20. contains ESTs
C22359(C11461),C22360(C11461).

AAK21965.1 AY028699 Brassica napus
DESCRIPTION: receptor protein kinase PERK1.

5 BAA87853.1 AP000816 Oryza sativa
DESCRIPTION: EST AU030604(E51294) corresponds to a region of the
predicted gene. Similar to putative NAK-like Ser/Thr protein kinase.
(AF001308).

10 BAB16871.1 AP002537 Oryza sativa
DESCRIPTION: putative protein kinase APK1A Arabidopsis thaliana.
P0001B06.24. contains ESTs C22608(R3192),D25110(R3192).

15 AAC27894.1 AF023164 Zea mays
DESCRIPTION: leucine-rich repeat transmembrane protein kinase 1. ltk1.

20 AAK00425.1 AC069324 Oryza sativa
DESCRIPTION: Putative protein kinase. OSJNBa0071K19.11.

25 AAG59657.1 AC084319 Oryza sativa
DESCRIPTION: putative protein kinase. OSJNBa0004B24.20.

30 BAA94519.1 AP001800 Oryza sativa
DESCRIPTION: ESTs AU032341(R3918),AU071016(R10613) correspond to a
region
of the predicted gene. Similar to Arabidopsis thaliana chromosome 4, BAC
F9D16; putative receptor kinase (AL035394).

35 BAB07903.1 AP002835 Oryza sativa
DESCRIPTION: putative receptor kinase. P0417G05.10. contains ESTs
AU032341(R3918),AU071016(R10613).

40 921

BAA96250.1 AB027617 Pyrus pyrifolia
DESCRIPTION: UDP-glucose pyrophosphorylase.

45 BAA25917.1 AB013353 Pyrus pyrifolia
DESCRIPTION: UDP-glucose pyrophosphorylase.

- CAA62689.1 X91347 *Hordeum vulgare*
 DESCRIPTION: UDP-glucose pyrophosphorylase.
- 5
- AAF62555.1 AF249880 *Oryza sativa* subsp. *indica*
 DESCRIPTION: UDP-glucose pyrophosphorylase. UDPGase.
- 10 922
-
- AAD03415.1 AF069494 *Sinapis alba*
 DESCRIPTION: converts tyrosine to para-hydroxyphenylacetaldoxime in
 para-hydroxybenzylglucosinolate biosynthesis. cytochrome P450. CYP79B1.
- 15
- AAA85440.1 U32624 *Sorghum bicolor*
 DESCRIPTION: cytochrome P-450. CYP79. P450TYR; N-hydroxylase.
- 20
- AAF27289.1 AF140613 *Manihot esculenta*
 DESCRIPTION: N-hydroxylating cytochrome P450. CYP79D1.
- 25
- AAF27290.1 AF140614 *Manihot esculenta*
 DESCRIPTION: N-hydroxylating cytochrome P450. CYP79D2.
- 30
- AAG59648.1 AC084319 *Oryza sativa*
 DESCRIPTION: putative cytochrome p450tyr. OSJNBa0004B24.15.
- 35
- AAF66543.1 AF140609 *Triglochin maritimum*
 DESCRIPTION: cytochrome P450 CYP79E1. CYP79E1.
- 40
- AAF66544.1 AF140610 *Triglochin maritimum*
 DESCRIPTION: cytochrome P450 CYP79E2. CYP79E2.
- 45
- BAA92894.1 AB006790 *Petunia x hybrida*
 DESCRIPTION: cytochrome P450. IMT-2.
- AAD56282.1 AF155332 *Petunia x hybrida*
 DESCRIPTION: flavonoid 3'-hydroxylase. Ht1. cytochrome P450; CYP75B2.

- CAA50155.1 X70824 *Solanum melongena*
DESCRIPTION: flavonoid hydroxylase (P450). CYP75.
- 5
- AAC32274.1 AF081575 *Petunia x hybrida*
DESCRIPTION: flavonoid 3',5'-hydroxylase. Hfl. P450 enzyme.
- 10
- AAG34695.1 AF313492 *Matthiola incana*
DESCRIPTION: putative cytochrome P450.
- 15
- AAA32913.1 M32885 *Persea americana*
DESCRIPTION: cytochrome P-450LXXIA1 (cyp71A1).
- 20
- CAA64635.1 X95342 *Nicotiana tabacum*
DESCRIPTION: cytochrome P450. hsr515. hypersensitivity-related gene.
- 25
- CAA65580.1 X96784 *Nicotiana tabacum*
DESCRIPTION: cytochrome P450. hsr515.
- 30
- AAB94587.1 AF022458 *Glycine max*
DESCRIPTION: CYP98A2p. CYP98A2. cytochrome P450 monooxygenase.
- 35
- AAG09208.1 AF175278 *Pisum sativum*
DESCRIPTION: wound-inducible P450 hydroxylase. CYP82A1.
- 40
- AAD37433.1 AF150881 *Lycopersicon esculentum x Lycopersicon peruvianum*
DESCRIPTION: catalyzes the hydroxylation of ferulic acid to 5-hydroxyferulic acid. ferulate-5-hydroxylase. CYP84. cytochrome P450-dependent monooxygenase; F5H; FAH1.
- 45
- CAA04117.1 AJ000478 *Helianthus tuberosus*
DESCRIPTION: fatty acid in-chain hydroxylase. cytochrome P450. CYP81B11.

chimeric sequence (from 5'-race).

CAA04116.1 AJ000477 Helianthus tuberosus
5 DESCRIPTION: fatty acid in-chain hydroxylase. cytochrome P450. CYP81B1c.

CAB43505.1 AJ239051 Cicer arietinum
10 DESCRIPTION: cytochrome P450. cyp81E2.

AAC49188.2 U29333 Pisum sativum
15 DESCRIPTION: cytochrome P450 monooxygenase. CYP82. new cytochrome P450 family.

AAG14963.1 AF214009 Brassica napus
20 DESCRIPTION: cytochrome p450-dependent monooxygenase. BNF5H3.

AAD38930.1 AF135485 Glycine max
25 DESCRIPTION: cytochrome P450 monooxygenase CYP93D1. CYP93E1.

AAG14962.1 AF214008 Brassica napus
DESCRIPTION: cytochrome p450-dependent monooxygenase. BNF5H2.

30 AAG44132.1 AF218296 Pisum sativum
DESCRIPTION: cytochrome P450. P450 isolog.

AAB94588.1 AF022459 Glycine max
35 DESCRIPTION: CYP71D10p. CYP71D10. cytochrome P450 monooxygenase.

AAG14961.1 AF214007 Brassica napus
40 DESCRIPTION: cytochrome p450-dependent monooxygenase. BNF5H1.

AAB94590.1 AF022461 Glycine max
DESCRIPTION: CYP82C1p. CYP82C1. cytochrome P450 monooxygenase.

45 CAA71513.1 Y10489 Glycine max

DESCRIPTION: putative cytochrome P450.

5 BAA84071.1 AB028151 Antirrhinum majus
DESCRIPTION: flavone synthase II. cytochrome P450. AFNS2.

10 CAA50442.1 X71130 Petunia x hybrida
DESCRIPTION: P450 hydroxylase. PET 1.
924

15 BAB20581.1 AB042268 Zea mays
DESCRIPTION: response regulator 6. ZmRR6.

20 AAK14395.1 AF339732 Dianthus caryophyllus
DESCRIPTION: response regulator protein. RR.

BAB20580.1 AB042267 Zea mays
DESCRIPTION: response regulator 5. ZmRR5.

25 BAB20579.1 AB042261 Zea mays
DESCRIPTION: response regulator 4. ZmRR4.

30 BAA85113.1 AB031012 Zea mays
DESCRIPTION: response regulator 2. ZmRR2. cytokinin-inducible.

35 BAA82873.1 AB024291 Zea mays
DESCRIPTION: response regulator. ZmRR2.

BAA75253.1 AB004882 Zea mays
DESCRIPTION: response regulator. ZmCip1, cytokinin-inducible protein.

40 BAA85112.1 AB031011 Zea mays
DESCRIPTION: response regulator 1. ZmRR1. cytokinin-inducible.

45 BAB17300.1 AB042260 Zea mays
DESCRIPTION: response regulator. ZmRR3.

BAB20582.1 AB042269 Zea mays
 DESCRIPTION: response regulator 7. ZmRR7.
 5

BAB41137.1 AB060130 Zea mays
 DESCRIPTION: response regulator 8. ZmRR8.
 10 925

AAA33280.1 L20475 Datura stramonium
 DESCRIPTION: 29kDa protein; high homology to aa sequence of tropinone
 reductases.
 15

AAA33281.1 L20473 Datura stramonium
 DESCRIPTION: catalyses a stereospecific reduction of tropinone to
 tropine. tropinone reductase-I.
 20

BAA85844.1 AB026544 Hyoscyamus niger
 DESCRIPTION: tropinone reductase-I. tr1.
 25

CAC34420.1 AJ307584 Solanum tuberosum
 DESCRIPTION: tropine forming tropinone reductase. tropinone reductase I.
 TRI.
 30

BAA13547.1 D88156 Hyoscyamus niger
 DESCRIPTION: tropinone reductase-I.
 35

AAA33282.1 L20474 Datura stramonium
 DESCRIPTION: catalyses a stereospecific reduction of tropinone to
 pseudotropine. tropinone reductase-II.
 40

BAA85845.1 AB026545 Hyoscyamus niger
 DESCRIPTION: tropinone reductase-II. tr2.
 45

AAB09776.1 L20485 Hyoscyamus niger
 DESCRIPTION: tropinone reductase-II.

DESCRIPTION: enoyl-ACP reductase. enr-T1.

927

- 5 AAD43046.1 AF124045 Sorghum bicolor
DESCRIPTION: GTP-binding protein-like. 110K5.8. terminal exon, defined by
homology to maize ESTs.

928

- 10 CAA09619.1 AJ011418 Lycopersicon esculentum
DESCRIPTION: ubiquitin activating enzyme.

- 15 AAC32140.1 AF051239 Picea mariana
DESCRIPTION: probable ubiquitin activating enzyme 2. Sb53. similar to
Arabidopsis thaliana ubiquitin activating enzyme 2 encoded by GenBank
Accession Number U40566.

- 20 AAA34308.1 M55604 Triticum aestivum
DESCRIPTION: ubiquitin-activating enzyme E1. UBA1.

- 25 AAA34265.1 M90663 Triticum aestivum
DESCRIPTION: ubiquitin activating enyme. E1.

- 30 AAA34266.1 M90664 Triticum aestivum
DESCRIPTION: ubiquitin activating enzyme. E1.

- CAA71762.1 Y10804 Nicotiana tabacum
DESCRIPTION: Ubiquitin activating enzyme E1. UBA1.

35 929

- CAA55693.1 X79086 Zea mays
DESCRIPTION: initiator-binding protein. IBP2.

40

- CAC19789.1 AJ251686 Catharanthus roseus
DESCRIPTION: putative transcription factor. MYB-like DNA-binding protein.
bpf-1.

45

CAA55691.1 X79085 Zea mays
DESCRIPTION: initiator binding protein. IBP1.

- 5 AAF97508.1 AF242298 Oryza sativa
DESCRIPTION: telomere binding protein-1. TBP1.

930

- 10 AAK15447.1 AC037426 Oryza sativa
DESCRIPTION: putative flavin-containing monooxygenase.
OSJNBb0014I11.12.

- 15 AAK15439.1 AC037426 Oryza sativa
DESCRIPTION: putative flavin-containing monooxygenase.
OSJNBb0014I11.8.

- 20 BAA88198.1 AP000837 Oryza sativa
DESCRIPTION: Similar to human dimethylaniline monooxygenase
(AC002376).

- 25 BAA88195.1 AP000837 Oryza sativa
DESCRIPTION: Similar to human dimethylaniline monooxygenase
(AC002376).

- 30 BAB32703.1 AP002902 Oryza sativa
DESCRIPTION: dimethylaniline monooxygenase-like protein. P0492F05.5.
contains EST C72123(E1029).

- 35 BAB07916.2 AP002835 Oryza sativa
DESCRIPTION: dimethylaniline monooxygenase-like protein. P0417G05.24.
contains EST C72123(E1029).

931

- 40 AAG38521.1 AF283536 Citrus x paradisi
DESCRIPTION: cystatin-like protein. cystein proteinase inhibitor.

- 45 AAA97905.1 U51853 Glycine max
DESCRIPTION: cysteine proteinase inhibitor.

CAA79954.1 Z21954 *Vigna unguiculata*
DESCRIPTION: cysteine proteinase inhibitor.

5

AAB66355.1 U54702 *Oryza sativa*
DESCRIPTION: thiol proteinase inhibitor; cysteine proteinase inhibitor.
oryzacystatin. has potential for insect resistance in rice and for cancer
10 therapeutics.

AAB24010.1 S49967 *Oryza*
DESCRIPTION: oryzacystatin. oryzacystatin. cysteine protease inhibitor;
15 This sequence comes from Fig. 1.

CAA60610.1 X87126 *Zea mays*
DESCRIPTION: cysteine proteinase inhibitor. zmc-II.

20

BAA09666.1 D63342 *Zea mays*
DESCRIPTION: cysteine proteinase inhibitor. gCC.

25

AAA32672.1 L16624 *Ambrosia artemisiifolia*
DESCRIPTION: cystatin proteinase inhibitor.

30

BAA07327.1 D38130 *Zea mays*
DESCRIPTION: inhibition against cysteine proteinases. cystatin II.

35

AAA97907.1 U51855 *Glycine max*
DESCRIPTION: cysteine proteinase inhibitor.

40

BAB18766.1 AB038392 *Triticum aestivum*
DESCRIPTION: cysteine proteinase inhibitor. WC61. cystatin.

BAB18767.1 AB038393 *Triticum aestivum*
DESCRIPTION: cysteine proteinase inhibitor. WC92. cystatin.

45

CAA11899.1 AJ224331 *Castanea sativa*

DESCRIPTION: cysteine proteinase inhibitor. cystatin.

AAB71505.1 U82220 *Pyrus communis*

5 DESCRIPTION: cysteine protease inhibitor.

AAA79239.1 L48182 *Brassica rapa*

10 DESCRIPTION: cysteine proteinase inhibitor. N-terminal deletion clone; putative.

CAA60634.1 X87168 *Sorghum bicolor*

15 DESCRIPTION: cysteine proteinase inhibitor. CPI1.

AAA68150.1 L42819 *Brassica rapa*

20 DESCRIPTION: cysteine protenase inhibitor. N-terminal deletion clone; putative.

BAB18765.1 AB038391 *Triticum aestivum*

25 DESCRIPTION: cysteine proteinase inhibitor. gWC2. cystatin.

BAB18768.1 AB038394 *Triticum aestivum*

DESCRIPTION: cysteine proteinase inhibitor. WC83. cystatin.

30 AAC37479.1 L41355 *Brassica rapa*

DESCRIPTION: cysteine proteinase inhibitor.

BAA28867.1 AB014760 *Cucumis sativus*

35 DESCRIPTION: root-specific cystein protease inhibitor. cystein proteinase inhibitor.

AAD33907.1 AF143677 *Artemisia vulgaris*

40 DESCRIPTION: cysteine proteinase inhibitor. CPI. pollen cystatin.

BAA89582.1 AP001073 *Oryza sativa*

45 a DESCRIPTION: ESTs AU067919(C10906),AU067918(C10906) correspond to region of the predicted gene. Similar to cysteine proteinase inhibitor

(D31700).

- CAA72790.1 Y12068 Hordeum vulgare
5 DESCRIPTION: cysteine proteinase inhibitor. CPI.
- AAA96316.1 U51119 Brassica rapa
10 DESCRIPTION: cysteine proteinase inhibitor. BCPI-2.
- AAK15090.1 AF240007 Sesamum indicum
DESCRIPTION: cystatin. cysteine proteinase inhibitor.
- 15 AAF23127.1 AF198389 Lycopersicon esculentum
DESCRIPTION: cysteine proteinase inhibitor. cystatin. STC. expression
induced by arachidonic acid and gamma linolenic acid.
- 20 BAA19610.1 D64115 Glycine max
DESCRIPTION: cysteine proteinase inhibitor. cystatin.
- 25 BAA19608.1 D31700 Glycine max
DESCRIPTION: cysteine proteinase inhibitor. cystatin.
- 30 CAA89697.1 Z49697 Ricinus communis
DESCRIPTION: cysteine proteinase inhibitor.
- AAF72202.1 AF265551 Manihot esculenta
35 DESCRIPTION: cysteine protease inhibitor.
- AAA97906.1 U51854 Glycine max
DESCRIPTION: cysteine proteinase inhibitor.
- 40 CAA50437.1 X71124 Carica papaya
DESCRIPTION: cysteine proteinase inhibitor (cystatin).
- 45 AAF23126.1 AF198388 Lycopersicon esculentum
DESCRIPTION: cysteine proteinase inhibitor. cystatin. LTC. expression

induced by arachidonic acid and gamma linolenic acid.

- 5 AAD13812.1 AF117334 *Ipomoea batatas*
DESCRIPTION: cysteine proteinase inhibitor. cystatin.
- 10 AAF64480.1 AF241536 *Ipomoea batatas*
DESCRIPTION: cysteine protease inhibitor. CYSPI.
- 15 AAK30004.1 AY028994 *Dianthus caryophyllus*
DESCRIPTION: cysteine proteinase inhibitor. DC-CPI.
- 20 BAB18769.1 AB038395 *Triticum aestivum*
DESCRIPTION: cysteine proteinase inhibitor. WC81. cystatin.
- 938

- 25 AAC32853.1 AF083253 *Lycopersicon esculentum*
DESCRIPTION: cysteine protease inhibitor.
- 940

- 30 BAB17350.1 AP002747 *Oryza sativa*
DESCRIPTION: putative nodulin. P0698G03.34. contains ESTs
D39891(S1543),D41717(S4395),AU033037(S1543).
- 35 BAA85440.1 AP000616 *Oryza sativa*
DESCRIPTION: ESTs AU055729(S20023),AU055730(S20023) correspond to a
region of the predicted gene.; similar to Medicago nodulin N21-like
protein (AC004218).
- 40 CAB53493.1 AJ245900 *Oryza sativa*
DESCRIPTION: CAA303720.1 protein. q3037.20. Similar to Medicago nodulin
N21 (MtN21).
- 45 941

- BAA21921.1 AB006599 Petunia x hybrida
DESCRIPTION: ZPT2-12. C2H2 zinc finger protein, 2 finger.
- 5 BAA21922.1 AB006600 Petunia x hybrida
DESCRIPTION: ZPT2-13. C2H2 zinc finger protein, 2finger.
- 10 BAA19110.1 AB000451 Petunia x hybrida
DESCRIPTION: PETHy;ZPT2-5. Cys(2) His(2) zinc finger protein, 2 fingers.
- 15 BAA21923.1 AB006601 Petunia x hybrida
DESCRIPTION: ZPT2-14. C2H2 zinc finger protein, 2 finger.
- 20 BAA21925.1 AB006603 Petunia x hybrida
DESCRIPTION: ZPT2-8. C2H2 zinc finger protein, 2 finger.
- BAA21924.1 AB006602 Petunia x hybrida
DESCRIPTION: ZPT2-7. C2H2 zinc finger protein, 2finger.
- 25 BAA21920.1 AB006598 Petunia x hybrida
DESCRIPTION: ZPT2-11. C2H2 zinc finger protein, 2finger.
- 30 CAA60828.1 X87374 Pisum sativum
DESCRIPTION: putative zinc finger protein.
- 35 BAA19111.1 AB000452 Petunia x hybrida
DESCRIPTION: PETHy;ZPT2-6. Cys(2) His(2) zinc finger protein, 2 fingers.
- 40 BAA21926.1 AB006604 Petunia x hybrida
DESCRIPTION: ZPT2-9. C2H2 zinc finger protein, 2 finger.
- 45 BAA21927.1 AB006605 Petunia x hybrida
DESCRIPTION: ZPT3-3. C2H2 zinc finger protein, 3 finger.
- BAA96071.1 AB035133 Petunia x hybrida
DESCRIPTION: C2H2 zinc-finger protein ZPT3-3. ZPT3-3.

- 5 BAA21919.1 AB006597 *Petunia x hybrida*
DESCRIPTION: ZPT2-10. C2H2 zinc finger protein, 2 finger.
- 10 BAA96070.1 AB035132 *Petunia x hybrida*
DESCRIPTION: C2H2 zinc-finger protein ZPT2-10. PETHy;ZPT2-10.
- 15 CAB77055.1 Y18788 *Medicago sativa*
DESCRIPTION: putative TFIIIA (or kruppel)-like zinc finger protein.
- 20 AAB53260.1 U76554 *Brassica rapa*
DESCRIPTION: transcription factor. zinc-finger protein-1. BR42.
- AAB53261.1 U76555 *Brassica rapa*
DESCRIPTION: zinc-finger protein BcZFP1. BcZFP1(3-2z).
- 25 BAA19114.1 AB000455 *Petunia x hybrida*
DESCRIPTION: PETHy;ZPT4-1. Cys(2) His(2) zinc finger protein, 4 fingers.
- BAA05078.1 D26085 *Petunia x hybrida*
DESCRIPTION: zinc-finger DNA binding protein.
- 30 AAD26942.1 AF119050 *Datisca glomerata*
DESCRIPTION: zinc-finger protein 1. zfp1. DgZFP1.
- 35 BAA05077.1 D26084 *Petunia x hybrida*
DESCRIPTION: zinc-finger DNA binding protein.
- 40 AAB39638.1 U68763 *Glycine max*
DESCRIPTION: putative transcription factor. SCOF-1. scof-1. zinc-finger protein.
- 45 AAC06243.1 AF053077 *Nicotiana tabacum*
DESCRIPTION: transcription factor. osmotic stress-induced zinc-finger protein. zfp.

BAA19112.1 AB000453 Petunia x hybrida
DESCRIPTION: PETHy;ZPT3-1. Cys(2) His(2) zinc finger protein, 3 fingers.

5

AAK01713.1 AF332876 Oryza sativa
DESCRIPTION: zinc finger transcription factor ZF1.

10

BAA05076.1 D26083 Petunia x hybrida
DESCRIPTION: zinc-finger DNA binding protein.

15 BAA05079.1 D26086 Petunia x hybrida
DESCRIPTION: zinc-finger protein.

20 BAA21928.1 AB006606 Petunia x hybrida
DESCRIPTION: ZPT4-4. C2H2 zinc finger protein, 4 finger.

25 BAA19926.1 AB000456 Petunia x hybrida
DESCRIPTION: PETHy; ZPT4-2. C2H2 zinc finger protein, 4 finger.

BAA19113.1 AB000454 Petunia x hybrida
DESCRIPTION: PETHy;ZPT3-2. Cys(2) His(2) zinc finger protein, 3 fingers.

30 945

AAG10793.1 AF296158 Citrus unshiu
DESCRIPTION: beta-carotene hydroxylase. CHX1.

35

AAG33636.1 AF315289 Citrus unshiu
DESCRIPTION: beta-carotene hydroxylase. CHX2. similar to beta-carotene
hydroxylase of Citrus unshiu encoded by GenBank Accession Number
AF296158.

40

AAG10430.1 AF251018 Tagetes erecta
DESCRIPTION: beta hydroxylase.

45

CAB55625.1 Y14809 Lycopersicon esculentum

DESCRIPTION: beta-carotene hydroxylase. CrtR-b1.

CAA70888.1 Y09722 Capsicum annuum

5 DESCRIPTION: beta-carotene hydroxylase 2.

CAB55626.1 Y14810 Lycopersicon esculentum

10 DESCRIPTION: beta-carotene hydroxylase. CrtR-b2.

CAA70427.1 Y09225 Capsicum annuum

DESCRIPTION: beta-carotene hydrolase.

15

CAC06712.1 AJ278882 Narcissus pseudonarcissus

DESCRIPTION: synthesis of zeaxanthin. beta-carotene hydroxylase.

20 AAD54243.1 AF162276 Haematococcus pluvialis

DESCRIPTION: carotenoid hydroxylase.

946

25 AAC18914.1 U94748 Petunia x hybrida

DESCRIPTION: AN11. An11. No functional information available. Protein is involved in transcriptional regulation of anthocyanin biosynthesis in petunia. Protein contains five WD 40 repeats; WD 40 repeat protein.

30 948

AAG52887.1 AF333386 Nicotiana tabacum

DESCRIPTION: beta-expansin-like protein. PPAL. pollen allergen-like protein.

35

AAF72986.1 AF261273 Oryza sativa

DESCRIPTION: putative cell wall loosening activity. beta-expansin. EXPB5.

40

AAF72990.1 AF261277 Oryza sativa

DESCRIPTION: putative cell wall loosening activity. beta-expansin. EXPB9. putative group-1 pollen allergen.

45

BAB20817.1 AB051899 Atriplex lentiformis

DESCRIPTION: beta-expansin. AI-EXP1.

AAAF72984.1 AF261271 Oryza sativa

5 DESCRIPTION: putative cell wall loosening activity. beta-expansin. EXPB3.

AAK15453.1 AC037426 Oryza sativa

10 DESCRIPTION: beta-expansin EXPB3. OSJNBb0014I11.1.

AAAF72991.1 AF261278 Oryza sativa

15 DESCRIPTION: putative cell wall loosening activity. beta-expansin.
EXPB10. putative group-1 pollen allergen.

AAK15442.1 AC037426 Oryza sativa

20 DESCRIPTION: beta-expansin EXPB6. OSJNBb0014I11.3.

AAAF72987.1 AF261274 Oryza sativa

DESCRIPTION: putative cell wall loosening activity. beta-expansin. EXPB6.

25 AAAF72983.1 AF261270 Oryza sativa

DESCRIPTION: putative cell wall loosening activity. beta-expansin. EXPB1.
putative group-1 pollen allergen Ory s1.

30 AAAF72988.1 AF261275 Oryza sativa

DESCRIPTION: putative cell wall loosening activity. beta-expansin. EXPB7.

AAAF72989.2 AF261276 Oryza sativa

35 DESCRIPTION: putative cell wall loosening activity. beta-expansin. EXPB8.

AAAF72985.1 AF261272 Oryza sativa

40 DESCRIPTION: putative cell wall loosening activity. beta-expansin. EXPB4.

AAK15440.1 AC037426 Oryza sativa

DESCRIPTION: beta-expansin EXPB2. OSJNBb0014I11.2.

45

AAB61710.1 U95968 Oryza sativa

DESCRIPTION: beta-expansin. EXPB2. cell wall loosening protein.

- 5 AAB37749.1 U30460 *Cucumis sativus*
DESCRIPTION: expansin S2 precursor. Cs-EXP2. similar to pollen allergen Lol pI, *Lolium perenne*, Swiss-Prot Accession Number P14946; former gene name CuExS2; expansin-30 (Ex30) protein.
- 10 AAD38296.1 AC007789 *Oryza sativa*
DESCRIPTION: putative expansin. OSJNBa0049B20.23.
- 15 BAB18336.1 AP002865 *Oryza sativa*
DESCRIPTION: putative expansin. P0034C11.27.
- 20 CAC19183.1 AJ291816 *Cicer arietinum*
DESCRIPTION: expansin.
- AAG13983.1 AF297522 *Prunus avium*
DESCRIPTION: expansin 2. Exp2. PruavExp2.
- 25 AAG01875.1 AF291659 *Striga asiatica*
DESCRIPTION: alpha-expansin 3. Exp3.
- 30 AAG32920.1 AF184232 *Lycopersicon esculentum*
DESCRIPTION: expansin. Exp8.
- 35 AAC96077.1 AF049350 *Nicotiana tabacum*
DESCRIPTION: involved in acid-growth response. alpha-expansin precursor. Nt-EXP1. cell wall protein.
- 40 AAC96078.1 AF049351 *Nicotiana tabacum*
DESCRIPTION: involved in acid-growth response. alpha-expansin precursor. Nt-EXP2. cell wall protein.
- 45 AAF35902.1 AF230333 *Zinnia elegans*
DESCRIPTION: expansin 3.

BAA88200.1 AP000837 *Oryza sativa*
DESCRIPTION: EST AU078708(E60526) corresponds to a region of the
predicted gene. Similar to expansin (U85246).

AAC39512.1 AF043284 *Gossypium hirsutum*
DESCRIPTION: expansin. GhEX1. contains N-terminal signal peptide.

AAD38297.1 AC007789 *Oryza sativa*
DESCRIPTION: putative expansin. OSJNBa0049B20.24.

AAF32411.1 AF230278 *Triphysaria versicolor*
DESCRIPTION: alpha-expansin 1.

BAB18338.1 AP002865 *Oryza sativa*
DESCRIPTION: putative expansin. P0034C11.29.

AAG32921.1 AF184233 *Lycopersicon esculentum*
DESCRIPTION: expansin. Exp10.

CAC19184.1 AJ291817 *Cicer arietinum*
DESCRIPTION: expansin.

AAC96079.1 AF049352 *Nicotiana tabacum*
DESCRIPTION: involved in acid-growth response. alpha-expansin precursor.
Nt-EXP3. cell wall protein.

950

CAA52213.1 X74115 *Picea abies*
DESCRIPTION: short-chain alcohol dehydrogenase.

AAC35342.1 AF072449 *Ipomoea trifida*
DESCRIPTION: short-chain alcohol dehydrogenase. SSP.
self-incompatibility-locus specific stigma protein.

AAC35340.1 AF072447 *Ipomoea trifida*

DESCRIPTION: short-chain alcohol dehydrogenase. SSP.
self-incompatibility-locus specific stigma protein.

5 CAA11153.1 AJ223177 *Nicotiana tabacum*

DESCRIPTION: short chain alcohol dehydrogenase.

10 CAA11154.1 AJ223178 *Nicotiana tabacum*

DESCRIPTION: short chain alcohol dehydrogenase. SCANT.

AAK29646.1 AF349916 *Solanum tuberosum*

15 DESCRIPTION: putative short-chain type alcohol dehydrogenase. GAN;
similar to tomato Leert10 and maize Ts2.

AAC37345.1 L20621 *Zea mays*

20 DESCRIPTION: alcohol dehydrogenase. short chain.

AAC35341.1 AF072448 *Ipomoea trifida*

25 DESCRIPTION: short-chain alcohol dehydrogenase. SSP.
self-incompatibility-locus specific stigma protein.

AAC35343.1 AF072450 *Ipomoea trifida*

30 DESCRIPTION: short-chain alcohol dehydrogenase. SSP.
self-incompatibility-locus specific stigma protein.

AAB57737.1 U89270 *Tripsacum dactyloides*

35 DESCRIPTION: short-chain alcohol dehydrogenase. gynomonocious sex form
1. similar to *Zea mays* tasselseed 2: SwissProt Accession Number P50160.

AAF89645.1 AF169018 *Glycine max*

40 DESCRIPTION: seed maturation protein PM34. PM34. similar to bacterial
glucose and ribitol dehydrogenase.

AAF04253.1 AF097651 *Pisum sativum*

45 DESCRIPTION: short-chain alcohol dehydrogenase SAD-C. sadC. contains the
entire nucleotide binding motif of 3(alpha), 20(beta)-hydroxysteroid
dehydrogenases, GXXXXXXGXXG(A)XGXXXXA (Ghosh et al., 1991, Proc.
Natl.

Acad. Sci. USA 88, 10064-10068).

AAF04193.1 AF053638 *Pisum sativum*

- 5 DESCRIPTION: short-chain alcohol dehydrogenase. sadA. contains the entire nucleotide binding motif of the 3(alfa),20(beta)-hydroxysteroid dehydrogenase: GXXXXXXGXXG(A)XGXXXA (Ghosh et al. (1991) Proc. Natl. Acad. Sci. USA 88, 10064-10068); similar to *Lycopersicon esculentum* product encoded by GenBank Accession Number U21801 and *Streptomyces hydrogenans* steroid alcohol dehydrogenase.
- 10

AAB57738.1 U89271 *Tripsacum dactyloides*

- 15 DESCRIPTION: short-chain alcohol dehydrogenase. gynomonoecious sex form 1. similar to *Zea mays tasselseed 2*: SwissProt Accession Number P50160.

CAB91875.1 AJ277945 *Lycopersicon esculentum*

- 20 DESCRIPTION: putative alcohol dehydrogenase. yfe37.

AAF04194.1 AF053639 *Pisum sativum*

- 25 DESCRIPTION: short-chain alcohol dehydrogenase. sadB. contains the Prosite pattern no. PS00061 for short-chain alcohol dehydrogenases; contains a deletion in the nucleotide binding motif of the 3(alfa),20(beta)-hydroxysteroid dehydrogenase: GXXXXXXGXXG(A)XGXXXA (Ghosh et al. (1991) Proc. Natl. Acad. Sci. USA 88, 10064-10068).
- 30

AAB00109.1 U21801 *Lycopersicon esculentum*

- DESCRIPTION: alcohol dehydrogenase homolog. GAD3. mRNA is supressed in the presence of gibberellin; similar to nonmetallo-short-chain alcohol dehydrogenases, PIR Accession Number A47542.
- 35

952

40 CAB63264.1 AJ251808 *Lotus japonicus*

DESCRIPTION: calcium-binding protein. cbp1.

AAG43547.1 AF211529 *Nicotiana tabacum*

- 45 DESCRIPTION: Avr9/Cf-9 rapidly elicited protein 31. ACRE31. similar to *Solanum tuberosum* CAST calcium binding protein encoded by GenBank

Accession Number L02830.

5 AAA34014.1 L01432 Glycine max
DESCRIPTION: calcium-binding regulatory protein. calmodulin. SCaM-3.
putative.

10 AAA34013.1 L01430 Glycine max
DESCRIPTION: calcium-binding regulatory protein. calmodulin. SCaM-1.
putative.

15 AAA92681.1 U13882 Pisum sativum
DESCRIPTION: calcium-binding protein. calmodulin.

20 CAA78301.1 Z12839 Lilium longiflorum
DESCRIPTION: calcium binding protein, signal transduction. calmodulin.

25 AAA33397.1 L18912 Lilium longiflorum
DESCRIPTION: calcium binding protein, signal transduction. calmodulin.
putative.

30 AAA19571.1 U10150 Brassica napus
DESCRIPTION: calcium binding. calmodulin. bcm1.

AAA85157.1 U20297 Solanum tuberosum
DESCRIPTION: calcium-binding protein. calmodulin.

35 AAA85156.1 U20296 Solanum tuberosum
DESCRIPTION: calcium-binding protein. calmodulin.

40 AAA62351.1 U20295 Solanum tuberosum
DESCRIPTION: calcium-binding protein. calmodulin.

45 AAA85155.1 U20294 Solanum tuberosum
DESCRIPTION: calcium-binding protein. calmodulin.

AAC49587.1 U49105 *Triticum aestivum*
DESCRIPTION: calmodulin TaCaM4-1. calcium-binding protein.

5 AAC49586.1 U49104 *Triticum aestivum*
DESCRIPTION: calmodulin TaCaM3-3. calcium-binding protein.

10 AAC49585.1 U49103 *Triticum aestivum*
DESCRIPTION: calmodulin TaCaM3-2. calcium-binding protein.

15 AAC49584.1 U48693 *Triticum aestivum*
DESCRIPTION: calmodulin TaCaM3-1. calcium-binding protein.

20 AAC49580.1 U48689 *Triticum aestivum*
DESCRIPTION: calmodulin TaCaM1-3. calcium-binding protein.

AAC49579.1 U48688 *Triticum aestivum*
DESCRIPTION: calmodulin TaCaM1-2. calcium binding protein.

25 AAC49578.1 U48242 *Triticum aestivum*
DESCRIPTION: calmodulin TaCaM1-1. calcium-binding.

30 CAA78287.1 Z12827 *Oryza sativa*
DESCRIPTION: calcium binding protein, signal transduction. calmodulin.

35 AAA03580.1 L01431 *Glycine max*
DESCRIPTION: calcium-binding regulatory protein. calmodulin. SCaM-2.
putative.

40 AAA33901.1 L18913 *Oryza sativa*
DESCRIPTION: calcium binding protein, signal transduction. calmodulin.
putative.

45 AAA34015.1 L01433 *Glycine max*
DESCRIPTION: calcium-binding regulatory protein. calmodulin. SCaM-4.
putative.

Table 27 DESCAl Blast report:

DeCypher Results for: NCBI BLASTX Translated Search against

Genbank nonredundant proteins

Results by Query

5 *Click on a query below to view its search results.*

Your_Query starting with: ACTGCGTACCAATTCTAGAG

Search Details

10 **Results for: Your_Query starting with:**

ACTGCGTACCAATTCTAGAG; (Length=166)

[Return to query summary](#)

	RANK	Sequences producing significant alignments:	(bits)	Value
15	<u>1</u>	gb AAAF18415.1 AF191051 apical membrane antigen 1 [Plasmodium...	30	
	4.4			
	<u>2</u>	gb AAAF18424.1 AF191060 apical membrane antigen 1 [Plasmodium...	30	
	4.4			

20 RANK 1 ITERATION 0>gb|AAAF18415.1| AF191051 apical membrane antigen 1 [Plasmodium falciparum]
Length = 140

25 Score = 29.7 bits (65), Expect = 4.4
Identities = 8/20 (40%), Positives = 15/20 (75%)
Frame = +1Query: 67 EFPSIYDDFNSTCHVWYVCS 126
++P++YDD N CH+ Y+ +
Sbjct: 78 KYPVYDDKNKKCHILYIAA 97

30 RANK 2 ITERATION 0>gb|AAAF18424.1| AF191060 apical membrane antigen 1 [Plasmodium falciparum]
Length = 147

35 Score = 29.7 bits (65), Expect = 4.4
Identities = 8/20 (40%), Positives = 15/20 (75%)
Frame = +1Query: 67 EFPSIYDDFNSTCHVWYVCS 126
++P++YDD N CH+ Y+ +

40 Sbjct: 83 KYPVYDDKNKKCHILYIAA 102
[END ALIGNMENTS]

Job Details

[Return to top](#)[BEGIN JOB STATUS][VERSION]
[SEARCH ID]
[EOL] CRLF
5 [COMMENT] /Comment=NCBI BLASTX Translated Search
[COMMENT] /
[ALGORITHM] BLASTX
[MATRIX] D:\DECYPHER\MATRIX\BLOSUM62.MAA
[QUERY FORMAT] FASTA/PEARSON
10 [QUERY TYPE] NT
[QUERY FILTER] T
[QUERY SEARCH] -1 -2 -3 1 2 3
[QUERY PATH] d:\decypher\query
[QUERY SET]
15 [TARGET TYPE] AA
[TARGET FRAMES] 1
[TARGET PATH] d:\decypher\target\blast
[TARGET SET] nr
[MAX SCORES] 30
20 [MAX ALIGNMENTS] 20
[THRESHOLD] 1
[RESULT PATH] d:\decypher\output
[OUTPUT FORMAT] TEXT EXTRACTALIGNED[SHOW GI] F
[EXPECTATION] 10
25 [GAPPED ALIGNMENT] TBLASTX
BLASTX
Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
30 programs", Nucleic Acids Res. 25:3389-3402.Query= Your_Query starting with:
ACTGCGTACCAATTCTAGAG /QuerySize=166
(166 letters)Database: Nonredundant Proteins
598,029 sequences; 189,012,571 total letters Database: Nonredundant
Proteins
35 Number of letters in database: 189,012,571
Number of sequences in database: 598,029

Lambda K H
0.318 0.135 0.401 Gapped
40 Lambda K H
0.270 0.0470 0.230 Matrix: BLOSUM62.MAA
Gap Penalties: Existence: 11, Extension: 1
Number of Hits to DB: 48853644
Number of Sequences: 598029
45 Number of extensions: 613365
Number of successful extensions: 2623

Number of sequences better than 10.0: 4
 Number of HSP's better than 10.0 without gapping: 2
 Number of HSP's successfully gapped in prelim test: 0
 Number of HSP's that attempted gapping in prelim test: 2621
 5 Number of HSP's gapped (non-prelim): 2
 length of query: 55
 length of database: 189,012,571
 effective HSP length: 33
 effective length of query: 21
 10 effective length of database: 169,277,614
 effective search space: 3554829894
 effective search space used: 3554829894
 frameshift window, decay const: 50, 0.1
 T: 12
 15 A: 40
 X1: 16 (7.3 bits)
 X2: 38 (14.8 bits)
 X3: 64 (24.9 bits)
 S1: 41 (21.7 bits)
 20 S2: 62 (28.6 bits)[JOB MESSAGES]
 [END JOB STATUS]
DESCA1 Blast against RICE V4
DeCypher Results for: NCBI TBLASTX Similarity Search
Results by Query

25 *Click on a query below to view its search results.*
 Your Query starting with: ACTGCGTACCAATTCTAGAG

Search Details

30 **Results for: Your_Query starting with:**
ACTGCGTACCAATTCTAGAG; (Length=166)

[Return to query summary](#)

	RANK	Sequences producing significant alignments:	(bits)	Value
35	<u>1</u>	CL033500.112	36	0.014
	<u>2</u>	CL011993.98	33	0.093
	<u>3</u>	CL023356.123	33	0.13
	<u>4</u>	CL038420.235.116	32	0.24
	<u>5</u>	CL009226.83.95	32	0.24
40	<u>6</u>	CL031366.112	32	0.24
	<u>7</u>	CL030944.62	32	0.24
	<u>8</u>	CL004532.88	32	0.24
	<u>9</u>	CL002685.132	32	0.24

5	<u>10</u>	CL012934.185	31 0.33
	<u>11</u>	CL016176.135	31 0.45
	<u>12</u>	CL022848.85.91	31 0.45
	<u>13</u>	CL004164.216	30 0.62
	<u>14</u>	CL017104.233	30 0.62
10	<u>15</u>	CL057296.104.93	30 0.86
	<u>16</u>	CL011101.255	30 0.86
	<u>17</u>	CL015029.130	29 1.2
	<u>18</u>	CL036024.74	29 1.2
	<u>19</u>	CL006787.80	29 1.2
15	<u>20</u>	CL002050.179	29 1.2
	21	CL001965.99	29 1.2
	22	CL063976.22.22	29 1.6
	23	CL014112.193.150	29 1.6
	24	CL023572.39	29 1.6
20	25	CL018854.33	29 1.6
	26	CL018796.102	29 1.6
	27	CL003436.377	29 1.6
	28	CL023961.93.109	29 1.6
	29	CL015998.53	29 1.6
	30	CL003436.341	29 1.6

25 RANK 1 ITERATION 0>CL033500.112
 Length = 2169

Score = 35.9 bits (72), Expect = 0.014
 Identities = 13/26 (50%), Positives = 16/26 (61%)
 Frame = +1 / +1

30 Query: 82 YDDFNSTCHVWYVCSITLL*HPSYSG 159
 +D STCH WYVC +T+ S SG
 Sbjct: 1492 FDALLSTCHFVWVCCMTVCMGGSASG 1569

```

35      RANK 2 ITERATION 0>CL011993.98
      Length = 6921

      Score = 33.1 bits (66), Expect = 0.093
      Identities = 9/24 (37%), Positives = 16/24 (66%)
      Frame = +3 / -2

40      Query: 69  ISINL**L*FNMSCMVCM*YHFIM 140
      I ++L L ++C++CM Y FI+
      Sbjct: 1427 IRLHLQELEQIVNCIICMSYQFII 1356

```

45

RANK 3 ITERATION 0>CL023356.123

Length = 4626

Score = 32.7 bits (65), Expect = 0.13
Identities = 13/24 (54%), Positives = 19/24 (79%)
Frame = -2 / +2

Query: 72 KFNMYMCNKLELDVLVSSALELVRS 1
KFN+Y+C+ +LDV+V SA++L S
Sbjct: 26 KFN+YICHT*KLDV+MVISAVKLALS 97

RANK 4 ITERATION 0>CL038420.235.116
Length = 7170

Score = 31.8 bits (63), Expect = 0.24
Identities = 11/37 (29%), Positives = 17/37 (45%)
Frame = -1 / +1

Query: 127 YYIHTIHDMLN*SHHRLMEIQLYV**ARARCSCKFSS 17
++H ML+ H++L RCSC+F S
Sbjct: 499 FLLHFDSHMLHSDSHTIXQKDLATREKNIRCSCRFPS 609

RANK 5 ITERATION 0>CL009226.83.95
Length = 6638

Score = 31.8 bits (63), Expect = 0.24
Identities = 10/22 (45%), Positives = 14/22 (63%)
Frame = +3 / +1

Query: 81 L**L*FNMSCMVCM*YHFIMTP 146
L L N+SC+VC+ Y + M P
Sbjct: 2953 LINLEVNISCIVCLPYQYSMAP 3018

RANK 6 ITERATION 0>CL031366.112
Length = 965

Score = 31.8 bits (63), Expect = 0.24
Identities = 11/24 (45%), Positives = 15/24 (61%)
Frame = +3 / +3

Query: 66 *ISINL**L*FNMSCMVCM*YHFI 137
+S **L +SC+VCM Y F+
Sbjct: 135 QLSSTA**LEDVLSCLVCMVYDFL 206

RANK 7 ITERATION 0>CL030944.62

Score = 30.8 bits (61), Expect = 0.45
Identities = 10/37 (27%), Positives = 18/37 (48%)
Frame = -1 / +3

5

Query: 160 VLSNSGVIIK*YYIHTIHDMLN*SHHRLMEIQLYV** 50
+ S +I Y++ IH+ +H+ MIQ+Y
Sbjct: 750 IYSQKYINIHKYFLREIHNRRQGRAHYVFMGIQMYTQD 860

10

RANK 12 ITERATION 0>CL022848.85.91
Length = 8101

Score = 30.8 bits (61), Expect = 0.45
Identities = 11/34 (32%), Positives = 15/34 (43%)
Frame = -3 / -2

15

Query: 125 LHTYHT*HVELKSS*IDGNSTICVIS*S*MFL*V 24
LH Y+ H E K+ ST+C +L V
Sbjct: 6882 LHVYYHQHSERKTGLQGLQSTVCQYLELECYLQV 6781

20

RANK 13 ITERATION 0>CL004164.216
Length = 643

Score = 30.4 bits (60), Expect = 0.62
Identities = 12/27 (44%), Positives = 16/27 (58%)
Frame = -1 / -2

25

Query: 85 HRLMEIQLYV**ARARCCKFSSRIGT 5
H+L+ +L+V R R C C S R GT
Sbjct: 306 HQLIRTRLFVSGTRMRCVCVCSLRSGT 226

30

RANK 14 ITERATION 0>CL017104.233
Length = 3603

Score = 30.4 bits (60), Expect = 0.62
Identities = 9/24 (37%), Positives = 13/24 (53%)
Frame = -1 / +3

35

Query: 130 *YYIHTIHDMLN*SHHRLMEIQLY 59
Y+ +HD N +HH L+ LY
Sbjct: 2010 EVYVIYLDQYNSAHHHLLPFLLY 2081

40

RANK 15 ITERATION 0>CL057296.104.93
Length = 5174

45

Frame = +3 / -1
Query: 51 YYTYS*ISINL**L*FNMSCMVCM*YHFIMTPEL 152
YYT IS+ LF+S C HF P++
Sbjct: 3116 YYTTCQISAD*CTLNFTLSVCSCFFLHFFSLPDV 3015

5

RANK 20 ITERATION 0>CL002050.179
Length = 11518

10 Score = 29.5 bits (58), Expect = 1.2
Identities = 12/23 (52%), Positives = 14/23 (60%)
Frame = +2 / +2
Query: 35 TSSSSLHI*LNFHQSMMTLIQH 103
TSSSSL H +H SMT +H
15 Sbjct: 2138 TSSSLYHTATSIHDSMSTTARH 2206
[END
ALIGNMENTS]

20 Job Details[Return to top](#)
[BEGIN JOB STATUS]
[VERSION]
[SEARCH ID]
[EOL] CRLF
25 [COMMENT] /Comment=NCBI TBLASTX Similarity Search
[COMMENT] /
[ALGORITHM] TBLASTX
[MATRIX] D:\DECYPHER\MATRIX\BLOSUM62.MAA
[QUERY FORMAT] FASTA/PEARSON
30 [QUERY TYPE] NT
[QUERY FILTER] T
[QUERY SEARCH] -1 -2 -3 1 2 3
[QUERY PATH] d:\decypher\query
[QUERY SET]
35 [TARGET TYPE] NT
[TARGET FRAMES] -1 -2 -3 1 2 3
[TARGET PATH] d:\decypher\target\blast
[TARGET SET] rice_contigs_
[MAX SCORES] 30
40 [MAX ALIGNMENTS] 20
[THRESHOLD] 1
[RESULT PATH] d:\decypher\output
[OUTPUT FORMAT] TEXT EXTRACTALIGNED[SHOW GI] F
[EXPECTATION] 10
45 [GAPPED ALIGNMENT] T
TBLASTX 2.0.12
TBLASTX 7.0.12.08

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402. Query= Your_Query starting with:

5 ACTGCGTACCAATTCTAGAG /QuerySize=166
(166 letters) Database: rice contigs
154,797 sequences; 359,911,975 total letters
Database: rice contigs

10 Number of letters in database: 359,911,975
Number of sequences in database: 154,797

Lambda K H
0.318 0.135 0.401

15 Matrix: BLOSUM62.MAA
Number of Hits to DB: 135828925
Number of Sequences: 154797
Number of extensions: 1347611
Number of successful extensions: 97244
20 Number of sequences better than 10.0: 824
length of query: 55
length of database: 119,970,658
effective HSP length: 47
effective length of query: 7
25 effective length of database: 112,695,199
effective search space: 788866393
effective search space used: 788866393
frameshift window, decay const: 50, 0.1
T: 13
30 A: 40
X1: 16 (7.3 bits)
X2: 0 (0.0 bits)
S1: 41 (21.7 bits)
S2: 51 (26.3 bits)[JOB MESSAGES]
35 [END JOB STATUS]

DESCA2 Blast Report against nonredundant protein database

DeCypher Results for: NCBI BLASTX Translated Search

Results by Query

Click on a query below to view its search results.

40 Your_Query starting with: GATGAGTCCTGAGTAAATAT

Search Details

**Results for: Your_Query starting with:
GATGAGTCCTGAGTAAATAT; (Length=245)**

[Return to query summary](#)

	RANK	Sequences producing significant alignments:	(bits)	Value
5	<u>1</u>	gb AAF19716.1 AC008047_23 AC008047 F2K11.7 [Arabidopsis thali...	66	6e-011
	<u>2</u>	pir T04835 probable serine/threonine-specific protein kinase (...	61	3e-009
10	<u>3</u>	gb AAD21872.1 AF078082 receptor-like protein kinase homolog ...	61	3e-009
	<u>4</u>	gb AAD21420.1 AC005882 55659 [Arabidopsis thaliana]	61	3e-009
	<u>5</u>	gb AAF19714.1 AC008047_21 AC008047 F2K11.9 [Arabidopsis thali...	57	3e-008
15	<u>6</u>	gb AAF19715.1 AC008047_22 AC008047 F2K11.8 [Arabidopsis thali...	57	4e-008
	<u>7</u>	pir T04834 hypothetical protein F21P8.60 - Arabidopsis thalian...	57	4e-008
	<u>8</u>	pir T06082 protein kinase homolog T9A14.110 - Arabidopsis thal...	57	4e-008
20	<u>9</u>	pir T04840 hypothetical protein F21P8.120 - Arabidopsis thalia...	57	5e-008
	<u>10</u>	dbj BAB01391.1 AB028622 contains similarity to receptor kina...	56	7e-008
	<u>11</u>	gb AAF19719.1 AC008047_26 AC008047 F2K11.4 [Arabidopsis thali...	55	1e-007
25	<u>12</u>	emb CAB81062.1 AL161503 receptor protein kinase-like protein...	55	1e-007
	<u>13</u>	gb AAF09156.1 AC011622_13 AC011622 unknown protein; 87064-861...	55	1e-007
30	<u>14</u>	pir T05149 protein kinase homolog F18E5.30 - Arabidopsis thali...	54	3e-007
	<u>15</u>	gb AAF19717.1 AC008047_24 AC008047 F2K11.6 [Arabidopsis thali...	54	3e-007
	<u>16</u>	pir T47526 protein kinase-like - Arabidopsis thaliana >gi 7339...	54	3e-007
35	<u>17</u>	dbj BAB11106.1 AB019225 contains similarity to unknown prote...	53	4e-007
	<u>18</u>	pir T04833 hypothetical protein F21P8.50 - Arabidopsis thalian...	53	6e-007
	<u>19</u>	pir T04831 probable serine/threonine-specific protein kinase (...	53	6e-007
40	<u>20</u>	pir T04848 protein kinase homolog F16G20.10 - Arabidopsis thal...	52	1e-006
	<u>21</u>	dbj BAB11104.1 AB019225 contains similarity to unknown prote...	52	1e-006
	<u>22</u>	pir T04845 probable serine/threonine-specific protein kinase (...	51	3e-006
45	<u>23</u>	pir T05148 protein kinase homolog F18E5.20 - Arabidopsis thali...	51	3e-006

24 dbj|BAB11105.1| AB019225 contains similarity to unknown prote... 50
4e-006
25 gb|AAF19718.1|AC008047_25 AC008047 F2K11.5 [Arabidopsis thali...
50 5e-006
5 26 pir|T04844 probable serine/threonine-specific protein kinase (... 49 1e-005
27 pir|T04954 hypothetical protein F7J7.170 - Arabidopsis thalian... 48 2e-
005
28 dbj|BAA96974.1| AB020745 33 kDa secretory protein-like [Arabi... 47
4e-005
10 29 dbj|BAB01372.1| AB028622 contains similarity to receptor prot... 46 6e-
005
30 dbj|BAB01368.1| AB028622 contains similarity to receptor prot... 46 1e-
004

15 RANK 1 ITERATION 0>gb|AAF19716.1|AC008047_23 AC008047 F2K11.7
[Arabidopsis thaliana]
Length = 337

20 Score = 66.3 bits (159), Expect = 6e-011
Identities = 33/76 (43%), Positives = 44/76 (57%)
Frame = -1Query: 236
TNSRINYGFYNLSVGXKLDEVYGVALCRGDIPTSKCKTCVDYAAARIGLDX
PSYKSAXGX 57
25 T+S ++Y N ++G D VYG+ LCRGDI T+ C CV AA I + K A
Sbjct: 111 TSSLVHY--
LNATIGLSPDTVYGMFLCRGDINTTSCSDCVQTAAIEIATNCTLNKRAFIY
168Query: 56 YDECMIRYSXTDIFTQ 9
YDECM+RYS F++
30 Sbjct: 169 YDECMVRYSNVSFFSE 184

RANK 2 ITERATION 0>pir|T04835 probable serine/threonine-specific protein
kinase (EC
35 2.7.1.-) F21P8.70 - Arabidopsis thaliana
>gi|3021270|emb|CAA18465.1| (AL022347) serine/threonine
kinase-like protein [Arabidopsis thaliana]
>gi|7269165|emb|CAB79273.1| (AL161558) serine/threonine
kinase-like protein [Arabidopsis thaliana]
40 Length = 633

Score = 60.5 bits (144), Expect = 3e-009
Identities = 29/74 (39%), Positives = 41/74 (55%)
Frame = -1Query: 233
45 NSRINYGFYNLSVGXKLDEVYGVALCRGDIPTSKCKTCVDYAAARIGLDXP
SYKSAXGXY 54

Sbjct: 123 FLRYSSRKIFS 133

RANK 5 ITERATION 0>gb|AAF19714.1|AC008047_21 AC008047 F2K11.9

5 [Arabidopsis thaliana]

Length = 323

Score = 57.4 bits (136), Expect = 3e-008

Identities = 30/71 (42%), Positives = 40/71 (56%)

10 Frame = -1Query: 242

LRTNSRINYGFYNLSVGXKLDEVYGVALCRGDIPTSKCKTCVDYAAARIGL
DXPSYKSAX 63

LR+S+++N+G DV+G+LCRGDIT+C CV A I + K A

Sbjct: 59 LRESSSLGH-

15 YSNATEGLSPDTVHGMFLCRGDITTASCVDCVQTATTEIASNCTLNKRAV

117Query: 62 GXYDECMIRYS 30

YDECM+RYS

Sbjct: 118 IYYDECMVRYS 128

RANK 6 ITERATION 0>gb|AAF19715.1|AC008047_22 AC008047 F2K11.8

[Arabidopsis thaliana]

Length = 284

25 Score = 57.0 bits (135), Expect = 4e-008

Identities = 31/72 (43%), Positives = 41/72 (56%), Gaps = 3/72 (4%)

Frame = -1Query: 227 RINYGFY-

NLSVGXKLDEVYGVALCRGDIPTSKCKTCVDYAAARI--GLDXPSYKSAXGX
57

30 R+GYN++G D VYG+LCRGD+ +C CV A I + S K+A

Sbjct: 64

RSSLGTYSNATIGLSPDTVYGMFLCRGDLTKTSCSDCVKTATLEITKNNNCT
SRKTALIF 123Query: 56 YDECMIRYSXTDIFT 12

Y+ECM+RYS FT

35 Sbjct: 124 YEECMVRYSNVSFFT 138

RANK 7 ITERATION 0>pir|T04834 hypothetical protein F21P8.60 - Arabidopsis
thaliana

40 >gi|3021269|emb|CAA18464.1| (AL022347) putative protein

[Arabidopsis thaliana] >gi|7269164|emb|CAB79272.1|

(AL161558) putative protein [Arabidopsis thaliana]

Length = 265

45 Score = 57.0 bits (135), Expect = 4e-008

Identities = 27/74 (36%), Positives = 41/74 (54%)

Frame = -1Query: 233
 NSRINYGFYNLSVGXKLDEVYGVALCRGDIPTSKCKTCVDYAAARIGLDXP
 SYKSAXGXY 54

N+ + GF N++VG D V G+ LCRGD+ C CV ++ PS + A Y

5 Sbjct: 60
 NASYSTGFQNVTVGQTPDLVTGLFLCRGDLSPEVCSNCVAFSVDEALTRCPS
 QREAVFY 119Query: 53 DECMIRYSXTDIFT 12

+EC++RYS +I +

Sbjct: 120 EECILRYSDKNILS 133

10

RANK 8 ITERATION 0>pir|T06082 protein kinase homolog T9A14.110 -
 Arabidopsis thaliana

15 >gi|4490335|emb|CAB38617.1| (AL035656) receptor-like
 protein kinase-like protein [Arabidopsis thaliana]

>gi|7270866|emb|CAB80546.1| (AL161594) receptor-like
 protein kinase-like protein [Arabidopsis thaliana]

Length = 665

20 Score = 57.0 bits (135), Expect = 4e-008
 Identities = 27/69 (39%), Positives = 37/69 (53%)

Frame = -1Query: 215

GFYNLSVGXKLDEVYGVALCRGDIPTSKCKTCVDYAAARIGLDXPSYKSAX
 GXYDECMIR 36

25 GFYN+SVG ++V ++ CRGD+ C C+ A R+ P K A YD+C R

Sbjct: 64

GFYNISVGDSDEKVNSISQCRGDVKLEVCINCIAMAGKRLVTLCVPVQKEAII
 WYDKCTFR 123Query: 35 YSXTDIFTQ 9

YS IF +

30 Sbjct: 124 YSNRTIFNR 132

RANK 9 ITERATION 0>pir|T04840 hypothetical protein F21P8.120 - Arabidopsis
 thaliana

35 >gi|3021275|emb|CAA18470.1| (AL022347) putative protein
 [Arabidopsis thaliana] >gi|7269171|emb|CAB79278.1|

(AL161559) putative protein [Arabidopsis thaliana]

Length = 485

40 Score = 56.6 bits (134), Expect = 5e-008
 Identities = 26/74 (35%), Positives = 41/74 (55%)

Frame = -1Query: 233

NSRINYGFYNLSVGXKLDEVYGVALCRGDIPTSKCKTCVDYAAARIGLDXP
 SYKSAXGXY 54

45 N+ + GF + G D V G+ LCRGD+ + C+ CV ++ + PS ++ Y

Sbjct: 43
NASYSTGFQSARAGQAPDRVTGLFLCRGDVSPA VCRNCVAFSINDTLVQCP
SERKSVFY 102Query: 53 DECMIRYSXTDIFT 12
DECM+RYS +I +

5 Sbjct: 103 DECMLRYSDQNILS 116

RANK 10 ITERATION 0>dbj|BAB01391.1| AB028622 contains similarity to
receptor

10 kinase~gene_id:MZN24.26 [Arabidopsis thaliana]
Length = 252

Score = 56.2 bits (133), Expect = 7e-008
Identities = 25/67 (37%), Positives = 39/67 (57%)

15 Frame = -1Query: 215
GFYNLSVGXKLDEVYGVALCRGDIPTSKCKTCVDYAAARIGLDXPSYKSAX
GXYDECMIR 36

GF S G + V G+ALCRGD +S C++C++ A + P+ K+ YD C+++

Sbjct: 71

20 GFAASSTGNTPNNVNGLALCRGDASSSDCRSCLETAIPELRQRCPPNNKAGIV
WYDNCLVK 130Query: 35 YSXTDIF 15

YS T+ F

Sbjct: 131 YSSTNFF 137

25 RANK 11 ITERATION 0>gb|AAF19719.1|AC008047_26 AC008047 F2K11.4
[Arabidopsis thaliana]
Length = 305

30 Score = 55.4 bits (131), Expect = 1e-007
Identities = 29/72 (40%), Positives = 38/72 (52%), Gaps = 1/72 (1%)
Frame = -1Query: 227 RINYGFY-
NLSVGXKLDEVYGVALCRGDIPTSKCKTCVDYAAARIGLDXPSYKSAXGXY
D 51

35 R + G Y N + G D V G+ LCRGDI + C CV A I + K A Y+

Sbjct: 67

RSSLGSYSNATAGISPDTV RGMFLCRGDISETSCSDCVQTATLEISRNCTYQK
EAFIFYE 126Query: 50 ECMIRYSXTDIFT 12

ECM+RYS + F+

40 Sbjct: 127 ECMVRYSDSSFFS 139

RANK 12 ITERATION 0>emb|CAB81062.1| AL161503 receptor protein kinase-
like protein

45 [Arabidopsis thaliana]
Length = 675

Score = 55.4 bits (131), Expect = 1e-007

Identities = 31/68 (45%), Positives = 37/68 (53%), Gaps = 2/68 (2%)

Frame = -1Query: 212 FYNLSVGXKLDE--

5 VYGVALCRGDIPTSKCKTCVDYAAARIGLDXPSYKSAXGXYDECM 39

F N + G + D VYGV LCRGD+ C+ CV +AA P K A YDECM+

Sbjct: 68

FDNAAAGEENDSNRVYGVFLCRGDVSAEICRDCVAFAANETLQRCPREKV

AVIWYDECMV 127Query: 38 RYSXTDIFTQ 9

10 RYS I Q

Sbjct: 128 RYSNQSIVGQ 137

RANK 13 ITERATION 0>gb|AAAF09156.1|AC011622_13 AC011622 unknown

15 protein; 87064-86156

[Arabidopsis thaliana]

Length = 302

Score = 55.4 bits (131), Expect = 1e-007

20 Identities = 29/72 (40%), Positives = 38/72 (52%), Gaps = 1/72 (1%)

Frame = -1Query: 227 RINYGFY-

NLSVGXKLDEVYGVLCRGDIPTSKCKTCVDYAAARIGLDXPSYKSAXGXY

D 51

R + G Y N + G D V G+ LCRGDI + C CV A I + K A Y+

25 Sbjct: 64

RSSLGSYSNATAGISPDTVRGMFLCRGDISETSCSDCVQTATLEISRNCTYQK

EAFIFYE 123Query: 50 ECMIRYSXTDIFT 12

ECM+RYS + F+

Sbjct: 124 ECMVRYS DSSFFS 136

30

RANK 14 ITERATION 0>pir|T05149 protein kinase homolog F18E5.30 -

Arabidopsis thaliana

35 >gi|3080385|emb|CAA18705.1| (AL022603) serine/threonine
protein kinase [Arabidopsis thaliana]

>gi|3402760|emb|CAA20206.1| (AL031187) serine/threonine
kinase-like protein [Arabidopsis thaliana]

>gi|7268938|emb|CAB81248.1| (AL161555) serine/threonine
kinase-like protein [Arabidopsis thaliana]

40 Length = 683

Score = 54.3 bits (128), Expect = 3e-007

Identities = 27/68 (39%), Positives = 34/68 (49%), Gaps = 1/68 (1%)

Frame = -1Query: 218 YGFYNLSVGXKLDE-

45 VYGVALCRGDIPTSKCKTCVDYAAARIGLDXPSYKSAXGXYDECM 42

YGFYNLS G E Y + LCR ++ C +C+ AA + P K A Y CM

Sbjct: 67
YGFYNLSSGDSSGERAYAIGLCRREVKRDDCVSCIQTAARNLTKQCPLTKQ
AVVWYTHCM 126Query: 41 IRYSXTDIF 15

RYS I+

5 Sbjct: 127 FRYSNRTIY 135

RANK 15 ITERATION 0>gb|AAAF19717.1|AC008047_24 AC008047 F2K11.6
[Arabidopsis thaliana]

10 Length = 254

Score = 53.9 bits (127), Expect = 3e-007
Identities = 25/77 (32%), Positives = 40/77 (51%)
Frame = -1Query: 242

15 LRTNSRINYGFYNLSVGXKLDEVYGVALCRGDIPTSKCKTCVDYAAARIGL
DXPSYKSAX 63

LR+S+ ++N+G +VYG+LCG+I +C CV A + S++

Sbjct: 48

LRNHSSLGSYYFNATAGLSPNTVYGMFLCIGNISKTSNCVHSATLEMDKS

20 CESHDTSF 107Query: 62 GXYDECMIRYSXTDIFT 12

DECM+RYS F+

Sbjct: 108 MFSDECMVRYSDNSFFS 124

25 RANK 16 ITERATION 0>pir|T47526 protein kinase-like - Arabidopsis thaliana
>gi|7339487|emb|CAB82810.1| (AL162459) protein
kinase-like [Arabidopsis thaliana]
Length = 676

30 Score = 53.9 bits (127), Expect = 3e-007
Identities = 26/74 (35%), Positives = 37/74 (49%)
Frame = -1Query: 233

NSRINYGFYNLSVGXKLDEVYGVALCRGDIPTSKCKTCVDYAAARIGLDXP
SYKSAXGXY 54

35 N+ +GF +G DVG+LCRGD+ C+CV++ P K Y

Sbjct: 64

NASYSTGFQTATAGQAPDRVTGLFLCRGDVSQEVCRNCVAFSVKETLYWC
PYNKEVVLYY 123Query: 53 DECMIRYSXTDIFT 12

DECM+RYS +I+

40 Sbjct: 124 DECMLRYSHRNILS 137

RANK 17 ITERATION 0>dbj|BAB11106.1| AB019225 contains similarity to
unknown

45 protein~gb|AAAF19719.1~gene_id:K1O13.10 [Arabidopsis
thaliana]

Length = 287

Score = 53.5 bits (126), Expect = 4e-007

Identities = 24/60 (40%), Positives = 34/60 (56%)

5 Frame = -1Query: 209

YNLSVGXKLDEVYGVALCRGDIPTSKCKTCVDYAAARIGLDXPSYKSAXGX
YDECMIRYS 30

YNL+ G D VYG+ LC GD+ + C CV A I + +++ A Y +CM+RYS

Sbjct: 71

10 YNLTGLASDTVYGMFLCTGDVNITTCNNCVKNATIEIVKNCTNHREALIYYI
DCMVRYS 130

RANK 18 ITERATION 0>pir|[T04833] hypothetical protein F21P8.50 - Arabidopsis
15 thaliana

>gi|3021268|emb|CAA18463.1| (AL022347) putative protein

[Arabidopsis thaliana] >gi|7269163|emb|CAB79271.1|

(AL161558) putative protein [Arabidopsis thaliana]

Length = 1240

20

Score = 53.1 bits (125), Expect = 6e-007

Identities = 24/68 (35%), Positives = 36/68 (52%)

Frame = -1Query: 233

25 NSRINYGFYNLSVGXKLDEVYGVALCRGDIPTSKCKTCVDYAAARIGLDXP
SYKSAXGXY 54

N+ + GF N+ G D V G+ LCRGD+ C CV ++ P++ A Y

Sbjct: 657

NASYSTGFQNIAGQTPDRVTGLFLCRGDLSPVCSNCVAFSVNESLTRCPN
QREAVFYY 716Query: 53 DECMIRYS 30

30 +EC++RYS

Sbjct: 717 EECILRYS 724

RANK 19 ITERATION 0>pir|[T04831] probable serine/threonine-specific protein
35 kinase (EC

2.7.1.-) F21P8.30 - Arabidopsis thaliana

>gi|3021266|emb|CAA18461.1| (AL022347) serine/threonine
kinase-like protein [Arabidopsis thaliana]

40 >gi|3292840|emb|CAA19830.1| (AL031018) serine/threonine
kinase-like protein [Arabidopsis thaliana]

>gi|7269161|emb|CAB79269.1| (AL161558) serine/threonine
kinase-like protein [Arabidopsis thaliana]

Length = 658

45 Score = 53.1 bits (125), Expect = 6e-007

Identities = 24/74 (32%), Positives = 40/74 (53%)

Frame = -1Query: 233
NSRINYGFYNLSVGXKLDEVYGVALCRGDIPTSKCKTCVDYAAARIGLDXP
SYKSAXGXY 54

N+ + GF N + G D V G+ LCRGD+ C+ CV ++ + P + A Y

5 Sbjct: 61
NASYSTGFQNATAGKAPDRVTGLFLCRGDVSPEVCRNCVAFSVNQTNLCP
KVREAVFYY 120Query: 53 DECMIRYSXTDIFT 12

++C++RYS +I +

Sbjct: 121 EQCILRYSHKNILS 134

10

RANK 20 ITERATION 0>pir|[T04848 protein kinase homolog F16G20.10 -
Arabidopsis thaliana

15 >gi|3021283|emb|CAA18478.1| (AL022347) serine/threonine
kinase-like protein [Arabidopsis thaliana]

>gi|7269179|emb|CAB79286.1| (AL161559) serine/threonine
kinase-like protein [Arabidopsis thaliana]

Length = 830

20 Score = 52.3 bits (123), Expect = 1e-006
Identities = 24/68 (35%), Positives = 33/68 (48%)

Frame = -1Query: 215

GFYNLSVGXKLDEVYGVALCRGDIPTSKCKTCVDYAAARIGLDXPSYKSAX
GXYDECMIR 36

25 GF N + G D V G+ CRGD+ C+ CV +A P K YD+C +R

Sbjct: 179

GFQNATAGKHPDRVTGLFNCRGDVSPEVCRRCVSVFAVNETSTRCPIEKEVTL
YYDQCTLR 238Query: 35 YSXTDIFT 12

YS +I +

30 Sbjct: 239 YSNRNILS 246

Score = 52.3 bits (123), Expect = 1e-006

Identities = 26/68 (38%), Positives = 36/68 (52%)

Frame = -1Query: 233

NSRINYGFYNLSVGXKLDEVYGVALCRGDIPTSKCKTCVDYAAARIGLDXP
35 SYKSAXGXY 54

+S + GF N +VG D V G+ CRGD+P C CV +A + P+ + Y

Sbjct: 62

SSSYSSGFRNDAVGTFPDRVTGLFDCRGDLPPEVCHNCVAFVKTDLIRCPN
ERDVTLFY 121Query: 53 DECMIRYS 30

40 DEC +RYS

Sbjct: 122 DECTLRYS 129

[END ALIGNMENTS]

Job Details[Return to top](#)

45 [BEGIN JOB STATUS][VERSION]
[SEARCH ID]

Number of HSP's that attempted gapping in prelim test: 3239

Number of HSP's gapped (non-prelim): 114

length of query: 81

length of database: 189,012,571

5 effective HSP length: 50

effective length of query: 31

effective length of database: 159,111,121

effective search space: 4932444751

effective search space used: 4932444751

10 frameshift window, decay const: 50, 0.1

T: 12

A: 40

X1: 16 (7.3 bits)

X2: 38 (14.8 bits)

15 X3: 64 (24.9 bits)

S1: 41 (21.7 bits)

S2: 63 (29.0 bits)[JOB MESSAGES]

[END JOB STATUS]

DESCA2 Blast result against NADI Rice database V4

20 **DeCypher Results for: NCBI TBLASTX Similarity Search**

Results by Query

Click on a query below to view its search results.

Your_Query starting with: GATGAGTCCTGAGTAAATAT

25 **Search Details**

Results for: Your_Query starting with:

GATGAGTCCTGAGTAAATAT; (Length=245)

[Return to query summary](#)

30	RANK	Sequences producing significant alignments:	(bits)	Value
	<u>1</u>	CL034536.100	59	8e-009
	<u>2</u>	CL016911.215	57	3e-008
	<u>3</u>	CL009506.298	45	3e-008
35	<u>4</u>	CL012328.109	53	4e-007
	<u>5</u>	CL024390.112.86	53	5e-007
	<u>6</u>	CL024378.22	52	7e-007
	<u>7</u>	CL008402.402.230	51	2e-006
	<u>8</u>	CL016911.223	51	2e-006
40	<u>9</u>	CL014204.347	50	3e-006
	<u>10</u>	CL041580.79.95	46	4e-005
	<u>11</u>	CL030694.100	46	6e-005
	<u>12</u>	CL018476.267	46	6e-005
	<u>13</u>	CL002737.272.140	45	2e-004

+ VG ++V ALCRGD+ S C C+ A A + ++ A YD CM+ YS
Sbjct: 1549
VDVGAVPEQVTAALCRGDVSASSCLGCLTQAFADLPNACGNSREAATYY
DRCMVSYS AI 1728

5

Query: 23 DIFT 12
+ +
Sbjct: 1729 NFLS 1740

10

RANK 10 ITERATION 0>CL041580.79.95
Length = 6443

Score = 46.4 bits (95), Expect = 4e-005
15 Identities = 22/61 (36%), Positives = 31/61 (50%)
Frame = -1 / +1

Query: 212
FYNLSVGXKLDEVYGV ALCRGDIPTSKCKTCVDYAAARIGLDXPSYKSAXG
20 XYDECMIRY 33
F + S G D +Y +ALCRGD +S C TCV A P K+ D C++R+
Sbjct: 4525
FASGSSGTVPDAIYALALCRGDTNSSSCATCVAAAIQSAQELCPLVKTIVIVY
DDTCILRF 4704

25

Query: 32 S 30
+
Sbjct: 4705 A 4707

30

RANK 11 ITERATION 0>CL030694.100
Length = 3881

Score = 46.0 bits (94), Expect = 6e-005
35 Identities = 20/62 (32%), Positives = 30/62 (48%)
Frame = -1 / -1

Query: 200
SVGXKLDEVYGV ALCRGDIPTSKCKTCVDYAAARIGLDXPSYKSAXGXYDE
40 CMIRYSXTD 21
++G D VYG+ LCRGD+ +S C C A + + A Y++C R+S
Sbjct: 2531
ALGAAPDAVYGLILCRGDVSSSDCYDCGTRAGQDVAPACNRTRDAILVYN
QCYTRFSAAG 2352

45

Query: 20 IF 15

F
Sbjct: 2351 DF 2346

5 RANK 12 ITERATION 0

>CL018476.267

Length = 5783

Score = 44.1 bits (90), Expect = 2e-004

10 Identities = 18/50 (36%), Positives = 26/50 (52%)

Frame = -1 / +2

Query: 245

*LRTNSRINYGFYNLSVGXKLDEVYGVALCRGDIPTSKCKTCVDYAAARI 96

15 L T GF + G ++YG+ CRGD+ TS C+ C+ AA +I

Sbjct: 1280

DLVTKGSTGVGFATSTAGKGNVYGLVQCRGDVSTSDCQACLASAANQI

1429 Score = 46.0 bits (94), Expect = 6e-005

Identities = 18/40 (45%), Positives = 25/40 (62%)

20 Frame = -1 / +2

Query: 215 GFYNLSVGXKLDEVYGVALCRGDIPTSKCKTCVDYAAARI 96

GF S G ++YG+A CRGD+ TS C+ C+ AA +I

Sbjct: 5231 GFATSSAGKANNVIYGLAQCRGDVSTSDCQACLASAANQI 5350

25 Score = 35.9 bits (72), Expect = 0.063

Identities = 14/48 (29%), Positives = 21/48 (43%)

Frame = -1 / +3

Query: 176

30 VYGVALCRGDIPTSKCKTCVDYAAARIGLDXPSYKSAXGXYDECMIRY 33

+YG A C D+ C C+ A +R ++ Y CM+RY

Sbjct: 1773

IYGFAQCTRDLSPILTCAQCLSTAVSRFDQYCGAQQGCRILYSSCMVRY 1916

35 RANK 13 ITERATION 0>CL002737.272.140

Length = 7746

Score = 32.7 bits (65), Expect = 0.58

40 Identities = 11/27 (40%), Positives = 16/27 (58%)

Frame = -1 / +1

Query: 176 VYGVALCRGDIPTSKCKTCVDYAAARI 96

V GVA C GD+P + C C+ A ++

Sbjct: 3199 VQGVAQCLGDPANDCTACLAEAVGQL 3279 Score = 44.6 bits

45 (91), Expect = 2e-004

Identities = 18/51 (35%), Positives = 24/51 (46%)

Frame = -1 / +1
Query: 173
YGVALCRGDIPTSKCKTCVDYAAARIGLDXPSYKSAXGXYDECMIRYSXTD
21
5 YG+ CRGD+ C CV AR+G + +A D C +RY D
Sbjct: 2902
YGLYQCRGDLSPGDCVACVRQTVARLGAVCANAYAASLQVDGCYVRYDA
AD
3054

10 RANK 14 ITERATION 0>CL022853.16.17
Length = 3000

Score = 44.1 bits (90), Expect = 2e-004
15 Identities = 20/51 (39%), Positives = 26/51 (50%)
Frame = -1 / +1

Query: 182
DEVYGVALCRGDIPTSKCKTCVDYAAARIGLDXPSYKSAXGXYDECMIRYS
20 30
DE+Y V C DI + CK+CV A +++ S A YD C IR S
Sbjct: 1042
DEMYAVGWCHADIDNTTCKSCVTDALRKVKVVCASKMEAIIFYDFCGIRIS
1194

25 RANK 15 ITERATION 0>CL020233.82
Length = 5396

Score = 44.1 bits (90), Expect = 2e-004
30 Identities = 16/33 (48%), Positives = 21/33 (63%)
Frame = -1 / +3

Query: 215 GFYNLSVGXKLDEVYGVALCRGDIPTSKCKTCV 117
35 GF + G D+VY +ALCRGD+ S C+ CV
Sbjct: 1284 GFAVRTAGAAPDQVYALALCRGDVNASACRACV 1382

40 RANK 16 ITERATION 0>HTC062340-A01.R.23.23
Length = 2705

Score = 43.7 bits (89), Expect = 3e-004
Identities = 17/55 (30%), Positives = 28/55 (50%)
Frame = -1 / -3

Query: 182
DEVYGVALCRGDIPTSKCKTCVDYAAARIGLDXPSYKSAXGXYDECMIRYS
XTDI 18

+++Y + CRGD T+ CK CV A ++ S A Y+ C+R S ++

5 Sbjct: 1584
EKIYAITQCRGDTNTNTCKRCVSEAVRDVQVVCDSRVEASVYYNFCSLRVS
SENV 1420

10 RANK 17 ITERATION 0>CL014204.310
Length = 5391

Score = 43.2 bits (88), Expect = 4e-004
Identities = 15/33 (45%), Positives = 22/33 (66%)

15 Frame = -1 / +1

Query: 215 GFYNLSVGXKLDEVYGVALCRGDIPTSKCKTCV 117
GF +VG D+V+ +ALCRGD+ + C+ CV
Sbjct: 661 GFAVATVGADPDQVFALALCRGDVNATACRACV 759

20 RANK 18 ITERATION 0>CL006774.121
Length = 7708

25 Score = 42.8 bits (87), Expect = 5e-004
Identities = 16/39 (41%), Positives = 23/39 (58%)
Frame = -1 / +3

Query: 233 NSRINYGFYNLSVGXKLDEVYGVALCRGDIPTSKCKTCV 117
N+ +GF S+G D VYG+ LCRGD+ + C C+
30 Sbjct: 4071 NASASGGFSAGSIGAAPDTVYGLTLCRGDVTGADCAACL 4187

35 RANK 19 ITERATION 0>CL004955.165.57
Length = 5126

Score = 42.8 bits (87), Expect = 5e-004
Identities = 19/33 (57%), Positives = 19/33 (57%)
Frame = -1 / +2

40 Query: 200 SVGXKLDEVYGVALCRGDIPTSKCKTCVDYAAA 102
S G D VY VALCRGD S C CVD A A
Sbjct: 2807 SRGAAPDTVYAVALCRGDANASACSGCVDAAYA 2905

45 RANK 20 ITERATION 0>CL024336.75

Length = 3989

Score = 42.8 bits (87), Expect = 5e-004

Identities = 18/39 (46%), Positives = 22/39 (56%)

5 Frame = -1 / -2

Query: 221 NYGFYNLSVGXKLDEVYGVALCRGDIPTSKCKTCVDYAA 105

N GF S G + YG+A CRGD+ S CK C+ AA

Sbjct: 2944 NGGFATSSAGKGNNVFYGLAQCRGDVSASDCKACLVEAA

10 2828[END ALIGNMENTS]

Job Details

[Return to top](#)

15 [BEGIN JOB STATUS]
[SEARCH ID]
[EOL] CRLF
[COMMENT] /Comment=NCBI TBLASTX Similarity Search
[COMMENT] /

20 [ALGORITHM] TBLASTX
[MATRIX] D:\DECYPHER\MATRIX\BLOSUM62.MAA
[QUERY FORMAT] FASTA/PEARSON
[QUERY TYPE] NT
[QUERY FILTER] T

25 [QUERY SEARCH] -1 -2 -3 1 2 3
[QUERY PATH] d:\decypher\query
[QUERY SET]
[TARGET TYPE] NT
[TARGET FRAMES] -1 -2 -3 1 2 3

30 [TARGET PATH] d:\decypher\target\blast
[TARGET SET] rice_contigs_
[MAX SCORES] 30
[MAX ALIGNMENTS] 20
[THRESHOLD] 1

35 [RESULT PATH] d:\decypher\output
[OUTPUT FORMAT] TEXT EXTRACTALIGNED[SHOW GI] F
[EXPECTATION] 10
[GAPPED ALIGNMENT] TTBLASTX
TBLASTX Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A.

40 Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs", Nucleic Acids Res. 25:3389-3402.Query= Your_Query starting with:
GATGAGTCCTGAGTAAATAT /QuerySize=245

45 (245 letters) Database
Number of letters in database: 359,911,975

Number of sequences in database: 154,797
 Lambda K H
 0.318 0.135 0.401 Matrix: BLOSUM62.MAA
 Number of Hits to DB: 165214302
 5 Number of Sequences: 154797
 Number of extensions: 1734115
 Number of successful extensions: 78575
 Number of sequences better than 10.0: 238
 length of query: 81
 10 length of database: 119,970,658
 effective HSP length: 49
 effective length of query: 32
 effective length of database: 112,385,605
 effective search space: 3596339360
 15 effective search space used: 3596339360
 frameshift window, decay const: 50, 0.1
 T: 13
 A: 40
 X1: 16 (7.3 bits)
 20 X2: 0 (0.0 bits)
 S1: 41 (21.7 bits)
S2: 56 (28.6 bits)[JOB MESSAGES][END JOB STATUS]DESCA3 Blast

report against nonredundant protein database:

DeCypher Results for: NCBI BLASTX Translated Search

25 **Results by Query**

Click on a query below to view its search results.

Your Query starting with: GATGAGTCCTGAGTAAGCAA

Search Details

30 **Results for: Your Query starting with:**

GATGAGTCCTGAGTAAGCAA; (Length=217)

[Return to query summary](#)

35	RANK	Sequences producing significant alignments:	(bits)	Value
	<u>1</u>	gb <u>AAB60922.1</u> <u>AC001229</u> F5I14.14 [Arabidopsis thaliana]	96	4e-
	020			
	<u>2</u>	emb <u>CAB51903.1</u> <u>AJ242807</u> cellulase [Brassica napus]	93	4e-019
	<u>3</u>	pir <u>S71215</u> endo-1,4-beta-D-glucanase (EC 3.2.1.-) KORRIGAN [im...	90	
40	3e-018			
	<u>4</u>	dbj <u>BAA94257.1</u> <u>AB040769</u> endo-1,4-beta-glucanase Cell [Hordeu...	90	
	4e-018			

RANK 1 ITERATION 0>gb|AAB60922.1| AC001229 F5I14.14 [Arabidopsis thaliana]

5 Length = 623
 Score = 96.3 bits (236), Expect = 4e-020
 Identities = 40/67 (59%), Positives = 55/67 (81%)
 Frame = +3
 Query: 15

10 KQFQVYNRTRGGLIELNSGGPKPLQYVANTAFLANLFADYMDSTGVPGWY
 CGPYFLRQSD 194
 KQ+ V+NRT GGL++LN G P+PL+YVA+
 +FLA+LFADY++STGVPGWYCGP F+
 Sbjct: 423

15 KQYNVFNRTSGGLMQLNLGKPRPLEYVAHASFLASLFADYLNSTGVPGWY
 CGPTFVENHV 482Query: 195 LRELVRS 215
 L++ +S
 Sbjct: 483 LKDFFAQS 489

20 RANK 2 ITERATION 0>emb|CAB51903.1| AJ242807 cellulase
 [Brassica napus]
 Length = 621

 Score = 92.8 bits (227), Expect = 4e-019

25 Identities = 40/65 (61%), Positives = 48/65 (73%)
 Frame = +3Query: 21
 FQVYNRTRGGLIELNSGGPKPLQYVANTAFLANLFADYMDSTGVPGWYCG
 PYFLRQSDLR 200
 F +NRTRGGLIELN G P+PLQY AN AFLA L++DY+D+ PGWYCGP F

30 + LR
 Sbjct: 421
 FNKFNRTTRGGLIELNHGDPQPLQYAANAAFLATLYSDYLDAADTPGWYCGP
 NFYSTNVLR 480Query: 201 ELVRS 215
 E R+

35 Sbjct: 481 EFART 485

RANK 3 ITERATION 0>pir|S71215 endo-1,4-beta-D-glucanase (EC 3.2.1.-) KORRIGAN

40 [imported] - Arabidopsis thaliana
 >gi|1022807|gb|AAB60304.1| (U37702) cellulase
 [Arabidopsis thaliana] >gi|3493633|gb|AAC33467.1|
 (AF074092) cellulase [Arabidopsis thaliana]
 >gi|3598956|gb|AAC35344.1| (AF074375) cellulase
 [Arabidopsis thaliana] >gi|3978258|gb|AAC83240.1|

45 (AF073875) endo-1,4-beta-D-glucanase KORRIGAN
 [Arabidopsis thaliana] >gi|8978269|dbj|BAA98160.1|

(AB025613) cellulase homolog OR16pep precursor
[Arabidopsis thaliana]
Length = 621

5 Score = 90.1 bits (220), Expect = 3e-018
Identities = 39/65 (60%), Positives = 46/65 (70%)
Frame = +3Query: 21
FQVYNRTRGGLIELNSGGPKPLQYVANTAFLANLFADYMDSTGVPGWYCG
PYFLRQSDLR 200
10 F +NRT GGLIELN G P+PLQY N AFLA L++DY+D+ PGWYCGP F S
LR
Sbjct: 421
FNKFNRTNGGLIELNHGAPQPLQYSVNAAFLATLYSDYLDAADTPGWYCGP
NFYSTSVLR 480Query: 201 ELVRS 215
15 + RS
Sbjct: 481 DFARS 485

20 RANK 4 ITERATION 0>dbj|BAA94257.1| AB040769 endo-1,4-beta-
glucanase Cell [Hordeum
vulgare]
Length = 621

25 Score = 89.7 bits (219), Expect = 4e-018
Identities = 38/65 (58%), Positives = 48/65 (73%)
Frame = +3Query: 21
FQVYNRTRGGLIELNSGGPKPLQYVANTAFLANLFADYMDSTGVPGWYCG
PYFLRQSDLR 200
F +N T+GGLI+LN GGP+PLQYV N AFLA+L+ADY+D+ PGWYCGP F
LR
30 Sbjct: 421
FNSFNFTKGGLIQLNHGGPQPLQYVVNAAFLASLYADYLDTADTPGWYCGP
NFYT TDVLR 480Query: 201 ELVRS 215
+ +S
Sbjct: 481 KFAKS 485

35 RANK 5 ITERATION 0>pir|T09889 cellulase homolog T22A6.90 -
Arabidopsis thaliana
40 >gi|5051768|emb|CAB45061.1| (AL078637) endo-1,
4-beta-glucanase like protein [Arabidopsis thaliana]
>gi|7269276|emb|CAB79336.1| (AL161561) endo-1,
4-beta-glucanase like protein [Arabidopsis thaliana]
Length = 620

45 Score = 87.8 bits (214), Expect = 1e-017
Identities = 38/65 (58%), Positives = 47/65 (71%)

Frame = +3Query: 21
 FQVYNRTRGGLIELNSGGPKPLQYVANTAFLANLFADYMDSTGVPGWYCG
 PYFLRQSDLR 200

++ +NRT GGLI+LN G P+PLQYVAN AFLA LF+DY+++ PGWYCGP F

5 LR

Sbjct: 422

YKKFNRTNGGLIQLNHGAPQPLQYVANAAFLAALFSDYLEAADTPGWYCG
 PNFYTTEFLR 481Query: 201 ELVRS 215

RS

10 Sbjct: 482 NFSRS 486

RANK 6 ITERATION 0>pir|T07612 cellulase (EC 3.2.1.4) Cel3,
 membrane-anchored - tomato

>gi|2065531|gb|AAC49704.1| (U78526)

15 endo-1,4-beta-glucanase [Lycopersicon esculentum]

Length = 617

Score = 83.9 bits (204), Expect = 2e-016

Identities = 36/65 (55%), Positives = 45/65 (68%)

20 Frame = +3Query: 21

FQVYNRTRGGLIELNSGGPKPLQYVANTAFLANLFADYMDSTGVPGWYCG
 PYFLRQSDLR 200

F +NRT+GGLI+LN G P+PLQYV N AFLA LF+DY+ + PGWYCGP F

LR

25 Sbjct: 419

FTSFNRTKGGGLIQLNHGRPQPLQYVVNAAFLATLFS DYLAADTPGWYCGP
 NFYSTDVLR 478Query: 201 ELVRS 215

+ +

Sbjct: 479 KFAET 483

30

RANK 7 ITERATION 0>gb|AAG12562.1|AC007797_22 AC007797
 Similar to

endo-beta-1,4-glucanase [Arabidopsis thaliana]

Length = 515

35

Score = 44.5 bits (103), Expect = 1e-004

Identities = 25/61 (40%), Positives = 37/61 (59%)

Frame = +3Query: 33

NRTRGGLIELNSGGPKPLQYVANTAFLANLFADYMDSTGVPGWYCGPYFLR
 QSDLRELVR 212

40

+RT GGLI ++ LQ+ ++AFLA L++DYM ++GV C + SDLR+ R

Sbjct: 347 SRTDGGLIWVSEWNA--

LQHPVSSAFLATLYSDYMLTSGVKELSCSDQSFKPSDLRK FAR 404Query:
 213 S 215

45

S

Sbjct: 405 S 405

Sbjct: 158
LLETQFGGSQRASIVSAAA VSTAFATGNSQTGLSAWYLSMYLLKEQHSR
207

5 RANK 11 ITERATION 0>gb|AAF02887.1|AC009525_21 AC009525
endo-1,4-beta glucanase
 [*Arabidopsis thaliana*]
 Length = 501

10 Score = 30.5 bits (67), Expect = 2.4
 Identities = 20/58 (34%), Positives = 29/58 (49%)
 Frame = +3Query: 39
 TRGG L I E L N S G G P K P L Q Y V A N T A F L A N L F A D Y M D S T G V P G W Y C G P Y F L R Q S
 D L R E L V R 212

15 T G G L L G +QYV +T+FL +A Y+ S YCG + +LR ++
Sbjct: 339 T P G G L --L F K M G E S N M Q Y V T S T S F L L L T Y A K Y L T S A R T V A -
Y C G G S V V T P A R L R S I A K 393

20 RANK 12 ITERATION 0>gb|AAC16418.1| AF034573 endo-1,4-beta
glucanase; ATCEL2
 [*Arabidopsis thaliana*]
 Length = 501

25 Score = 30.5 bits (67), Expect = 2.4
 Identities = 20/58 (34%), Positives = 29/58 (49%)
 Frame = +3Query: 39
 TRGG L I E L N S G G P K P L Q Y V A N T A F L A N L F A D Y M D S T G V P G W Y C G P Y F L R Q S
 D L R E L V R 212

30 T G G L L G +QYV +T+FL +A Y+ S YCG + +LR ++
Sbjct: 339 T P G G L --L F K M G E S N M Q Y V T S T S F L L L T Y A K Y L T S A R T V A -
Y C G G S V V T P A R L R S I A K 393

35 RANK 13 ITERATION 0>gb|AAD19548.1| AF103912 envelope
glycoprotein [Human
 immunodeficiency virus type 1]
 Length = 115

40 Score = 29.7 bits (65), Expect = 4.2
 Identities = 15/35 (42%), Positives = 21/35 (59%)
 Frame = +1Query: 76 QSHCNM*RIQHFWQISLQIIWTLTGFLDGIVALIF 180
 Q+HCN+ R+Q W +LQ+ T L G L +IF
Sbjct: 52 Q A H C N I S R V Q --W N K T L Q Q V A T K L G G L F N Q T T I I F 84

45 RANK 14 ITERATION 0>gb|AAB61572.1| U92803 CC-chemokine-
binding receptor JAB61 [*Rattus*
 norvegicus]

Length = 382

Score = 29.7 bits (65), Expect = 4.2

Identities = 16/45 (35%), Positives = 25/45 (55%), Gaps = 2/45 (4%)

5 Frame = +1Query: 61 *TVEDQSHCNM*RIQH--

FWQISLQIIWTLLGFLDGIVALIFFVNLI 195

T++ HC H W++ L+ LLGFL ++A+IFF +I

Sbjct: 187

QTLDGVWHCYADFGGHATIWKLYLRFQMNLLGFLFPLLAMIFFYSRI 233

10

RANK 15 ITERATION 0>emb|CAA67111.1| X98485 putative

[Plasmodium vivax]

Length = 101

15 Score = 29.3 bits (64), Expect = 5.5

Identities = 14/35 (40%), Positives = 23/35 (65%), Gaps = 1/35 (2%)

Frame = +1Query: 100 IQHFWQISLQIIWTLLGFLDGIVALI-FFVNLIFVN 204

++ FW +SLQI +++L FL + +I F + L F N

Sbjct: 53 LEEFWPLSLQIFFSVLPFLSNYMCIIPFEIVLQFTN 88

20

RANK 16 ITERATION 0>gb|AAD08699.1| AF098292 endo-beta-1,4-D-

glucanase [Lycopersicon

esculentum]

Length = 625

25

Score = 29.3 bits (64), Expect = 5.5

Identities = 21/70 (30%), Positives = 34/70 (48%)

Frame = +3Query: 6

VLSKQFQVYNRTRGGGLIELNSGGPKPLQYVANTAFLANLFADYMDSTGVPG

30 WYCGPYFLR 185

+L K + +T GGLI +Q+V + AFLA ++DY+ S G C F+

Sbjct: 316 MLGKGNRNTQKTPGGLIYRQRWNN--

MQFVTSAAFLATTYS DYLASAG-KYLCSSGFVS 372Query: 186

QSDLRELVR 215

35

++L +S

Sbjct: 373 PNELLSFAKS 382

RANK 17 ITERATION 0>gb|AAF15367.1| AF206716 endoglucanase

[Bacillus pumilus]

40

Length = 659

Score = 29.3 bits (64), Expect = 5.5

Identities = 16/33 (48%), Positives = 22/33 (66%)

Frame = +3Query: 39 TRGGLIELNSGGPKPLQYVANTAFLANLFADYM 137

45

T GGL L+ G L+Y AN AFLA ++AD++

Sbjct: 346 TPGGLAWLDQWGS--LRYTANAAFLAFVYADWV 376

RANK 18 ITERATION 0>pir||40807 cellulase (EC 3.2.1.4) engC -
Clostridium cellulovorans
Length = 553

5

Score = 29.3 bits (64), Expect = 5.5
Identities = 16/33 (48%), Positives = 22/33 (66%)
Frame = +3Query: 39 TRGGLIELNSGGPKPLQYVANTAFLANLFADYM 137
T GGL L+ G L+Y AN AFLA ++AD++

10 Sbjet: 346 TPGGLAWLDQWGS--LRYTANAAFLAFVYADWV 376

RANK 19 ITERATION 0>sp|P28622|GUN4_BACS5
ENDOGLUCANASE 4 PRECURSOR
(ENDO-1,4-BETA-GLUCANASE 4) (CELLULASE 4) (EG-IV)
15 >gi|7474377|pir||JC5874 cellulase (EC 3.2.1.4) precursor
- Bacillus sp >gi|2897802|dbj|BAA24918.1| (AB004098)
endo-1,4-beta-glucanase [Bacillus sp.]
Length = 636

20

Score = 29.3 bits (64), Expect = 5.5
Identities = 16/33 (48%), Positives = 22/33 (66%)
Frame = +3Query: 39 TRGGLIELNSGGPKPLQYVANTAFLANLFADYM 137
T GGL L+ G L+Y AN AFLA ++AD++

Sbjet: 327 TPGGLAWLDQWGS--LRYTANAAFLAFVYADWV 357

25

RANK 20 ITERATION 0>emb|CAA73379.1| Y12879 beta-chemokine
receptor D6 [Mus musculus]
Length = 378

30

Score = 29.0 bits (63), Expect = 7.2
Identities = 16/45 (35%), Positives = 25/45 (55%), Gaps = 2/45 (4%)
Frame = +1Query: 61 *TVEDQSHCNM*RIQH--
FWQISLQIIWTLGFLDGIVALIFFVNLI 195

T++ HC H W++ L+ LLGFL ++A+IFF +I

35

Sbjet: 186
QTLDGVWHCYADFGGHATIWKLYLRFQLNLLGFLPLLAMIFFYSRI 232
[END ALIGNMENTS]

Job Details

40 [Return to top](#)

[BEGIN JOB STATUS]

[SEARCH ID]

[EOL] CRLF

45

[COMMENT] /Comment=NCBI BLASTX Translated Search
[COMMENT] /CGI_


```

[ALGORITHM] BLASTX
[MATRIX] D:\DECYPHER\MATRIX\BLOSUM62.MAA
[QUERY FORMAT] FASTA/PEARSON
[QUERY TYPE] NT
5 [QUERY FILTER] T
[QUERY SEARCH] -1 -2 -3 1 2 3
[QUERY PATH] d:\decypher\query
[QUERY SET]
[TARGET TYPE] AA
10 [TARGET FRAMES] 1
[TARGET PATH] d:\decypher\target\blast
[TARGET SET] nr
[MAX SCORES] 30
[MAX ALIGNMENTS] 20
15 [THRESHOLD] 1
[RESULT PATH] d:\decypher\output
[OUTPUT FORMAT] TEXT EXTRACTALIGNED[SHOW GI] F
[EXPECTATION] 10
[GAPPED ALIGNMENT] TBLASTX
20 BLASTX Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A.
Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs", Nucleic Acids Res. 25:3389-3402.Query= Your_Query starting with:
25 GATGAGTCCTGAGTAAGCAA /QuerySize=217
(217 letters)
Database: Nonredundant Proteins
598,029 sequences; 189,012,571 total letters
Database: Nonredundant Proteins
30 Number of letters in database: 189,012,571
Number of sequences in database: 598,029
Lambda K H
0.318 0.135 0.401
Gapped
35 Lambda K H
0.270 0.0470 0.230 Matrix: BLOSUM62.MAA
Gap Penalties: Existence: 11, Extension: 1
Number of Hits to DB: 78221013
Number of Sequences: 598029
40 Number of extensions: 1409131
Number of successful extensions: 6695
Number of sequences better than 10.0: 60
Number of HSP's better than 10.0 without gapping: 17
Number of HSP's successfully gapped in prelim test: 13
45 Number of HSP's that attempted gapping in prelim test: 6678
Number of HSP's gapped (non-prelim): 30

```

length of query: 72
length of database: 189,012,571
effective HSP length: 50
effective length of query: 21
5 effective length of database: 159,111,121
effective search space: 3341333541
effective search space used: 3341333541
frameshift window, decay const: 50, 0.1
T: 12
10 A: 40
X1: 16 (7.3 bits)
X2: 38 (14.8 bits)
X3: 64 (24.9 bits)
S1: 41 (21.7 bits)
15 **S2: 62 (28.6 bits)[JOB MESSAGES][END JOB STATUS]DeCypher**

Results for: NCBI TBLASTX Similarity Search

Results by Query

Click on a query below to view its search results.
Your_Query starting with: GATGAGTCCTGAGTAAGCAA

20 **Search Details**

Results for: Your_Query starting with:
GATGAGTCCTGAGTAAGCAA; (Length=217)

25 [Return to query summary](#)

	RANK	Sequences producing significant alignments:	(bits)	Value
	<u>1</u>	CL014572.178.121	97	2e-020
	<u>2</u>	CL039258.100	92	6e-019
30	<u>3</u>	CL014123.176.147	89	4e-018
	<u>4</u>	CL003768.44	36	0.032
	<u>5</u>	CL015561.165	34	0.15
	<u>6</u>	CL003630.19	34	0.21
	<u>7</u>	CL011752.109	34	0.21
35	<u>8</u>	CL005473.68.117	34	0.21
	<u>9</u>	CL039250.11	33	0.29
	<u>10</u>	CL015463.45	33	0.29
	<u>11</u>	CL017322.121	33	0.29
	<u>12</u>	CL004643.389.153	33	0.29
40	<u>13</u>	CL056684.22.32	33	0.40
	<u>14</u>	CL012270.93	33	0.40
	<u>15</u>	CL029430.34.48	33	0.40
	<u>16</u>	CL021562.87	32	0.55

RANK 2 ITERATION 0>CL039258.100

Length = 6683

5 Score = 91.8 bits (194), Expect = 6e-019
Identities = 34/60 (56%), Positives = 43/60 (71%)
Frame = +3 / +2

Query: 36

10 RTRGGLIELNSGGPKPLQYVANTAFLANLFADYMDSTGVPGWYCGPYFLRQ
SDLRELVRS 215

R GG+I+LN G P+PLQYV N AFLA+L++DY+D+ PGWYCGP F LR+

RS

Sbjct: 4127

15 RFTGGMIQLNHGRPQPLQYVVNA AFLASLYSDYLDAAADTPGWYCGPTFYTT
EVLRFKARS 4306 Score = 32.2 bits (64), Expect = 0.55

Identities = 15/45 (33%), Positives = 23/45 (50%)

Frame = +2 / +1

20 Query: 44

RRIDRAEQWRTKAIAICSEYSIFGKSLCRLYGLYWGSWMVLWPLF 178

RR D A+ + A ++C + S+ RL G +W+VLW F

Sbjct: 4135

RRNDTAQPRKASATSVCCQCGFPCLSIQRLPGCCRYTWVVLWITYF 4269

25 Score = 48.7 bits (100), Expect = 6e-006

Identities = 26/54 (48%), Positives = 29/54 (53%)

Frame = -1 / -3

Query: 205

30 NSRRSD*RRK*GPQYHPGTPVESI*SAKRFAKNAVFATYCNGFGPPLFSSINPP
44

N RR+ K GPQYHPG S *S R A+ A TY +G G P S I PP

Sbjct: 4296

NLRRTSVV*KVGPQYHPGVSAASR*SLYREARKAALTTY*SG*GLPWLSCIIP

35 P 4135

RANK 3 ITERATION 0>CL014123.176.147

Length = 9524

40 Score = 89.0 bits (188), Expect = 4e-018
Identities = 32/57 (56%), Positives = 41/57 (71%)
Frame = +3 / -3

Query: 45

45 GGLIELNSGGPKPLQYVANTAFLANLFADYMDSTGVPGWYCGPYFLRQSDL
RELVRS 215

GGLI+LN G P+PLQYV N AFLA+L+ DY+++ PGWYCGP+F LR R+
Sbjct: 3705
GGLIQLNHGRPQPLQYVVNA AFLASLYGDYLEAADTPGWYCGPHFYPIETL
RNFART 3535

5

RANK 4 ITERATION 0

>CL003768.44

Length = 4180

10

Score = 36.3 bits (73), Expect = 0.032

Identities = 16/44 (36%), Positives = 25/44 (56%)

Frame = +3 / +2

15

Query: 84

LQYVANTAFLANLFADYMDSTGVPGWYCGPYFLRQSDLREL VRS 215

LQ+ +AFLA +++DYM S+G C +DLR+ +S

Sbjct: 1403

LQHPVASAFLAAVYSDYMQSSGKTELSCSGQGFSPADLRKFAKS 1534

20

RANK 5 ITERATION 0>CL015561.165

Length = 4917

Score = 34.1 bits (68), Expect = 0.15

25 Identities = 16/44 (36%), Positives = 24/44 (54%)

Frame = +3 / -1

Query: 84

LQYVANTAFLANLFADYMDSTGVPGWYCGPYFLRQSDLREL VRS 215

30

LQ+ +AFLA +++DYM S+ C SDLR+ +S

Sbjct: 822 LQHPVASAFLAAVYSDYMQSSRKTELTCSGQGFSPSDLRKFAKS
691

RANK 6 ITERATION 0>CL003630.19

35

Length = 2204

Score = 33.6 bits (67), Expect = 0.21

Identities = 12/24 (50%), Positives = 17/24 (70%)

Frame = +1 / -3

40

Query: 136 WTLLGFLDGIVALIFFVNLFVNW 207

W ++ LD V +IFFV L+F+NW

Sbjct: 1761 WRVIL*LDSSVRIFFVKLMFMNW 1690

RANK 7 ITERATION 0>CL011752.109

45

Length = 2467

Sbjct: 1459 LRY*LLTVYLIYSFCSFHFITGITGLYCNHYFLR 1358

RANK 11 ITERATION 0>CL017322.121

Length = 5655

5

Score = 33.1 bits (66), Expect = 0.29

Identities = 10/44 (22%), Positives = 19/44 (42%)

Frame = +1 / +1

10 Query: 43 EED**S*TVEDQSHCNM*RIQHFQISLQIIWTLLGFLDGIVAL
174

E + D+ CN ++QH W + + T + D +A+

Sbjct: 3721 EREERERERERDKEFCNFQKLQHIWYLKFKRSVTCMQKCDFRIAI
3852

15

RANK 12 ITERATION 0>CL004643.389.153

Length = 9365

Score = 33.1 bits (66), Expect = 0.29

20 Identities = 14/43 (32%), Positives = 26/43 (59%)

Frame = -2 / -3

Query: 132 NLQRDLPKMLYSLHIAMALVLHCSALSILLEYDYKPEIAYSGL 4

++RDL +L+ ++ +L +LS+ L Y YKP+I Y++

Sbjct: 2154 DMVRDLRMVLFV FYL*ESLSHVYNGLSLYLRYKYKPQIIYTNI

25 2026

RANK 13 ITERATION 0>CL056684.22.32

Length = 4603

30 Score = 32.7 bits (65), Expect = 0.40

Identities = 14/50 (28%), Positives = 25/50 (50%)

Frame = +1 / +3

Query: 61

*TVEDQSHCNM*RIQHFQISLQIIWTLLGFLDGIVALIFFVNLI FVNWY 210

35 +++ CN * + +W + F + I+A+IFF NL + NW+

Sbjct: 3603

ESLKSLLMCNS*SVVEYWMTRVFAPCNTRDFKNLIMAIIF FANL*YKNWH
3752

40 RANK 14 ITERATION 0>CL012270.93

Length = 430

Score = 32.7 bits (65), Expect = 0.40

Identities = 15/44 (34%), Positives = 22/44 (49%)

45 Frame = -2 / +1

RANK 19 ITERATION 0>CL035133.150

Length = 4282

- 5 Score = 31.8 bits (63), Expect = 0.75
 Identities = 13/28 (46%), Positives = 16/28 (56%)
 Frame = +2 / -3
 Query: 62 EQWRTKAIAICSEYSIFGKSLCRLYGLY 145
 EQW ++A C IF KS CRL L+
 10 Sbjct: 1643 EQWDVDSLAHCVTLPFPKSYCRLSQLF 1560

RANK 20 ITERATION 0>CL016566.130

Length = 3700

- 15 Score = 31.3 bits (62), Expect = 1.0
 Identities = 15/54 (27%), Positives = 29/54 (52%)
 Frame = -2 / +1
 Query: 201
 HEDQIDEENKGHNTIQEPQ*SPYNLQRDLPKMLYSLHIAMALVLHCSALSILL
 20 E 40
 H +ID +H +EP+ + +N + P +L ++HIA V ++ S L++
 Sbjct: 3457
 HVRKIDMSGREHLRCKEPRSNQWNGKIPTPILLSAVHIARTQVAQMASNSQL
 IK 3618
 25 [END
 ALIGNMENTS]

Job Details[Return to top](#)

- 30 [BEGIN JOB STATUS]
 [BEGIN SEARCH TIME]
 [END SEARCH TIME]
 [VERSION]
 [SEARCH ID]
 35 [EOL] CRLF
 [COMMENT] /Comment=NCBI TBLASTX Similarity Search
 [COMMENT] /CGI_
 [ALGORITHM] TBLASTX
 [MATRIX] D:\DECYPHER\MATRIX\BLOSUM62.MAA
 40 [QUERY FORMAT] FASTA/PEARSON
 [QUERY TYPE] NT
 [QUERY FILTER] T
 [QUERY SEARCH] -1 -2 -3 1 2 3
 [QUERY PATH] d:\decypher\query
 45 [QUERY SET]
 [TARGET TYPE] NT
 [TARGET FRAMES] -1 -2 -3 1 2 3

```

[TARGET PATH] d:\decypher\target\blast
[TARGET SET] rice_contigs
[MAX SCORES] 30
[MAX ALIGNMENTS] 20
5 [THRESHOLD] 1
[RESULT PATH] d:\decypher\output
[OUTPUT FORMAT] TEXT EXTRACTALIGNED[SHOW GI] F
[EXPECTATION] 10
[GAPPED ALIGNMENT] TTBLASTX
10 TBLASTX
Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs", Nucleic Acids Res. 25:3389-3402.Query= Your_Query starting with:
15 GATGAGTCCTGAGTAAGCAA /QuerySize=217
(217 letters)Database
154,797 sequences; 359,911,975 total letters Database:
Posted date:
Number of letters in database: 359,911,975
20 Number of sequences in database: 154,797

Lambda K H
0.318 0.135 0.401
Matrix: BLOSUM62.MAA
25 Number of Hits to DB: 174955088
Number of Sequences: 154797
Number of extensions: 1959937
Number of successful extensions: 104549
Number of sequences better than 10.0: 383
30 length of query: 72
length of database: 119,970,658
effective HSP length: 49
effective length of query: 22
effective length of database: 112,385,605
35 effective search space: 2472483310
effective search space used: 2472483310
frameshift window, decay const: 50, 0.1
T: 13
A: 40
40 X1: 16 ( 7.3 bits)
X2: 0 ( 0.0 bits)
S1: 41 (21.7 bits)
S2: 55 (28.1 bits)
[JOB MESSAGES]
45 [END JOB STATUS]

```

DESCA4 Blast report against nonredundant proteins:

DeCypher Results for: NCBI BLASTX Translated Search

Results by Query

Click on a query below to view its search results.

5 Your Query starting with: CTCCAAGTTGCCAGAAGATA

Search Details

Results for: Your Query starting with:

10 **CTCCAAGTTGCCAGAAGATA; (Length=247)**

[Return to query summary](#)

	RANK	Sequences producing significant alignments:	(bits)	Value
15	<u>1</u>	gb <u>AAF71978.1</u> <u>AC013453_3</u> <u>AC013453</u> Putative ABC transporter [A...		
	129	6e-030		
	<u>2</u>	emb <u>CAA94437.1</u> <u>Z70524</u> PDR5-like ABC transporter [Spirodela p...	120	
		2e-027		
	<u>3</u>	gb <u>AAG31197.1</u> <u>AC083891_6</u> <u>AC083891</u> ABC transporter, putative [...	108	
		1e-023		
20	<u>4</u>	gb <u>AAF98206.1</u> <u>AC007152_2</u> <u>AC007152</u> Putative ABC transporter [...	108	
		1e-023		
	<u>5</u>	dbj <u>BAB02609.1</u> <u>AP002043</u> ABC transporter-like protein [Arabid...	105	
		8e-023		
25	<u>6</u>	pir <u>T02644</u> ABC-type transport protein homolog F12C20.5 - Arabi...	99	1e-020
	<u>7</u>	gb <u>AAD39329.1</u> <u>AC007258_18</u> <u>AC007258</u> Putative ABC transporter [...	96	
		5e-020		
	<u>8</u>	gb <u>AAD24623.1</u> <u>AC006919_2</u> <u>AC006919</u> putative ABC transporter [A...		
	95	2e-019		
30	<u>9</u>	gb <u>AAD39650.1</u> <u>AC007591_15</u> <u>AC007591</u> Similar to gb Z70524 PDR5-...		
	94	4e-019		
	<u>10</u>	gb <u>AAB63643.1</u> <u>AC001645</u> ABC transporter (PDR5-like) isolog [A...	92	
		8e-019		
35	<u>11</u>	pir <u>T02491</u> hypothetical protein F23F1.14 - Arabidopsis thalian...	80	4e-015
	<u>12</u>	pir <u>T45888</u> ABC transporter-like protein - Arabidopsis thaliana...	76	5e-014
	<u>13</u>	gb <u>AAC98048.1</u> <u>AC005896</u> putative ABC transporter [Arabidopsis...	75	
		2e-013		
40	<u>14</u>	pir <u>D71416</u> probable PDR5-like ABC transporter - Arabidopsis th...	73	6e-013
	<u>15</u>	emb <u>CAB45997.1</u> <u>Z97338</u> ABC transporter like protein [Arabidop...	73	
		6e-013		

- 16 pir|[T05915 probable ABC transport protein - barley (fragment) ... 52 2e-006
- 17 gb|AAF51130.1| AE003580 CG9663 gene product [Drosophila melan... 34 0.32
- 5 18 sp|Q11180|YPC3_CAEEL PUTATIVE ABC TRANSPORTER C05D10.3 IN CHROM... 33 0.71
- 19 emb|CAB46279.1| AJ243112 putative ABC transporter [Mycosphaer... 32 1.2
- 20 sp|Q05360|WHIT_LUCCU WHITE PROTEIN >gi|1079667|gb|AAA82057.1| (... 32 1.2
- 10 21 gb|AAF61569.1|AF229609_1 AF229609 ATP dependent transmembrane... 32 1.6
- 22 pir|[T43022 ATP-binding multidrug cassette transport protein - ... 32 1.6
- 23 pir|[G81748 conserved hypothetical protein TC0035 [imported] - ... 31 2.7
- 15 24 gb|AAG12173.1|AF078834_1 AF078834 p33ING2 [Mus musculus] 31 2.7
- 25 dbj|BAA93677.1| AB028872 BMR1 [Botryotinia fuckeliana] 31 3.6
- 26 pir|[T30567 ATP-binding cassette multidrug transport protein - ... 31 3.6
- 27 gb|AAF51131.1| AE003580 CG9664 gene product [Drosophila melan... 30 4.7
- 20 28 pir|[T30541 ABC1 transport protein - rice blast fungus >gi|2625... 30 4.7
- 29 pir|[S61535 nucleotide-binding head-stalk protein 183K - Giardi... 30 4.7
- 30 gb|AAB18390.1| U70213 heat shock 70kDa protein [Mesocostoides... 30 4.7
- 25 RANK 1 ITERATION 0>gb|AAF71978.1|AC013453_3 AC013453 Putative ABC transporter
[Arabidopsis thaliana]
Length = 1423
- 30 Score = 129 bits (321), Expect = 6e-030
Identities = 57/79 (72%), Positives = 66/79 (83%)
Frame = -1Query: 238
NSELYRRNKA VIQELGTPRPGSQDLYFPTIYSQSFFS QVLACLWKQHLSYWR
35 NTPYTAVR 59
NSELY+RNK +I+EL P PGS+DLYFPT YS QSF +Q +A LWKQH SYWRN
PYTAVR
Sbjct: 1114
NSELYKRNKELIKELSQPAPGSKDLYFPTQYSQSFLTQCMASLWKQHWSYW
40 RNPPYTAVR 1173Query: 58 FVFTVAIALTFGTIFWQLG 2
F+FT+ IAL FGT+FW LG
Sbjct: 1174 FLFTIGIALMFGTMFWDLG 1192
- 45 RANK 2 ITERATION 0>emb|CAA94437.1| Z70524 PDR5-like ABC transporter
[Spirodela
polyrrhiza]

Length = 1441

Score = 120 bits (299), Expect = 2e-027
Identities = 55/79 (69%), Positives = 62/79 (77%)

5 Frame = -1Query: 238
NSELYRRNKAVIQELGTPRPGSQDLYFPTIYSQSFFSQVLACLWKQHLSYWR
NTPYTAVR 59

NS+LY+RNK +I+EL TP PGS+DL+F T +SQSF Q LACLWKQH SYWRN
YTA R

10 Sbjct: 1132
NSDLYKRNDLIKELSTPPPGSKDLFFATQFSQSFMQCLACLWKQHKSYSW
RNPSYTATR 1191Query: 58 FVFTVAIALTFGTIFWQLG 2

FTV IAL FGTIFW LG

Sbjct: 1192 LFFTIVIALIFGTIFWDLG 1210

15 RANK 3 ITERATION 0>gb|AAG31197.1|AC083891_6 AC083891 ABC
transporter, putative

[Arabidopsis thaliana]

Length = 1434

20 Score = 108 bits (268), Expect = 1e-023
Identities = 46/80 (57%), Positives = 61/80 (75%)
Frame = -1Query: 241

TNSELYRRNKAVIQELGTPRPGSQDLYFPTIYSQSFFSQVLACLWKQHLSYW
25 RNTPYTAV 62

+NS LYRRN+ +I++L TP PGS+D+YF T Y+QSF +Q AC WKQ+ SYWR+
Y A+

Sbjct: 1121

SNSSLYRRNQELIKDLSTPPPGSKDVYFKTKYAQSFSSTQTKACFWKQYWSY
30 WRHPQYNAI 1180Query: 61 RFVFTVAIALTFGTIFWQLG 2

RF+ TV I + FG IFWQ+G

Sbjct: 1181 RFLMTVVIGVLFGLIFWQIG 1200

35 RANK 4 ITERATION 0>gb|AAF98206.1|AC007152_2 AC007152 Putative ABC
transporter

[Arabidopsis thaliana]

Length = 1435

40 Score = 108 bits (268), Expect = 1e-023
Identities = 46/80 (57%), Positives = 61/80 (75%)

Frame = -1Query: 241

TNSELYRRNKAVIQELGTPRPGSQDLYFPTIYSQSFFSQVLACLWKQHLSYW
RNTPYTAV 62

45 +NS LYRRN+ +I++L TP PGS+D+YF T Y+QSF +Q AC WKQ+ SYWR+
Y A+

Sbjct: 1122
 SNSSLYRRNQELIKDLSTPPPGSKDVYFKTKYAQSFSTQTKACFWKQYWSY
 WRHPQYNAI 1181Query: 61 RFVFTVAIALTFGTIFWQLG 2
 RF+ TV I + FG IFWQ+G

5 Sbjct: 1182 RFLMTVVIGVLFGLIFWQIG 1201

RANK 5 ITERATION 0>dbj|BAB02609.1| AP002043 ABC transporter-like
 protein [Arabidopsis
 thaliana]
 10 Length = 1405

Score = 105 bits (260), Expect = 8e-023
 Identities = 47/78 (60%), Positives = 56/78 (71%)
 Frame = -1Query: 235

15 SELYRRNKAVIQELGTPRPGSQDLYFPTIYSQSFFSQVLACLWKQHLSYWRN
 TPYTAVRF 56
 S LYRRNK +I+EL P +QD++F T YSQS+ SQ ACLWKQH SYWRN PY
 AVRF

Sbjct: 1118

20 SNLYRRNKDLIKELNNIPPHAQDIHFSTKYSQSYLSQFQACLWKQHKSYSWR
 NVPYNAVR 1177Query: 55 VFTVAIALTFGTIFWQLG 2
 F A+ + +G IFW LG

Sbjct: 1178 SFGAAVGIMYGIIFWSLG 1195

25 RANK 6 ITERATION 0>pir|T02644 ABC-type transport protein homolog
 F12C20.5 - Arabidopsis
 thaliana >gi|3426037|gb|AAC32236.1| (AC005168) putative
 ABC transporter [Arabidopsis thaliana]
 Length = 1420

30 Score = 98.7 bits (242), Expect = 1e-020
 Identities = 45/79 (56%), Positives = 58/79 (72%)
 Frame = -1Query: 238

35 NSELYRRNKAVIQELGTPRPGSQDLYFPTIYSQSFFSQVLACLWKQHLSYWR
 NTPYTAVR 59
 NS L +RNK +I+ L P +++++ FPT YSQS +SQ +ACLWKQ+LSYWRN
 YTAVR

Sbjct: 1107

40 NSNLCQRNKELIEVLSKPSNIAKEIEFPTRYSQLYSQFVACLWKQNLSYWR
 NPQYTAVR 1166Query: 58 FVFTVAIALTFGTIFWQLG 2
 F +TV I+L GTI W+ G

Sbjct: 1167 FFYTVVISLMLGTICWKFG 1185

45 RANK 7 ITERATION 0>gb|AAD39329.1|AC007258_18 AC007258 Putative
 ABC transporter
 [Arabidopsis thaliana]

Length = 1469

Score = 96.3 bits (236), Expect = 5e-020
Identities = 41/82 (50%), Positives = 58/82 (70%)

5 Frame = -1Query: 247

LRTNSEL YRRNKAVIQELGTPRPGSQDLYFPTIYSQSFFSQVLACLWKQHLS
YWRNTPYT 68

L S L++RNKA+++EL P G+ DLYF T +SQ+ + Q +CLWKQ +YWR+ Y
Sbjct: 1153

10 LYNQSALHQRNKALVKELSVPPAGASDLYFATQFSQNTWGGQFKSCLWKQW
WTYWRSPDYN 1212Query: 67 AVR FVFTVAIALTFGTIFWQLG 2

VRF+FT+A +L GT+FWQ+G
Sbjct: 1213 LVR FIFTLATSL LIGTVFWQIG 1234

15 RANK 8 ITERATION 0>gb|AAD24623.1|AC006919_2 AC006919 putative ABC
transporter

[Arabidopsis thaliana]
Length = 1450

20 Score = 94.8 bits (232), Expect = 2e-019
Identities = 42/79 (53%), Positives = 53/79 (66%)
Frame = -1Query: 238

NSELYRRNKAVIQELGTPRPGSQDLYFPTIYSQSFFSQVLACLWKQHLSYWR
NTPYTAVR 59

25 NS + RRN+ +I+EL TP PGS DLYF T Y+Q F +Q AC WK + S WR Y A+R
Sbjct: 1138

NSSVNRRNQELIKELSTPPPGSNDLYFRTKYAQPFFSTQTKACFWKMYWSNW
RYPQYNAIR 1197Query: 58 FVFTVAIALTFGTIFWQLG 2

F+ TV I + FG +FWQ G
30 Sbjct: 1198 FLMTVVIGVLFGLLFWQTG 1216

RANK 9 ITERATION 0>gb|AAD39650.1|AC007591_15 AC007591 Similar to
gb|Z70524 PDR5-like ABC

35 transporter from Spirodela polyrrhiza and is a member of
the PF|00005 ABC transporter family. ESTs gb|N97039 and
gb|T43169 come from this gene. [Arabidopsis thaliana]
Length = 1451

40 Score = 93.6 bits (229), Expect = 4e-019
Identities = 40/78 (51%), Positives = 56/78 (71%)
Frame = -1Query: 235

SELYRRNKAVIQELGTPRPGSQDLYFPTIYSQSFFSQVLACLWKQHLSYWRN
TPYTAVRF 56

45 VRF
S L +RNKA++QEL P G+ DLYF T +SQ+ + Q +CLWKQ +YWR+ Y

Sbjct: 1139
 SALCQRNKALVQELSVPPQGATDLYFATQFSQNTWGGQFKSCLWKQWWTY
 WRSPDYNLVRF 1198Query: 55 VFTVAIALTFGTIFWQLG 2
 +FT+A +L G++FWQ+G

5 Sbjct: 1199 IFTLATSLMIGSVFWQIG 1216

RANK 10 ITERATION 0>gb|AAB63643.1| AC001645 ABC transporter (PDR5-
 like) isolog

10 [Arabidopsis thaliana] >gi|9279716|dbj|BAB01273.1|
 (AB023046) ABC transporter [Arabidopsis thaliana]
 Length = 1416

Score = 92.4 bits (226), Expect = 8e-019
 Identities = 39/78 (50%), Positives = 54/78 (69%)

15 Frame = -1Query: 235
 SELYRRNKAVIQELGTPRPGSQDL YFPTIYSQSFFSQVLACLWKQHLSYWRN
 TPYTAVRF 56

S LY++NK +++EL TP G+ DLYF T +SQS Q +CLWKQ ++YWR Y

RF

20 Sbjct: 1104
 SSLYQQNKNLVKELSTPPQGASDLYFSTRFSQSLLGQFKSCLWKQWITYWR
 TPDYNLARF 1163Query: 55 VFTVAIALTFGTIFWQLG 2
 FT+A A+ G+IFW++G

Sbjct: 1164 FFTLAAAVMLGSIFWKVG 1181

25 RANK 11 ITERATION 0>pir|T02491 hypothetical protein F23F1.14 - Arabidopsis
 thaliana

30 >gi|3420057|gb|AAC31858.1| (AC004680) putative ABC
 transporter [Arabidopsis thaliana]
 Length = 1443

Score = 80.4 bits (195), Expect = 4e-015
 Identities = 37/82 (45%), Positives = 50/82 (60%)
 Frame = -1Query: 247

35 LRTNSEL YRRNKAVIQELGTPRPGSQDL YFPTIYSQSFFSQVLACLWKQHLS
 YWRNTPYT 68

L S+ +R +A I++L P GS+ + F + YSQ+ SQ L CLWKQ+L YWR+ Y

Sbjct: 1129

40 LYKKSDQFREVEANIKQLSVPPEGSEPISTSRYSQNQLSQFLLCLWKQNLVY
 WRSPEYN 1188Query: 67 AVR FVFTVAIALTFGTIFWQLG 2
 VR VFT A GT+FW +G

Sbjct: 1189 LVRLVFTTIAAFILGTVFWDIG 1210

45 RANK 12 ITERATION 0>pir|T45888 ABC transporter-like protein - Arabidopsis
 thaliana

>gi|6729499|emb|CAB67655.1| (AL132966) ABC

transporter-like protein [Arabidopsis thaliana]

Length = 1450

Score = 76.5 bits (185), Expect = 5e-014

5 Identities = 31/79 (39%), Positives = 51/79 (64%)

Frame = -1Query: 238

NSELYRRNKAVIQELGTPRPGSQDLYFPTIYSQSFFSQVLACLWKQHLSYWR
NTPYTAVR 59

+S LY+RN ++++L P GS D+ F ++QS++ Q +LWK +LSYWR+ Y +R

10 Sbjct: 1139

DSALYKRNSELVKQLSQPDSSDIQFKRTFAQSWWGQFKSILWKMNLSY
WRSPSYNLMR 1198Query: 58 FVFTVAIALTFGTIFWQLG 2

+ T+ +L FG +FW+ G

Sbjct: 1199 MMHTLVSSLIFGALFWKQG 1217

15

RANK 13 ITERATION 0>gb|AAC98048.1| AC005896 putative ABC transporter

[Arabidopsis

thaliana]

Length = 1413

20

Score = 74.9 bits (181), Expect = 2e-013

Identities = 31/78 (39%), Positives = 47/78 (59%)

Frame = -1Query: 235

SELYRRNKAVIQELGTPRPGSQDLYFPTIYSQSFFSQVLACLWKQHLSYWRN
25 TPTYTAVRF 56

S+LY+ N +++EL P GS DL+F ++Q+++ Q +CLWK LSYWR+ Y +R

Sbjct: 1103

SDLYKNNSELVKELSKPDHGSSDLHFKRTFAQNWWEQFKSCLWKMSLSYW
RSPSYNLMRI 1162Query: 55 VFTVAIALTFGTIFWQLG 2

30

T + FG +FW G

Sbjct: 1163 GHTFISSFIFGLLFWNQG 1180

RANK 14 ITERATION 0>pir|D71416 probable PDR5-like ABC transporter -

Arabidopsis thaliana

35

Length = 1177

Score = 73.0 bits (176), Expect = 6e-013

Identities = 32/73 (43%), Positives = 46/73 (62%)

Frame = -1Query: 226

40 YRRNKAVIQELGTPRPGSQDLYFPTIYSQSFFSQVLACLWKQHLSYWRNTPY
TAVRFVFT 47

Y NK V+++L + GS+ L FP+ +SQ+ + Q+ ACLWKQH SYWRN + R VF

Sbjct: 672

YFENKMOVVEQLSSASLGSEALRFPSQFSQTAWVQLKACLWKQHYSYWRNP
45 SHNITRIVFI 731Query: 46 VAIALTFGTIFWQ 8

+ + G +FWQ

RANK 18 ITERATION 0>sp|Q11180|YPC3_CAEEL PUTATIVE ABC
TRANSPORTER C05D10.3 IN CHROMOSOME

III >gi|532111|gb|AAA20989.1| (U13645) similar to D.
melanogaster white protein [Caenorhabditis elegans]
Length = 559

Score = 32.8 bits (73), Expect = 0.71
Identities = 16/52 (30%), Positives = 28/52 (53%)
Frame = -1Query: 163

10 YFPTIYSQSFFSQVLACLWKQHLSYWRNTPYTAVRFVFTVAIALTFGTIFWQ
8

+F Y+ SF++Q LA W+ L+ R+ +VR+ + A G +F+Q

Sbjct: 306

15 FFNQDYNASFWTQFLALFWRSWLTVIRDPNLLSVRLQILITAFITGIVFFQ
357

RANK 19 ITERATION 0>emb|CAB46279.1| AJ243112 putative ABC transporter
[Mycosphaerella

20 graminicola]
Length = 1562

Score = 32.1 bits (71), Expect = 1.2
Identities = 15/49 (30%), Positives = 23/49 (46%)
Frame = -1Query: 148

25 YSQSFFSQVLACLWKQHLSYWRNTPYTAVRFVFTVAIALTFGTIFWQLG 2
++ S Q L+ YWR+ Y +F +V++ G FWQLG

Sbjct: 1212

30 FAASTMLQCTELLRRTRFYWRDPSYLYGKFFVSVIVGIFNGFTFWQLG
1260

RANK 20 ITERATION 0>sp|Q05360|WHIT_LUCCU WHITE PROTEIN
>gi|1079667|gb|AAA82057.1|

(U38899) white protein [Lucilia cuprina]
Length = 677

Score = 32.1 bits (71), Expect = 1.2
Identities = 14/46 (30%), Positives = 24/46 (51%)
Frame = -1Query: 151

40 IYSQSFFSQVLACLWKQHLSYWRNTPYTAVRFVFTVAIALTFGTIF 14
+Y S+F+Q A +W+ +S + VR + T +A+ G IF

Sbjct: 395

LYKASWFTQFRAIMWRSWISTLKEPLLVKVRLIQTMMVAVLIGLIF 440
[END

ALIGNMENTS]

45 [Job Details](#)[Return to top](#)

```

[BEGIN JOB STATUS]
[BEGIN SEARCH TIME]
[END SEARCH TIME]
5 [VERSION]
[SEARCH ID]
[EOL] CRLF
[COMMENT] /Comment=NCBI BLASTX Translated Search
[COMMENT] /CGI_
10 [ALGORITHM] BLASTX
[MATRIX] D:\DECYPHER\MATRIX\BLOSUM62.MAA
[QUERY FORMAT] FASTA/PEARSON
[QUERY TYPE] NT
[QUERY FILTER] T
15 [QUERY SEARCH] -1 -2 -3 1 2 3
[QUERY PATH] d:\decypher\query
[QUERY SET]
[TARGET TYPE] AA
[TARGET FRAMES] 1
20 [TARGET PATH] d:\decypher\target\blast
[TARGET SET] nr
[MAX SCORES] 30
[MAX ALIGNMENTS] 20
[THRESHOLD] 1
25 [RESULT PATH] d:\decypher\output
[OUTPUT FORMAT] TEXT EXTRACTALIGNED[SHOW GI] F
[EXPECTATION] 10
[GAPPED ALIGNMENT] TBLASTX
BLASTX
30 Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs", Nucleic Acids Res. 25:3389-3402.Query= Your_Query starting with:
CTCCAAGTTGCCAGAAGATA /QuerySize=247
35 (247 letters)Database: Nonredundant Proteins
598,029 sequences; 189,012,571 total letters Database: Nonredundant
Proteins
Posted date:
Number of letters in database: 189,012,571
40 Number of sequences in database: 598,029

Lambda K H
0.318 0.135 0.401 Gapped
Lambda K H
45 0.270 0.0470 0.230
Matrix: BLOSUM62.MAA
Gap Penalties: Existence: 11, Extension: 1

```

Number of Hits to DB: 85229441
 Number of Sequences: 598029
 Number of extensions: 1495114
 Number of successful extensions: 5979
 5 Number of sequences better than 10.0: 64
 Number of HSP's better than 10.0 without gapping: 26
 Number of HSP's successfully gapped in prelim test: 10
 Number of HSP's that attempted gapping in prelim test: 5944
 Number of HSP's gapped (non-prelim): 44
 10 length of query: 82
 length of database: 189,012,571
 effective HSP length: 50
 effective length of query: 31
 effective length of database: 159,111,121
 15 effective search space: 4932444751
 effective search space used: 4932444751
 frameshift window, decay const: 50, 0.1
 T: 12
 A: 40
 20 X1: 16 (7.3 bits)
 X2: 38 (14.8 bits)
 X3: 64 (24.9 bits)
 S1: 41 (21.7 bits)

S2: 63 (29.0 bits)[JOB MESSAGES] [END JOB STATUS]

25 **DeCypher Results for: NCBI TBLASTX Similarity Search**
Results by Query

Click on a query below to view its search results.

Your Query starting with: CTCCAAGTTGCCAGAAGATA

30 **Search Details**

Results for: Your Query starting with:
CTCCAAGTTGCCAGAAGATA; (Length=247)

[Return to query summary](#)

	RANK	Sequences producing significant alignments:	(bits)	Value
	<u>1</u>	CL006165.133	146	3e-035
	<u>2</u>	CL033427.97	144	2e-034
	<u>3</u>	CL007442.59	137	2e-032
40	<u>4</u>	CL030069.96	132	5e-031
	<u>5</u>	CL015806.71.73	131	1e-030
	<u>6</u>	CL019956.116	131	1e-030
	<u>7</u>	CL015979.62	130	2e-030

	<u>8</u>	CL005229.122	126 3e-029
	<u>9</u>	CL022029.79.92	125 8e-029
	<u>10</u>	CL034104.95.105	123 3e-028
	<u>11</u>	CL004519.125	114 1e-025
5	<u>12</u>	CL015320.117	114 1e-025
	<u>13</u>	CL011245.130	111 1e-024
	<u>14</u>	CL030907.51	109 5e-024
	<u>15</u>	HTC136628-B01.1.12	105 9e-023
	<u>16</u>	CL006941.193	104 1e-022
10	<u>17</u>	CL017221.107	101 1e-021
	<u>18</u>	CL029363.9	100 2e-021
	<u>19</u>	CL032337.38.39	100 2e-021
	<u>20</u>	CL004158.37.92	89 6e-018
	<u>21</u>	CL008664.122.49	89 6e-018
15	<u>22</u>	CL009086.91.106	88 2e-017
	<u>23</u>	CL004158.37.98	86 6e-017
	<u>24</u>	CL032965.81	85 1e-016
	<u>25</u>	CL032050.208	79 5e-015
	<u>26</u>	CL000720.227	79 7e-015
20	<u>27</u>	CL048383.82.87	71 2e-012
	<u>28</u>	CL032050.194	61 2e-009
	<u>29</u>	CL011454.199.122	59 8e-009
	<u>30</u>	CL002331.203	35 0.16
25	<u>RANK 1</u> ITERATION 0>CL006165.133 Length = 6699		
	Score = 95.0 bits (201), Expect = 1e-019 Identities = 44/74 (59%), Positives = 51/74 (68%)		
30	Frame = +3 / -2 Query: 3 PSCQKIVPKVRAIATVKTNLTA*GVLRQYDRCCFHKQARTCEKNDWEYIV GK*RSCEPG 182 P QK+VPK+RA+ VK +L A+*G QYDRCCFH+ AR K D EY VGK S		
35	EPG Sbjct: 1772 PRSQKMVPKMRAMTVVKNSLMAL*GGFLQYDRCCFHRHARH*IKKDCEYC VGKYSSLEPG 1593 Query: 183 RGV PNS*ITALFLL 224		
40	GV +S I ALFLL Sbjct: 1592 GGV LSSCINALFLL 1551 Score = 52.4 bits (108), Expect = 7e-007 Identities = 33/75 (44%), Positives = 40/75 (53%) Frame = +2 / -1		

RANK 2 ITERATION 0>CL033427.97

Length = 4922

- 5 Score = 42.8 bits (87), Expect = 5e-004
Identities = 28/75 (37%), Positives = 36/75 (47%)
Frame = +2 / +3
Query: 2
SKLPEDSSESESNHSGKDKSDSXVRSITPV*QVLF PQTSQDL*EE*LG VYSREI
10 EVL*TR 181
+K+PED ++ ES + S VR + PV*QV PQ L E V REI T
Sbjct: 2433
AKIPEDGAKEESYDSSEK*SYGIVRRVPPV*QVHLPQAC*ALI*ER*RVLCREI
*FTRTW 2612
15 Query: 182 SRRSQLLNHCFVSPV 226
+Q L C V P+
Sbjct: 2613 WWCAQFLYQCLVPPI 2657
Score = 90.9 bits (192), Expect = 2e-018
Identities = 44/74 (59%), Positives = 49/74 (65%)
20 Frame = +3 / +1
Query: 3
PSCQKIVPKVRAIATVKTNLTA V*GVL RQYDRCCFHKQARTCEKNDWEYIV
GK*RSCEPG 182
P QK+VPK RA+ VK NL A+*G QYDRC FH+ AR K D EY VGK S
25 EPG
Sbjct: 2434
PRSQKMVPKRRAMTVVKNNLMAL*GGFLQYDRCIFHRHARH*FKKDSEYF
VGKYSSLEPG 2613
Query: 183 RGV PNS*ITALFLL 224
30 GV +S I ALFLL
Sbjct: 2614 GGV LSSCINALFLL 2655
Score = 29.9 bits (59), Expect = 3.9
Identities = 20/46 (43%), Positives = 23/46 (49%)
Frame = +1 / +2
35 Query: 85
ASMTGAVSTNKPGLVRRMIGSI**GNRGPVNQVEAFPTPESLLCFS 222
+SMTGA ST G+ R I S *GN N V P S+ C S
Sbjct: 2516
SSMTGASSTGMLGIDLRKIASTL*GNIVHSNLVVVCSVPVSMPCSS 2653
40 Score = 144 bits (308), Expect = 2e-034
Identities = 55/76 (72%), Positives = 60/76 (78%)
Frame = -1 / -1
Query: 229
LYRRNKAVIQELGT PRPGSQDLYFPTIYSQSFFSQVLACLWKQHLSYWRNTP
45 YTAVRFVF 50

+YRRNKA+IQEL TP PGS +LYFPT YS SF +Q LACLWK HLSYWRN PY
A+R F
Sbjct: 2660
IYRRNKALIQELSTPPPGSSELYFPTKYSLSFNLQCLACLWKMHLASYWRNPP
5 YNAIRLFF 2481
Query: 49 TVALALTFGTIFWQLG 2
T IAL FGTIFW LG
Sbjct: 2480 TTVIALLFGTIFWDLG 2433
Score = 37.7 bits (76), Expect = 0.018
10 Identities = 21/73 (28%), Positives = 33/73 (44%)
Frame = -3 / -3
Query: 221
EKQSSDSGVGNASTWFTGXXXXXXXXXXXXXLTSPGLFVETAPVILA*YSLH
XCQICLYRG 42
15 E+Q D+G ++T F + P + VE APVIL SL +I +
Sbjct: 2652
EEQGIDTGTEHTTTRFE*TIFPYKVLAIFLKSMPSMPVEDAPVILEEPSLQCHKI
IFHYC 2473
Query: 41 YCSHFRNYLLATW 3
20 + S ++LL +W
Sbjct: 2472 HSSPLWHLLGSW 2434

RANK 3 ITERATION 0>CL007442.59
Length = 3798
25
Score = 51.0 bits (105), Expect = 2e-006
Identities = 28/74 (37%), Positives = 41/74 (54%)
Frame = +2 / -3
Query: 2
30 SKLPEDSSESESNSHGKDKSDSXVRSITPV*QVLF PQTSQDL*EE*LGVYSREI
EVL*TR 181
+K+PED ++ +SN + + + VR + PV*QVL PQ S L L + REI+V *
Sbjct: 2887
AKVPEDGTKEKSNDSSEKEPNGIVRRVPPV*QVLLPQASHALC*RRLRILGRE
35 IQVT*IG 2708
Query: 182 SRRSQLLNHCFVSP 223
+Q+L V P
Sbjct: 2707 GWLAQVLYQGLVPP 2666
Score = 92.2 bits (195), Expect = 7e-019
40 Identities = 45/74 (60%), Positives = 49/74 (65%)
Frame = +3 / -1
Query: 3
PSCQKIVPKVRAIATVKTNLTA*GVLRQYDRCCFHKQARTCEKNDWEYIV
GK*RSCEPG 182
45 P QK+VPK RA+ VK NLTA+*G QYDR CFH+QA C K D EY VGK RS
E G

Sbjct: 2761 TMHGLPVEAKPVILEEPSLQCR*VLFHYCHCSSLWYHLLGPW
2886

RANK 4 ITERATION 0>CL030069.96

5 Length = 5235

Score = 40.9 bits (83), Expect = 0.002
Identities = 26/72 (36%), Positives = 35/72 (48%)
Frame = +2 / -3

10 Query: 2
SKLPEDSSESESNHSGKDKSDSXVRSITPV*QVLFQTSQDL*EE*LGVYSREI
EVL*TR 181

SK+PE S+ N ++S V IP+* +L PQ S L E V RE+E+ R

Sbjct: 4426

15 SKVPEHCSKH*GNDDSEE*SHCSVGWIPPI*PILLPQAS*ALCNERSRVLRREV
EISRAR 4247

Query: 182 SRRSQLLNHCFV 217
+ LLN V

Sbjct: 4246 RWCA*LLNKFLV 4211

20 Score = 101 bits (215), Expect = 1e-021
Identities = 46/74 (62%), Positives = 53/74 (71%)
Frame = +3 / -1

Query: 3
PSCQKIVPKVRAIATVKTNLTA*GVLRQYDRCCFHKQARTCEKNDWEYIV
25 GK*RSCEPG 182

P Q IVP +RA+ VK+NLTA* QYD+ CFHKQAR C ND EY VGK RS
EPG

Sbjct: 4425

PRFQNI*V*PNIRAMTIVKSNLTAV*DGFLQYDQFCFHKQARHCVMNDLEYCV

30 GKLRSVEPG 4246

Query: 183 RGV*PNS*ITALFLL 224
GV +S I++LFL

Sbjct: 4245 GGVLS*SSSI*SLFLL 4204

35 Score = 132 bits (283), Expect = 5e-031
Identities = 51/75 (68%), Positives = 60/75 (80%)
Frame = -1 / +2

Query: 226
YRRNKAVIQELGT*PRPGSQDLYFPTIYSQSFFSQVLACLWKQHLSYWRNTPY
TAVRFVFT 47

40 +RRNK +I+EL TP PGS DL FPT YS+SF +Q LACLWKQ+ SYWRN
YTAVR +FT

Sbjct: 4202

FRRNKELIEELSTPPPGSTD*LN*FPTQYSRSFITQCLACLWKQNWSYWRNPSY
TAVRLLFT 4381

45 Query: 46 VAI*ALTFGTIFWQLG 2
+ IAL FGT+FW LG

Sbjct: 4286 GGALNSLIKFLFLL 4245
Score = 42.8 bits (87), Expect = 5e-004
Identities = 22/75 (29%), Positives = 34/75 (45%)
Frame = -3 / +3

5 Query: 227
IQEKQSSDSGVGNASTWFTGXXXXXXXXXXXXLTSPGLFVETAPVILA*YSL
HXCQICLY 48

+QE+Q D GV S F T GL +E ++L SL+ C++ L+

Sbjct: 4242

10 LQEEQKFD*GVKCTS*RFKRLIISNSIFTAFSYTMVGLPMEATSIVLEKSSLYC
CEVPLH 4421

Query: 47 RGYCSHFRNYLLATW 3

C+ RN++L W

Sbjct: 4422 YCSCTLVRNHVLGYW 4466

15 Score = 130 bits (278), Expect = 2e-030
Identities = 49/75 (65%), Positives = 58/75 (77%)

Frame = -1 / +1

Query: 226

YRRNKAVIQELGTPRPGSQDLYFPTIYSQSFFSQVLACLWKQHLSYWRNTPY

20 TAVRFVFT 47

YRRNK +I+EL P GS DL FPT YSQ F +Q LACLWKQHLSYWRN PY

VR++FT

Sbjct: 4243

YRRNKNLIKELSAPPEGSSDLSFPTQYSQFLTLQWLACLWKQHLSYWRNPP

25 YIVVRYLFT 4422

Query: 46 VAIALTFGTIFWQLG 2

+ +AL FGT+FW +G

Sbjct: 4423 IVVALLFGTMFWGIG 4467

30 RANK 8 ITERATION 0>CL005229.122

Length = 2407

Score = 85.8 bits (181), Expect = 6e-017
Identities = 41/74 (55%), Positives = 45/74 (60%)

35 Frame = +3 / -1

Query: 3

PSCQKIVPKVRAIATVKTNLTA V*GVL RQYDRCCFHKQARTCEKNDWEYIV

GK*RSCEPG 182

P +IVPK+RAI VK L AV QYD CCFH+QA C K E VGK RS +PG

40 Sbjct: 352

PRFKNIVPKMRAITVVKKILVAVYDGF LQYDLCCFHRQAMHCVKKGCEN*V

GKCRSVDPG 173

Query: 183 RGV PNS*ITALFLL 224

GV NS I L FLL

45 Sbjct: 172 GGVLNSLINVL FLL 131

Score = 31.3 bits (62), Expect = 1.5

Query: 183 RGVPNS*ITALFLL 224
 GV NS I++ F L
 Sbjct: 846 GGVLNSLISSWFFL 887
 Score = 114 bits (244), Expect = 1e-025
 5 Identities = 42/74 (56%), Positives = 56/74 (74%)
 Frame = -1 / -2
 Query: 223
 RRNKAVIQELGTPRPGSQDLYFPTIYSQSFFSQVLACLWKQHLSYWRNTPYT
 AVRFVFTV 44
 10 R+N+ +I+EL TP PG QDL FPT YSQ+F+SQ +A WKQ+ SYW+N PY
 A+R++ T+
 Sbjct: 886
 RKNQELIKELSTPPPGYQDLSFPTKYSQNFYSQCIANFWKQYRSYWKNPPYN
 AMRYLMTL 707
 15 Query: 43 AIALTFGTIFWQLG 2
 L FGT+FWQ G
 Sbjct: 706 LNGLVFGTVFWQKG 665
 RANK 13 ITERATION 0>CL011245.130
 20 Length = 9174
 Score = 59.7 bits (124), Expect = 4e-009
 Identities = 31/62 (50%), Positives = 36/62 (58%)
 Frame = +3 / +1
 25 Query: 3
 PSCQKIVPKVRAIATVKTNLTA V*GVL RQYDRCCFHKQARTCEKNDWEYIV
 GK*RSCEPG 182
 P QK+VP +A+ VK NLT +* LRQ CF +QA C D EY VGK RS PG
 Sbjct: 8308
 30 PIFQKMVPSSKAVNRVKENLTRL*SGLRQ*VSHCFQRQALNCPMVD*EYFV
 GKCRSDVPG 8487
 Query: 183 RG 188
 G
 Sbjct: 8488 SG 8493
 35 Score = 111 bits (237), Expect = 1e-024
 Identities = 41/76 (53%), Positives = 54/76 (70%)
 Frame = -1 / -2
 Query: 229
 LYRRNKAVIQELGTPRPGSQDLYFPTIYSQSFFSQVLACLWKQHLSYWRNTP
 40 YTAVRFVF 50
 ++R+NK ++ +L P PG+ DL+FPT YSQS Q ACLWKQ L+YWR+ Y
 VRF F
 Sbjct: 8534
 VFRQNKVLVNQLSQPEPGTSDLHFPTKYSQSTIGQFRACLWKQWLTYWRSP
 45 DYNLVRFSF 8355
 Query: 49 TVAIALTFGTIFWQLG 2

T+ AL GTIFW++G
Sbjct: 8354 TLFTALLGTIFWKIG 8307

RANK 14 ITERATION 0>CL030907.51

5 Length = 11233

Score = 49.2 bits (101), Expect = 6e-006
Identities = 31/74 (41%), Positives = 41/74 (54%)
Frame = +3 / -1

10 Query: 3

PSCQKIVPKVRAIATVKTNLTA*GVLRQYDRCCFHKQARTCEKNDWEYIV
GK*RSCEPG 182

P+ Q IVP ++A+ K LT +* L Q CF +Q+ K EY +GK*RS EPG

Sbjct: 7672

15 PTLQNIVPNIKAVNNAKKILTRL*SGLLQ*VHHCFQRQSLN*LKVLCEY*LGK
*RSSEPG 7493

Query: 183 RGV PNS*ITALFLL 224

G+ +S AL L

Sbjct: 7492 GGLLSSFTNALVRL 7451

20 Score = 47.3 bits (97), Expect = 2e-005
Identities = 24/71 (33%), Positives = 37/71 (51%)
Frame = +2 / -3

Query: 11

PEDSSESESNHKGKSDSXVRSITPV*QVLFPQTSQDL*EE*LGVSREIEVL
25 *TRSRR 190

P+ S + S+ K+ D + +PV LFP+ +L + L V +RE+EV+ TR

Sbjct: 7664

PKYSPQH*SSK*CKENPDKVIIRASVSPPLFPEAELELIKALRVLTREVEVIG
TRRWI 7485

30 Query: 191 SLLNHCFVSP 223

+Q CF SP

Sbjct: 7484 AQFFYQCFGSP 7452

Score = 109 bits (232), Expect = 5e-024
Identities = 41/76 (53%), Positives = 53/76 (68%)

35 Frame = -1 / +3

Query: 229

LYRRNKAVIQELGTTPRPGSQDLYFPTIYSQSFFSQVLACLWKQHLSYWRNTP
YTAVRFVF 50

++RR KA+++EL P PGS DLYFP+ YSQS F+Q CLWKQ +YWR+ Y VR

40 F

Sbjct: 7446

IFRRTKALVKELSNPPPGSDDL YFPSQYSQSTFNQFKLCLWKQWWTYWRSP
DYNLVRIFF 7625

Query: 49 TVAIALTFGTIFWQLG 2

45 + AL GTIFW++G

Sbjct: 7626 ALFTALMLGTIFWRVG 7673

RANK 15 ITERATION 0>HTC136628-B01.1.12

Length = 1249

- 5 Score = 63.4 bits (132), Expect = 3e-010
Identities = 33/74 (44%), Positives = 41/74 (54%)
Frame = +3 / +2
Query: 3
PSCQKIVPKVRAIATVKTNLTA V*GVL RQYDRCCFHKQARTCEKNDWEYIV
- 10 GK*RSCEPG 182
P Q VPK A+ V NL V* + QY++ CF+K R C K EY++GK RS E
Sbjct: 227
PRFQNTVPKSSAMTVVTKNLRPV**IFLQYNKFCFYKHIRHCLKKVCEYLLG
KRRSPELA 406
- 15 Query: 183 RGV PNS*ITALFLL 224
+ S I ALFLL
Sbjct: 407 GALLISSIKALFLL 448
Score = 105 bits (223), Expect = 9e-023
Identities = 43/75 (57%), Positives = 50/75 (66%)
- 20 Frame = -1 / -2
Query: 226
YRRNKAVIQELGTPRPGSQDLYFPTIYSQSFFSQVLACLWKQHLSYWRNTPY
TAVRFVFT 47
+RRNKA+I+E+ S DL FP YSQ+FF Q L CL KQ+L YWRN YT RF T
- 25 Sbjct: 450
FRRNKALIEEISRAPANS GDLLFPNKYSQTFFKQCLICL*KQNLLYWRNIHYT
GRRFFVT 271
Query: 46 VAIALTFGTIFWQLG 2
IAL FGT+FW LG
- 30 Sbjct: 270 TVIALLFGT VFWNLG 226

RANK 16 ITERATION 0>CL006941.193

Length = 2470

- 35 Score = 48.3 bits (99), Expect = 1e-005
Identities = 30/74 (40%), Positives = 38/74 (50%)
Frame = +3 / -2
Query: 3
PSCQKIVPKVRAIATVKTNLTA V*GVL RQYDRCCFHKQARTCEKNDWEYIV
- 40 GK*RSCEPG 182
P QK VP R +V T A+*G Q D CFH A + WEY+VG RS +PG
Sbjct: 2016
PLRQKTVPNTRP*RSVIT*RIAL*GGSFQ*D*NCFHVFATH*FRKFW EYLVGN
ERSWKPG 1837
- 45 Query: 183 RGV PNS*ITALFLL 224
G + I++ LL

[illegible]

5 Score = 41.4 bits (84), Expect = 0.001
Identities = 29/74 (39%), Positives = 33/74 (44%)
Frame = +3 / +2
Query: 3
PSCQKIVPKVRAIATVKTNLTA V*GVLRQYDRCCFHKQARTCEKNDWEYIV
10 GK*RSCEPG 182
P CQ VPK R V +* Q D CFHK A EY V RS PG
Sbjct: 482
PFCQNTVPKKRP*RNVVR*RKLL*DGFFQ*DL YCFHKFATHWI*KL*EYFVA
NKRSR*PG 661
15 Query: 183 RGV PNS*ITALFLL 224
G+ NS I++ F L
Sbjct: 662 GGMLN SSISSWFFL 703
Score = 100 bits (213), Expect = 2e-021
Identities = 38/74 (51%), Positives = 52/74 (69%)
20 Frame = -1 / -1
Query: 223
RRNKAVIQELGTPRPGSQDL YFPTIYSQSFFSQVLACLWKQHLSYWRNTPYT
AVRFVFTV 44
R+N+ +I+EL P PG +DL F T YSQSF+ Q +A LWKQ+ SYW+N Y ++R++
25 T
Sbjct: 702
RKNQELIEELSIPPPGYRDLLFATKYSQSFYIQC VANLWKQYKSYWKNPSYN
SLRYLTTF 523
Query: 43 AIALTFGTIFWQLG 2
30 L FGT+FWQ G
Sbjct: 522 LYGLFFGT VFWQKG 481

35 Score = 41.4 bits (84), Expect = 0.001
Identities = 29/74 (39%), Positives = 33/74 (44%)
Frame = +3 / -1
Query: 3
40 PSCQKIVPKVRAIATVKTNLTA V*GVLRQYDRCCFHKQARTCEKNDWEYIV
GK*RSCEPG 182
P C Q V P K R V + * Q D C F H K A E Y V R S P G
Sbjct: 649
PFCQNTVPKKRP*RN VVR*RKLL*DGFFQ*DL YCFHKFATHWI*KL*EYFVA
45 NKRSR*PG 470
Query: 183 RGV PNS*IT ALFLL 224

G+ NS I++ F L
 Sbjct: 469 GGMLNSSISSWFFL 428
 Score = 100 bits (213), Expect = 2e-021
 Identities = 38/74 (51%), Positives = 52/74 (69%)
 5 Frame = -1 / +3
 Query: 223
 RRNKAVIQELGTPRPGSQDLYFPTIYSQSFFSQVLACLWKQHLSYWRNTPYT
 AVRFVFTV 44
 R+N+ +I+EL P PG +DL F T YSQS F+ Q +A LWKQ+ SYW+N Y ++R++
 10 T
 Sbjct: 429
 RKNQELIEELSIPPPGYRDLLFATKYSQSFYIQC VANLWKQYKSYWKNPSYN
 SLRYLTTF 608
 Query: 43 AIALTFGTIFWQLG 2
 15 L FGT+FWQ G
 Sbjct: 609 LYGLFFGT VFWQKG 650

RANK 20 ITERATION 0>CL004158.37.92
 Length = 758
 20
 Score = 41.4 bits (84), Expect(2) = 0.001
 Identities = 24/63 (38%), Positives = 29/63 (45%)
 Frame = +3 / +1
 Query: 3
 25 PSCQKIVPKVRAIATVKTNLTA V*GVLRQYDRCCFHKQARTCEKNDWEYIV
 GK*RSCEPG 182
 P CQ PK + T +* L QYD+ CF QA +C N VGK RS P
 Sbjct: 316
 PCCQNNTPKTMQEIVMKNIRTRL*EGLLQYDKHCFQMQA FSCSLNFCGNRV
 30 GKWRSLVPR 495
 Query: 183 RGV 191
 G+
 Sbjct: 496 AGL 504
 Score = 19.4 bits (36), Expect(2) = 0.001
 35 Identities = 5/11 (45%), Positives = 7/11 (63%)
 Frame = +1 / +2
 Query: 193 PTPESLLCFSC 225
 P P +LC +C
 Sbjct: 668 PKPHCILCVTC 700
 40 Score = 89.0 bits (188), Expect = 6e-018
 Identities = 33/74 (44%), Positives = 45/74 (60%)
 Frame = -1 / -1
 Query: 223
 RRNKAVIQELGTPRPGSQDLYFPTIYSQSFFSQVLACLWKQHLSYWRNTPYT
 45 AVRFVFTV 44
 R A+++ L P G+ DL+FPT + Q F Q+ AC+WKQ LSYWR+ Y VR +F

Sbjct: 536
 RDKDALVKSLSKPALGTSDLHFPTFRFPQKFREQLKACIWKQCLSYWRSPSY
 NLVRILFIT 357
 Query: 43 AIALTFGTIFWQLG 2
 + FG +FWQ G
 Sbjct: 356 ISCIVFGVLFWQQG 315
 [END
 ALIGNMENTS]

10 Job Details [Return to top](#)

[BEGIN JOB STATUS][BEGIN SEARCH TIME]
 [END SEARCH TIME]
 [VERSION]

15 [SEARCH ID]

[EOL] CRLF
 [COMMENT] /Comment=NCBI TBLASTX Similarity Search
 [COMMENT] /CGI_
 [ALGORITHM] TBLASTX

20 [MATRIX] D:\DECYPHER\MATRIX\BLOSUM62.MAA

[QUERY FORMAT] FASTA/PEARSON
 [QUERY TYPE] NT
 [QUERY FILTER] T
 [QUERY SEARCH] -1 -2 -3 1 2 3

25 [QUERY PATH] d:\decypher\query

[QUERY SET]
 [TARGET TYPE] NT
 [TARGET FRAMES] -1 -2 -3 1 2 3
 [TARGET PATH] d:\decypher\target\blast

30 [TARGET SET] rice_contigs

[MAX SCORES] 30
 [MAX ALIGNMENTS] 20
 [THRESHOLD] 1
 [RESULT PATH] d:\decypher\output

35 [OUTPUT FORMAT] TEXT EXTRACTALIGNED[SHOW GI] F

[EXPECTATION] 10
 [GAPPED ALIGNMENT] TTBLASTX
 TBLASTX

40 Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
 Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
 "Gapped BLAST and PSI-BLAST: a new generation of protein database search
 programs", Nucleic Acids Res. 25:3389-3402.Query= Your_Query starting with:
 CTCCTAAGTTGCCAGAAGATA /QuerySize=247

(247 letters)Database:
 45 154,797 sequences; 359,911,975 total letters Database:
 Posted date:
 Number of letters in database: 359,911,975

Number of sequences in database: 154,797

Lambda K H
0.318 0.135 0.401

- 5 Matrix: BLOSUM62.MAA
Number of Hits to DB: 209872722
Number of Sequences: 154797
Number of extensions: 2535298
Number of successful extensions: 136774
- 10 Number of sequences better than 10.0: 277
length of query: 82
length of database: 119,970,658
effective HSP length: 49
effective length of query: 32
- 15 effective length of database: 112,385,605
effective search space: 3596339360
effective search space used: 3596339360
frameshift window, decay const: 50, 0.1
T: 13
- 20 A: 40
X1: 16 (7.3 bits)
X2: 0 (0.0 bits)
S1: 41 (21.7 bits)
S2: 56 (28.6 bits)[JOB MESSAGES]
- 25 [END JOB STATUS]

DESCA5 Blast report against swissprot:

DeCypher Results for: NCBI BLASTX Translated Search

Results by Query

Click on a query below to view its search results.

5 Your_Query starting with: GACTCCCCTTTTATTAGGAC

Search Details

Results for: Your_Query starting with:

10 **GACTCCCCTTTTATTAGGAC; (Length=160)**

[Return to query summary](#)

	RANK	Sequences producing significant alignments:	(bits)	Value
15	<u>1</u>	sp Q64685 CAG1_MOUSE CMP-N-ACETYLNEURAMINATE-BETA-GALACTOSAMIDE...	29	1.8
	<u>2</u>	sp P22082 SNF2_YEAST TRANSCRIPTION REGULATORY PROTEIN SNF2 (SWI...	28	3.0
	<u>3</u>	sp P19653 KILA_BPP1 KILA PROTEIN	27	6.8
20	<u>4</u>	sp P32597 STH1_YEAST NUCLEAR PROTEIN STH1/NPS1	27	6.8
	<u>5</u>	sp P36089 YKG6_YEAST HYPOTHETICAL 16.7 KD PROTEIN IN NDK1-MNR2 ...	27	6.8

RANK 1 ITERATION 0>sp|Q64685|CAG1_MOUSE
25 CMP-N-ACETYLNEURAMINATE-BETA-GALACTOSAMIDE-ALPHA-
2,
6-SIALYLTRANSFERASE (BETA-GALACTOSIDE
ALPHA-2,6-SIALYLTRANSFERASE) (ALPHA 2,6-ST)
(SIALYLTRANSFERASE 1) (ST6GALI)
30 Length = 403

Score = 28.6 bits (62), Expect = 1.8

Identities = 14/34 (41%), Positives = 21/34 (61%)

Frame = +3Query: 51 PQITSKVKKTPSL*LLSIDMSFSPINQCLLMNW 152

35 P++T+KVK PS L + D ++S +N LL W

Sbjct: 78 PRVTAKVKPQPS-LQVWDKDYSTYKLNPRLLKIW 110

RANK 2 ITERATION 0>sp|P22082|SNF2_YEAST TRANSCRIPTION
40 REGULATORY PROTEIN SNF2 (SWI/SNF
COMPLEX COMPONENT SNF2) (REGULATORY PROTEIN SWI2)
(REGULATORY PROTEIN GAM1) (TRANSCRIPTION FACTOR TYE3)
Length = 1703

Score = 27.8 bits (60), Expect = 3.0
Identities = 11/26 (42%), Positives = 15/26 (57%)
Frame = +3Query: 15 *DKMKLHYYNVTPQITSKVKKTPSLL 92
D + YYNV +I +KK PS+L

5 Sbjct: 737 DDNSNVDYYNVAHRIKEDIKKQPSIL 762

RANK 3 ITERATION 0>sp|P19653|KILA_BPP1 KILA PROTEIN
Length = 266

10 Score = 26.6 bits (57), Expect = 6.8
Identities = 12/25 (48%), Positives = 15/25 (60%)
Frame = -1Query: 115 DISIDNSHNEGVEFTLDVICGVTL 41
D++I N H N TL VICGV +
Sbjct: 8 DMNISNLHQNVDPSTTLPVICGVEI 32

15 RANK 4 ITERATION 0>sp|P32597|STH1_YEAST NUCLEAR PROTEIN
STH1/NPS1
Length = 1359

20 Score = 26.6 bits (57), Expect = 6.8
Identities = 10/26 (38%), Positives = 15/26 (57%)
Frame = +3Query: 15 *DKMKLHYYNVTPQITSKVKKTPSLL 92
++ K YY V +I K+ K PS+L
Sbjct: 440 EEREKTDYYEVAHRIKEKIDKQPSIL 465

25 RANK 5 ITERATION 0>sp|P36089|YKG6_YEAST HYPOTHETICAL 16.7 KD
PROTEIN IN NDK1-MNR2
INTERGENIC REGION
Length = 147

30 Score = 26.6 bits (57), Expect = 6.8
Identities = 8/25 (32%), Positives = 17/25 (68%)
Frame = +2Query: 71 EKNTFIIIVTIVY*YVFFSNQSMSFD 145
+KNT + T++Y ++ ++ SM+ D

35 Sbjct: 39 KKNTTYVATLIYEFIILNDASMTDP 63
[END
ALIGNMENTS]

40 Job Details[Return to top](#)

[BEGIN JOB STATUS][BEGIN SEARCH TIME]
[END SEARCH TIME]
[VERSION]
[SEARCH ID]

45 [EOL] CRLF
[COMMENT] /Comment=NCBI BLASTX Translated Search
[COMMENT]

```

[ALGORITHM] BLASTX
[MATRIX] D:\DECYPHER\MATRIX\BLOSUM62.MAA
[QUERY FORMAT] FASTA/PEARSON
[QUERY TYPE] NT
5 [QUERY FILTER] T
[QUERY SEARCH] -1 -2 -3 1 2 3
[QUERY PATH] d:\decypher\query
[QUERY SET]
[TARGET TYPE] AA
10 [TARGET FRAMES] 1
[TARGET PATH] d:\decypher\target\blast
[TARGET SET] swissprot
[MAX SCORES] 30
[MAX ALIGNMENTS] 20
15 [THRESHOLD] 1
[RESULT PATH] d:\decypher\output
[OUTPUT FORMAT] TEXT EXTRACTALIGNED[SHOW GI] F
[EXPECTATION] 10
[GAPPED ALIGNMENT] TBLASTX
20 BLASTX
Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs", Nucleic Acids Res. 25:3389-3402.Query= Your_Query starting with:
25 GACTCCCCTTTTATTAGGAC /QuerySize=160
(160 letters)Database: Swissprot
90,939 sequences; 32,775,839 total letters Database: Swissprot
Posted date:
Number of letters in database: 32,775,839
30 Number of sequences in database: 90,939

Lambda K H
0.318 0.135 0.401 Gapped
Lambda K H
35 0.270 0.0470 0.230
Matrix: BLOSUM62.MAA
Gap Penalties: Existence: 11, Extension: 1
Number of Hits to DB: 8359131
Number of Sequences: 90939
40 Number of extensions: 107544
Number of successful extensions: 419
Number of sequences better than 10.0: 10
Number of HSP's better than 10.0 without gapping: 4
Number of HSP's successfully gapped in prelim test: 1
45 Number of HSP's that attempted gapping in prelim test: 414
Number of HSP's gapped (non-prelim): 6

```

length of query: 53
length of database: 32,775,839
effective HSP length: 31
effective length of query: 21
5 effective length of database: 29,956,730
effective search space: 629091330
effective search space used: 629091330
frameshift window, decay const: 50, 0.1
T: 12
10 A: 40
X1: 16 (7.3 bits)
X2: 38 (14.8 bits)
X3: 64 (24.9 bits)
S1: 41 (21.7 bits)
15 S2: 56 (26.2 bits)[JOB MESSAGES].[END JOB STATUS] DeCypher

Results for: NCBI TBLASTX Similarity Search

Results by Query

Click on a query below to view its search results.
Your Query starting with: GACTCCCCTTTTATTAGGAC

20 **Search Details**

Results for: Your_Query starting with:
GACTCCCCTTTTATTAGGAC; (Length=160)

25 [Return to query summary](#)

	RANK	Sequences producing significant alignments:	(bits)	Value
	<u>1</u>	CL036159.49.55	34	0.049
	<u>2</u>	CL020648.137	32	0.18
30	<u>3</u>	CL015965.58	32	0.24
	<u>4</u>	CL026096.91.110	31	0.46
	<u>5</u>	CL010918.122	31	0.46
	<u>6</u>	CL022771.95	31	0.46
	<u>7</u>	CL017745.67	31	0.46
35	<u>8</u>	CL008574.139	31	0.46
	<u>9</u>	CL025010.68	30	0.63
	<u>10</u>	HTC029298-A01.67.71	30	0.63
	<u>11</u>	CL032651.106	30	0.63
	<u>12</u>	CL030741.61	30	0.86
40	<u>13</u>	CL022383.157	30	0.86
	<u>14</u>	CL022706.67.81	29	1.2
	<u>15</u>	CL020359.55	29	1.2
	<u>16</u>	HTC165637-B01.1.34	29	1.2

17 CL003682.107.101 29 1.2
 18 CL002685.134 29 1.2
 19 CL035824.124 29 1.2
 20 CL013521.189.10 29 1.2
 5 21 CL022031.78 29 1.2
 22 CL012099.118 29 1.6
 23 HTC137924-A01.F.54.59 29 1.6
 24 CL002542.57 29 1.6
 25 CL017083.123.78 29 1.6
 10 26 CL024763.48 29 1.6
 27 CL032385.114 29 1.6
 28 CL030846.260 29 1.6
 29 CL021667.116 29 1.6
 30 CL023837.102 29 1.6
 15
RANK 1 ITERATION 0>CL036159.49.55
 Length = 4230

 Score = 34.1 bits (68), Expect = 0.049
 20 Identities = 12/38 (31%), Positives = 23/38 (59%)
 Frame = +3 / -3
 Query: 27 KLHYYNVTPQITSKVKKTPSLL*LLSIDMSFSPINQCL 140
 ++HY++ TP ITS+ P + L+ M +P++Q +
 Sbjct: 2284 QIHYHHGTPNITSQRTGAPPMHQLMHAQMHSAPMHQLM 2171
 25
RANK 2 ITERATION 0>CL020648.137
 Length = 5539

 Score = 32.2 bits (64), Expect = 0.18
 30 Identities = 13/30 (43%), Positives = 20/30 (66%)
 Frame = +3 / -2
 Query: 54 QITSKVKKTPSLL*LLSIDMSFSPINQCLL 143
 +ITSK K P ++ L+S + FSP+N L+
 Sbjct: 2019 KITSKYLKDPIIIDLVSAFLLFSPVNSYLV 1930
 35
RANK 3 ITERATION 0>CL015965.58
 Length = 1092

 Score = 31.8 bits (63), Expect = 0.24
 40 Identities = 11/36 (30%), Positives = 20/36 (55%)
 Frame = +3 / +2
 Query: 39 YNVTPQITSKVKKTPSLL*LLSIDMSFSPINQCLLM 146
 Y + P +T ++ K P++ + F PIN CL++
 Sbjct: 239 YKIIPYLTYEIAKQPTSIHFYNNINKFLPINTCLII 346
 45
RANK 4 ITERATION 0>CL026096.91.110

Length = 7831

Score = 30.8 bits (61), Expect = 0.46
Identities = 14/34 (41%), Positives = 19/34 (55%)

5 Frame = +3 / +2

Query: 30 LHYYNVTPQITSKVKKTPSLL*LLSIDMSFSPIN 131
+ Y +VTP S VKKT S+L L ++ IN

Sbjct: 1418 IEYSHVTPLSKSTVKKTNLSILSLKKMESPMDAIN 1519

10 RANK 5 ITERATION 0>CL010918.122

Length = 5632

Score = 30.8 bits (61), Expect = 0.46
Identities = 14/30 (46%), Positives = 19/30 (62%)

15 Frame = +3 / +3

Query: 36 YYNVTPQITSKVKKTPSLL*LLSIDMSFSP 125
YY++ Q +KVK TP L L S+ SF+P

Sbjct: 678 YYHASIQRPKNVKITPFLRRLASVLRSFAP 767

20 RANK 6 ITERATION 0>CL022771.95

Length = 2860

Score = 30.8 bits (61), Expect = 0.46
Identities = 7/29 (24%), Positives = 15/29 (51%)

25 Frame = -3 / +1

Query: 125 WRKRHINRQ*SQ**RCFFHFRCDLWCDIV 39
WR+ + Q + +H R ++WC ++

Sbjct: 1096 WRQTGLREQEQLTNKLGYPHIRLEIWCTLM 1182

30 RANK 7 ITERATION 0>CL017745.67

Length = 4118

Score = 30.8 bits (61), Expect = 0.46
Identities = 8/21 (38%), Positives = 16/21 (76%)

35 Frame = +2 / -3

Query: 56 NHI*SEKNTFIIVTIVY*YVF 118
+HI EKN F+++T++ Y++

Sbjct: 2475 DHISDEKNIFVVITLIETYLY 2413

40 RANK 8 ITERATION 0>CL008574.139

Length = 883

Score = 30.8 bits (61), Expect = 0.46
Identities = 13/34 (38%), Positives = 17/34 (49%)

45 Frame = +2 / +2

Query: 44 CHTTNHI*SEKNTFIIVTIVY*YVFFSNQSMSFD 145

CH + E +VTI + YVF S +SFD
Sbjct: 557 CHAICSLQGEYWKPSTLTISFSYVFHSADELSFD 658

RANK 9 ITERATION 0>CL025010.68

5 Length = 5087

Score = 30.4 bits (60), Expect = 0.63
Identities = 13/30 (43%), Positives = 17/30 (56%)
Frame = +3 / +3

10 Query: 69 VKKTPSLL*LLSIDMSFSPINQCLLMNWYA 158
+K TPS L LLS S SP + + WY+

Sbjct: 1812 LKTTSPFLNLLSRPRSMSPSSWLEISTWYS 1901

RANK 10 ITERATION 0>HTC029298-A01.67.71

15 Length = 5419

Score = 30.4 bits (60), Expect = 0.63
Identities = 10/27 (37%), Positives = 16/27 (59%)
Frame = -3 / +1

20 Query: 104 RQ*SQ**RCFFHFRCDLWCDIVVM*LH 24
R+ S +C F F DL C+I+ + +H

Sbjct: 3022 RKESNTVQCFLFLCADLLCNIITILIH 3102

RANK 11 ITERATION 0>CL032651.106

25 Length = 8032

Score = 30.4 bits (60), Expect = 0.63
Identities = 10/32 (31%), Positives = 20/32 (62%)
Frame = +3 / -3

30 Query: 51 PQITSKVKKTPSLL*LLSIDMSFSPINQCLLM 146
P ++ + TP L ++++ S SPI+QC ++

Sbjct: 5411 PPLSLSAENTPPTLMPIALEPSLSPIHQCAIL 5316

RANK 12 ITERATION 0>CL030741.61

35 Length = 5245

Score = 29.9 bits (59), Expect = 0.86
Identities = 10/29 (34%), Positives = 17/29 (58%)
Frame = +2 / +3

40 Query: 50 TTNHI*SEKNTFIIIVTIVY*YVFFSNQSM 136
TT +E F + T++Y Y++ SN S+

Sbjct: 1539 TTQIFLTESTNFPVYTVIYAYIYSSNHSL 1625

RANK 13 ITERATION 0>CL022383.157

45 Length = 5241

Score = 29.9 bits (59), Expect = 0.86
Identities = 10/23 (43%), Positives = 12/23 (51%)
Frame = -3 / -1
Query: 122 RKRHINRQ*SQ**RCFFHFRCDL 54
5 R+RH Q CF+ F CDL
Sbjct: 1029 RRRHALGGEVQEKFCFYIFLCDL 961

RANK 14 ITERATION 0>CL022706.67.81
Length = 6339

10 Score = 29.5 bits (58), Expect = 1.2
Identities = 11/31 (35%), Positives = 17/31 (54%)
Frame = -2 / +1
Query: 102 TIVTIMKVFFSL*M*FVV*HCSNVASFCPNK 10
15 TI T++ F+SL ++ HC A+ P K
Sbjct: 82 TICTVLVFFYSLCFTDLLEHCRFAATTLPQK 174

RANK 15 ITERATION 0>CL020359.55
Length = 4387

20 Score = 29.5 bits (58), Expect = 1.2
Identities = 9/15 (60%), Positives = 13/15 (86%)
Frame = -3 / +2
Query: 143 QKTLIDWRKRHINRQ 99
25 +KTL +W+K+H NRQ
Sbjct: 3284 KKTLTNWQKKHFNRQ 3328

RANK 16 ITERATION 0>HTC165637-B01.1.34
Length = 3227

30 Score = 29.5 bits (58), Expect = 1.2
Identities = 10/15 (66%), Positives = 12/15 (79%)
Frame = +1 / +3
Query: 91 CDYCLLICLFLQSIN 135
35 C +CL ICLFL SI+
Sbjct: 210 CTFCLAICLFLPSIS 254

RANK 17 ITERATION 0>CL003682.107.101
Length = 7732

40 Score = 29.5 bits (58), Expect = 1.2
Identities = 9/15 (60%), Positives = 13/15 (86%)
Frame = -3 / -3
Query: 143 QKTLIDWRKRHINRQ 99
45 +KTL +W+K+H NRQ
Sbjct: 6359 KKTLTNWQKKHFNRQ 6315

RANK 18 ITERATION 0>CL002685.134
Length = 4653

5 Score = 29.5 bits (58), Expect = 1.2
Identities = 6/14 (42%), Positives = 12/14 (84%)
Frame = -3 / -2

Query: 53 WCDIVVM*LHFVLI 12
WC+++V+ HF+L+

10 Sbjct: 3746 WCNVIVLEFHFLLL 3705

RANK 19 ITERATION 0>CL035824.124
Length = 4694

15 Score = 29.5 bits (58), Expect = 1.2
Identities = 11/31 (35%), Positives = 17/31 (54%)
Frame = -2 / +2

Query: 102 TIVTIMKVFFSL*M*FVV*HCSNVASFCPNK 10
TI T++ F+SL ++ HC A+ P K

20 Sbjct: 3968 TICTVLVFFYSLCFTDLLEHCRFAATTL P Q K 4060

RANK 20 ITERATION 0>CL013521.189.10
Length = 1223

25 Score = 29.5 bits (58), Expect = 1.2
Identities = 10/26 (38%), Positives = 15/26 (57%)
Frame = -3 / -3

Query: 83 RCFFHFRCDLWCDIVVM*LHFVLI K G 6
RC+ RC CD V + L ++ +KG

30 Sbjct: 1161 RCWLXVRCPWRCDAVCLKLR Y L D L K G 1084
[END
ALIGNMENTS]

35 Job Details[Return to top](#)
[BEGIN JOB STATUS][BEGIN SEARCH TIME]
[END SEARCH TIME]
[VERSION]
[SEARCH ID]
40 [EOL] CRLF
[COMMENT] /Comment=NCBI TBLASTX Similarity Search
[COMMENT]
[ALGORITHM] TBLASTX
[MATRIX] D:\DECYPHER\MATRIX\BLOSUM62.MAA
45 [QUERY FORMAT] FASTA/PEARSON
[QUERY TYPE] NT
[QUERY FILTER] T

```

[QUERY SEARCH] -1 -2 -3 1 2 3
[QUERY PATH] d:\decypher\query
[QUERY SET]
[TARGET TYPE] NT
5 [TARGET FRAMES] -1 -2 -3 1 2 3
[TARGET PATH] d:\decypher\target\blast
[TARGET SET] rice_contigs
[MAX SCORES] 30
[MAX ALIGNMENTS] 20
10 [THRESHOLD] 1
[RESULT PATH] d:\decypher\output
[OUTPUT FORMAT] TEXT EXTRACTALIGNED[SHOW GI] F
[EXPECTATION] 10
[GAPPED ALIGNMENT] TTBLASTX
15 TBLASTX
Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs", Nucleic Acids Res. 25:3389-3402.Query= Your_Query starting with:
20 GACTCCCCTTTTATTAGGAC /QuerySize=160
(160 letters)Database:
154,797 sequences; 359,911,975 total letters Database:
Posted date:
Number of letters in database: 359,911,975
25 Number of sequences in database: 154,797

Lambda K H
0.318 0.135 0.401
Matrix: BLOSUM62.MAA
30 Number of Hits to DB: 130240129
Number of Sequences: 154797
Number of extensions: 1231076
Number of successful extensions: 85557
Number of sequences better than 10.0: 662
35 length of query: 53
length of database: 119,970,658
effective HSP length: 45
effective length of query: 7
effective length of database: 113,004,793
40 effective search space: 791033551
effective search space used: 791033551
frameshift window, decay const: 50, 0.1
T: 13
A: 40
45 X1: 16 ( 7.3 bits)
X2: 0 ( 0.0 bits)

```

S1: 41 (21.7 bits)

S2: 51 (26.3 bits)[JOB MESSAGES] [END JOB STATUS]

DESCA6 Blast report against Arabidopsis peptide database:

DeCypher Results for: NCBI BLASTX Translated Search

5 **Results by Query**

Click on a query below to view its search results.

Your Query starting with: GGACTGCGTACCAATTCGCC

Search Details

10 **Results for: Your_Query starting with:**

GGACTGCGTACCAATTCGCC; (Length=208)

[Return to query summary](#)

15	RANK	Sequences producing significant alignments:	(bits)	Value
	<u>1</u>	51098.m00067#F23M2.26 chr.2 hypothetical protein predicted by ...	29	0.93
	<u>2</u>	43859.m00036#T10J7.10 chr.2 hypothetical protein predicted by ...	29	0.93
	<u>3</u>	51098.m00067#F23M2.26 chr.2 hypothetical protein predicted by ...	29	0.93
20	<u>4</u>	43859.m00036#T10J7.10 chr.2 hypothetical protein predicted by ...	29	0.93

RANK 1 ITERATION 0>51098.m00067#F23M2.26 chr.2 hypothetical protein predicted by

25 genscan [Arabidopsis thaliana] Sequencing_group:
TIGR annotation_status: Finished TIGR-annotation
Length = 231

Score = 28.6 bits (62), Expect = 0.93

30 Identities = 12/22 (54%), Positives = 13/22 (58%)

Frame = +3Query: 141 *CFCVLTQD*IKAAI*LLRTH 206

CVLT + IK AI LLR H

Sbjct: 97 EALCVLTHERDIKGAINLLRPH 118

35 RANK 2 ITERATION 0>43859.m00036#T10J7.10 chr.2 hypothetical protein predicted by

genscan [Arabidopsis thaliana] Sequencing_group:
TIGR annotation_status: Finished TIGR-annotation
Length = 231

40 Score = 28.6 bits (62), Expect = 0.93

Identities = 12/22 (54%), Positives = 13/22 (58%)

Frame = +3Query: 141 *CFCVLTQD*IKAAI*LLRTH 206

CVLT + IK AI LLR H
Sbjct: 97 EALCVLTHERDIKGAINLLRPH 118

RANK 3 ITERATION 0>51098.m00067#F23M2.26 chr.2 hypothetical protein

5 predicted by
 genscan [Arabidopsis thaliana] Sequencing_group:
 TIGR annotation_status: Finished TIGR-annotation
 Length = 231

10 Score = 28.6 bits (62), Expect = 0.93
 Identities = 12/22 (54%), Positives = 13/22 (58%)
 Frame = +3Query: 141 *CFCVLTQD*IKA*AI*LLRTH 206
 CVLT + IK AI LLR H
Sbjct: 97 EALCVLTHERDIKGAINLLRPH 118

RANK 4 ITERATION 0>43859.m00036#T10J7.10 chr.2 hypothetical protein
predicted by

 genscan [Arabidopsis thaliana] Sequencing_group:
 TIGR annotation_status: Finished TIGR-annotation
20 Length = 231

Score = 28.6 bits (62), Expect = 0.93
Identities = 12/22 (54%), Positives = 13/22 (58%)
Frame = +3Query: 141 *CFCVLTQD*IKA*AI*LLRTH 206

25 CVLT + IK AI LLR H
Sbjct: 97 EALCVLTHERDIKGAINLLRPH 118
[END
ALIGNMENTS]

30 Job DetailsReturn to top

[BEGIN JOB STATUS][BEGIN SEARCH TIME]
[END SEARCH TIME]
[VERSION]
35 [SEARCH ID]
[EOL] CRLF
[COMMENT] /Comment=NCBI BLASTX Translated Search
[COMMENT]
[ALGORITHM] BLASTX
40 [MATRIX] D:\DECYPHER\MATRIX\BLOSUM62.MAA
[QUERY FORMAT] FASTA/PEARSON
[QUERY TYPE] NT
[QUERY FILTER] T
[QUERY SEARCH] -1 -2 -3 1 2 3
45 [QUERY PATH] d:\decypher\query
[QUERY SET]
[TARGET TYPE] AA

```

[TARGET FRAMES] 1
[TARGET PATH] d:\decypher\target\blast
[TARGET SET] arabpep
[MAX SCORES] 30
5  [MAX ALIGNMENTS] 20
   [THRESHOLD] 1
   [RESULT PATH] d:\decypher\output
   [OUTPUT FORMAT] TEXT EXTRACTALIGNED[SHOW GI] F
   [EXPECTATION] 10
10  [GAPPED ALIGNMENT] TBLASTX
    BLASTX
    Reference:Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
    Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
    "Gapped BLAST and PSI-BLAST: a new generation of protein database search
15  programs", Nucleic Acids Res. 25:3389-3402.Query= Your_Query starting with:
    GGACTGCGTACCAATTCGCC /QuerySize=208
        (208 letters)Database: Arabidopsis peptides
        34,190 sequences; 14,691,163 total letters Database: Arabidopsis peptides
        Posted date:
20  Number of letters in database: 14,691,163
    Number of sequences in database: 34,190

    Lambda  K  H
        0.318 0.135 0.401 Gapped
25  Lambda  K  H
        0.270 0.0470 0.230
    Matrix: BLOSUM62.MAA
    Gap Penalties: Existence: 11, Extension: 1
    Number of Hits to DB: 3629655
30  Number of Sequences: 34190
    Number of extensions: 34223
    Number of successful extensions: 104
    Number of sequences better than 10.0: 8
    Number of HSP's better than 10.0 without gapping: 4
35  Number of HSP's successfully gapped in prelim test: 0
    Number of HSP's that attempted gapping in prelim test: 100
    Number of HSP's gapped (non-prelim): 4
    length of query: 69
    length of database: 14,691,163
40  effective HSP length: 43
    effective length of query: 25
    effective length of database: 13,220,993
    effective search space: 330524825
    effective search space used: 330524825
45  frameshift window, decay const: 50, 0.1
    T: 12

```

A: 40

X1: 16 (7.3 bits)

X2: 38 (14.8 bits)

X3: 64 (24.9 bits)

5 S1: 41 (21.7 bits)

S2: 53 (25.1 bits)[JOB MESSAGES]

[END JOB STATUS]DESCA6 blast against NADI rice V4

DeCypher Results for: NCBI TBLASTX Similarity Search

Results by Query

10 *Click on a query below to view its search results.*

Your_Query starting with: GGACTGCGTACCAATTCGCC

Search Details

15 **Results for: Your_Query starting with:**

GGACTGCGTACCAATTCGCC; (Length=208)

[Return to query summary](#)

	RANK	Sequences producing significant alignments:	(bits)	Value
20	<u>1</u>	CL038406.52	31	0.94
	<u>2</u>	CL039253.78	31	1.3
	<u>3</u>	CL004633.63	30	1.8
	<u>4</u>	CL061327.46.58	29	3.4
	<u>5</u>	CL006249.99	29	4.6
25	<u>6</u>	HTC119539-A01.F.2.2	29	4.6
	<u>7</u>	CL031599.3	29	4.6
	<u>8</u>	CL000696.100	29	4.6
	<u>9</u>	HTC044121-A01.R.4.4	29	4.6
	<u>10</u>	CL022009.126	29	4.6
30	<u>11</u>	CL013659.161	29	4.6
	<u>12</u>	CL035453.30.34	24	4.6
	<u>13</u>	CL037679.83	29	6.3
	<u>14</u>	CL005825.40	28	8.7
	<u>15</u>	HTC081753-A01.F.8.8	28	8.7
35	<u>16</u>	CL008611.99	28	8.7

RANK 1 ITERATION 0>CL038406.52

Length = 4337

40 Score = 31.3 bits (62), Expect = 0.94

Identities = 12/24 (50%), Positives = 13/24 (54%)

Frame = -2 / +3

Query: 72 CMSSFSSWSQNHKYAHGRIGTQS 1

CM S SSSW + GRIG S
Sbjct: 3777 CMQSCSSSWKATK*FCGGRIGLAS 3848

RANK 2 ITERATION 0>CL039253.78

5 Length = 5864

Score = 30.8 bits (61), Expect = 1.3
Identities = 11/18 (61%), Positives = 14/18 (77%)
Frame = -2 / +3

10 Query: 66 SSFSSSWSQNHKYAHGRI 13
+S SSSWS+NH Y H R+
Sbjct: 2124 ASNSSSWSRNHYYHHPRL 2177

RANK 3 ITERATION 0>CL004633.63

15 Length = 2015

Score = 30.4 bits (60), Expect = 1.8
Identities = 10/18 (55%), Positives = 14/18 (77%)
Frame = -2 / +3

20 Query: 66 SSFSSSWSQNHKYAHGRI 13
+S SSSW +NH+Y H R+
Sbjct: 189 ASNSSSWPRNHRYPRL 242

RANK 4 ITERATION 0>CL061327.46.58

25 Length = 4097

Score = 29.5 bits (58), Expect = 3.4
Identities = 11/21 (52%), Positives = 13/21 (61%)
Frame = -1 / -3

30 Query: 88 REVTEVYELIFFMVTKSQIC 26
+EV E I FF+ TKS IC
Sbjct: 1500 KEVVE***TIFFL*TKSSIC 1438

RANK 5 ITERATION 0>CL006249.99

35 Length = 1774

Score = 29.0 bits (57), Expect = 4.6
Identities = 12/24 (50%), Positives = 13/24 (54%)
Frame = -2 / -3

40 Query: 72 CMSSFSWSQNHKYAHGRIGTQS 1
CM S SSSW + GRIG S
Sbjct: 1049 CMQSCSSSWKATK*FCGGRIGLAS 978

RANK 6 ITERATION 0>HTC119539-A01.F.2.2

45 Length = 800

RANK 11 ITERATION 0>CL013659.161

Length = 8841

5 Score = 29.0 bits (57), Expect = 4.6
 Identities = 12/24 (50%), Positives = 13/24 (54%)
 Frame = -2 / +1
 Query: 72 CMSSFSSWSQNHKYAHGRIGTQS 1
 CM S SSSW + GRIG S
 10 Sbjct: 8689 CMQSCSSSWKATK*FCGGRIGLAS 8760

RANK 12 ITERATION 0>CL035453.30.34

Length = 2732

15 Score = 24.4 bits (47), Expect(2) = 4.6
 Identities = 9/22 (40%), Positives = 12/22 (53%)
 Frame = +2 / -1
 Query: 8 VPIRP*AYL*FCDHEEENELIH 73
 +P+ AY F EEE L+H

20 Sbjct: 2369 LPLSVQAYEEFLLMEEELSLLH 2304
 Score = 23.1 bits (44), Expect(2) = 4.6
 Identities = 8/20 (40%), Positives = 12/20 (60%)
 Frame = +3 / -2
 Query: 147 FCVLTQD*IIKAAI*LLRTH 206
 FC+ +QD I A+ +R H

25 Sbjct: 2311 FCICSQDKEIAGALFGIRVH 2252

RANK 13 ITERATION 0>CL037679.83

Length = 2902

30 Score = 28.6 bits (56), Expect = 6.3
 Identities = 7/17 (41%), Positives = 13/17 (76%)
 Frame = -1 / +1
 Query: 58 FFFMVTKSQICSWANWY 8
 FF++V++ C++ NWY
 35 Sbjct: 1432 FFYVVSSNNACTFGNWy 1482

RANK 14 ITERATION 0>CL005825.40

Length = 645

40 Score = 28.1 bits (55), Expect = 8.7
 Identities = 10/22 (45%), Positives = 17/22 (76%)
 Frame = -1 / +1
 Query: 97 LIIREVTEVYELIFFFMVTKSQ 32
 45 LIIR +++Y +I +F++ KSQ
 Sbjct: 28 LIIRLIQKIYVIIIYFVMRKSQ 93

RANK 15 ITERATION 0>HTC081753-A01.F.8.8

Length = 1138

5 Score = 28.1 bits (55), Expect = 8.7
 Identities = 9/18 (50%), Positives = 14/18 (77%)
 Frame = -2 / +3
 Query: 66 SSFSSWSQNHKYAHGRI 13
 +S SSSW ++H+Y H R+
10 Sbjct: 216 ASNSSSWPRSHRYRHPRL 269

RANK 16 ITERATION 0>CL008611.99

Length = 2913

15 Score = 28.1 bits (55), Expect = 8.7
 Identities = 8/22 (36%), Positives = 16/22 (72%)
 Frame = -1 / -1
 Query: 76 EYELIFFFMVTKSQICSWANW 11
 ++++ +FFF+V +S IC +W
20 Sbjct: 2316 QLFKSMFFVVCESMICDRVSW 2251
 [END
 ALIGNMENTS]

25 Job Details[Return to top](#)

[BEGIN JOB STATUS][BEGIN SEARCH TIME]
[END SEARCH TIME]
[VERSION]
[SEARCH ID]
30 [EOL] CRLF
 [COMMENT] /Comment=NCBI TBLASTX Similarity Search
 [COMMENT]
 [ALGORITHM] TBLASTX
 [MATRIX] D:\DECYPHER\MATRIX\BLOSUM62.MAA
35 [QUERY FORMAT] FASTA/PEARSON
 [QUERY TYPE] NT
 [QUERY FILTER] T
 [QUERY SEARCH] -1 -2 -3 1 2 3
 [QUERY PATH] d:\decypher\query
40 [QUERY SET]
 [TARGET TYPE] NT
 [TARGET FRAMES] -1 -2 -3 1 2 3
 [TARGET PATH] d:\decypher\target\blast
 [TARGET SET] rice_contigs
45 [MAX SCORES] 30
 [MAX ALIGNMENTS] 20
 [THRESHOLD] 1

```

[RESULT PATH] d:\decypher\output
[OUTPUT FORMAT] TEXT EXTRACTALIGNED[SHOW GI] F
[EXPECTATION] 10
[GAPPED ALIGNMENT] TTBLASTX
5  TBLASTX
   Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
   Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
   "Gapped BLAST and PSI-BLAST: a new generation of protein database search
   programs", Nucleic Acids Res. 25:3389-3402.Query= Your_Query starting with:
10  GGACTGCGTACCAATTCGCC /QuerySize=208
   (208 letters)Database
   154,797 sequences; 359,911,975 total letters Database:
   Posted date:
   Number of letters in database: 359,911,975
15  Number of sequences in database: 154,797

   Lambda  K  H
   0.318  0.135  0.401
   Matrix: BLOSUM62.MAA
20  Number of Hits to DB: 112903379
   Number of Sequences: 154797
   Number of extensions: 724958
   Number of successful extensions: 42806
   Number of sequences better than 10.0: 56
25  length of query: 69
   length of database: 119,970,658
   effective HSP length: 48
   effective length of query: 20
   effective length of database: 112,540,402
30  effective search space: 2250808040
   effective search space used: 2250808040
   frameshift window, decay const: 50, 0.1
   T: 13
   A: 40
35  X1: 16 ( 7.3 bits)
   X2: 0 ( 0.0 bits)
   S1: 41 (21.7 bits)
   S2: 55 (28.1 bits)[JOB MESSAGES][END JOB STATUS]

```

DESCA7 Blast result against nonredundant proteins

DeCypher Results for: NCBI BLASTX Translated Search

Results by Query

Click on a query below to view its search results.

5 Your_Query starting with: GATGAGTCCTGAGTAATTGG

Search Details

Results for: Your_Query starting with:

10 **GATGAGTCCTGAGTAATTGG; (Length=342)**

[Return to query summary](#)

	RANK	Sequences producing significant alignments:	(bits)	Value
15	<u>1</u>	sp P56725 ZOX_PHAVU ZEATIN O-XYLOSYLTRANSFERASE (ZEATIN O-BETA-...	137	5e-032
	<u>2</u>	sp Q9ZSK5 ZOG_PHALU ZEATIN O-GLUCOSYLTRANSFERASE (ZEATIN O-BETA-...	135	2e-031
	<u>3</u>	dbj BAA36410.1 AB012114 UDP-glycose:flavonoid glycosyltransf...	104	5e-022
20	<u>4</u>	dbj BAB17061.1 AP002523 putative glucosyl transferase [Oryza...	103	8e-022
	<u>5</u>	dbj BAA36412.1 AB012116 UDP-glycose:flavonoid glycosyltransf...	102	2e-021
25	<u>6</u>	pir T01850 UTP-glucose glucosyltransferase homolog F9D12.4 - A...	102	2e-021
	<u>7</u>	gb AAF17551.1 AF198453 UDP-glycose:flavonoid glycosyltransfe...	100	5e-021
	<u>8</u>	dbj BAB17059.1 AP002523 putative glucosyl transferase [Oryza...	100	5e-021
30	<u>9</u>	emb CAB16822.1 Z99708 glucosyltransferase-like protein [Arab...	100	7e-021
	<u>10</u>	pir T03747 glucosyltransferase IS5a (EC 2.4.1.-), salicylate-i...	100	9e-021
	<u>11</u>	emb CAB88666.1 AJ400861 putative UDP-glycose [Cicer arietinum]	99	1e-020
35	<u>12</u>	pir T03745 glucosyltransferase IS10a (EC 2.4.1.-), salicylate-...	99	2e-020
	<u>13</u>	gb AAD20154.1 AC006282 putative glucosyl transferase [Arabid...	99	2e-020
	<u>14</u>	sp Q40287 UFO5_MANES FLAVONOL 3-O-GLUCOSYLTRANSFERASE 5 (UDP-GL...	99	2e-020
40	<u>15</u>	pir T05423 probable glucosyltransferase F28A23.110 (EC 2.4.1.-...	99	2e-020
	<u>16</u>	gb AAD12210.1 AC006135 putative flavonol 3-O-glucosyltransfe...	99	2e-020

- 17 dbj|BAB17060.1| AP002523 putative glucosyl transferase [Oryza... 99 2e-020
- 18 gb|AAD17393.1| AC006248 putative glucosyltransferase [Arabido... 98 3e-020
- 5 19 dbj|BAA98157.1| AB025613 anthocyanidin-3-glucoside rhamnosyl... 98 4e-020
- 20 gb|AAF97321.1|AC023628_2 AC023628 Similar to UTP-glucose gluc... 98 4e-020
- 21 gb|AAD32297.1|AC006533_21 AC006533 putative glucosyltransfera... 98 4e-020
- 10 22 pir|T07404 probable glucosyltransferase twi1 (EC 2.4.1.-) - to... 98 5e-020
- 23 dbj|BAB01151.1| AP000373 flavonol 3-O-glucosyltransferase-lik... 98 5e-020
- 24 gb|AAF97324.1|AC023628_5 AC023628 Putative UTP-glucose glucos... 98 5e-020
- 15 25 gb|AAD20153.1| AC006282 putative glucosyl transferase [Arabid... 97 6e-020
- 26 pir|T08395 UTP-glucose glucosyltransferase-like protein - Arab... 97 6e-020
- 20 27 pir|T01732 UTP-glucose glucosyltransferase homolog A_IG002N01.... 97 6e-020
- 28 emb|CAB80916.1| AL161491 putative flavonol glucosyltransferas... 97 6e-020
- 29 dbj|BAA83484.1| AB031274 UDP-glucose: flavonoid 7-O-glucosylt... 96 1e-019
- 25 30 gb|AAD17392.1| AC006248 putative glucosyltransferase [Arabido... 96 2e-019

RANK 1 ITERATION 0>sp|P56725|ZOX_PHAVU ZEATIN O-XYLOSYLTRANSFERASE (ZEATIN O-BETA-D-XYLOSYLTRANSFERASE)
 >gi|5802783|gb|AAD51778.1|AF116858_1 (AF116858) zeatin O-xylosyltransferase [Phaseolus vulgaris]
 Length = 454

35 Score = 137 bits (341), Expect = 5e-032
 Identities = 64/104 (61%), Positives = 79/104 (75%)
 Frame = +3Query: 18
 WXDKQKGKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLRADPNDF
 40 TEADKVK 197
 W DKQ SVIYVSFG+T +L D+QI ELA GLE+ +KFIWVLR AD DIF + +
 K
 Sbjct: 249
 WLDKQEPSSVIYVSFGTTTALRDEQIQELATGLEQSKQKFIWVLRDADKGDI
 45 F-DGSEAK 307Query: 198
 KPQLLADYEERVKDRGIIVRDWAPQLEILAHPSVGGFMSHCGWN 329

++L +EERV+ G++VRDWAPQ+EIL+H S GGFMSHCGWN
 Sbjct: 308
 RYELPEGFEERVEGMGLVVRDWAPQMEILSHSSTGGFMSHCGWN 351

5 RANK 2 ITERATION 0>sp|Q9ZSK5|ZOG_PHALU ZEATIN O-
 GLUCOSYLTRANSFERASE (ZEATIN
 O-BETA-D-GLUCOSYLTRANSFERASE) >gi|4140691|gb|AAD04166.1|
 (AF101972) zeatin O-glucosyltransferase [Phaseolus
 lunatus]
 10 Length = 459

Score = 135 bits (337), Expect = 2e-031
 Identities = 62/104 (59%), Positives = 79/104 (75%)
 Frame = +3Query: 18

15 WXD KQ GKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLRRADPN DIF
 TEADKVK 197

W D K Q S V I Y + S F G + T + L D + Q I + + A G L E + + K F I W V L R A D D I F + +
 K

Sbjct: 254
 20 WLDKQEPSSVIYISFGTTTALRDEQIQIATGLEQSKQKFIWVLREADKGDIF
 AGSE-AK 312Query: 198
 KPQLLADYEERVKDRGIIVRDWAPQLEILAHPSVGGFMSHCGWN 329

++L +EERV+ G++VRDWAPQLEIL+H S GGFMSHCGWN
 Sbjct: 313
 25 RYELPKGFEERVEGMGLVVRDWAPQLEILSHSSTGGFMSHCGWN 356

RANK 3 ITERATION 0>dbj|BAA36410.1| AB012114 UDP-glycose:flavonoid
 glycosyltransferase

[Vigna mungo]
 30 Length = 477

Score = 104 bits (256), Expect = 5e-022
 Identities = 48/104 (46%), Positives = 68/104 (65%)
 Frame = +3Query: 18

35 WXD KQ GKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLRRADPN DIF
 TEADKVK 197

W D + + D S V + Y + F G S + L + D Q + E L A N G L + G F I W V + R E + +
 Sbjct: 258

WLD SKERDSVLYICFGSLVLLSDKQLYELANGLDASGHSFIWVVHRKKKEG
 40 QEEEEEEKW 317Query: 198
 KPQLLADYEERVKDRGIIVRDWAPQLEILAHPSVGGFMSHCGWN 329

P+ + ER K R G + + + + W A P Q I L H P + V G G F + + H C G W N
 Sbjct: 318 LPEGFEEKIEREK-RGMLIKGWAPQLILNHPAVGGFLTHCGWN
 360

45

- Score = 102 bits (251), Expect = 2e-021
 Identities = 53/105 (50%), Positives = 74/105 (70%), Gaps = 8/105 (7%)
 Frame = +3Query: 15
 5 NWXDKQGKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLR----
 RADPNDIFTE 182
 +W +KQ +SV+Y+SFGS SLT Q+TELA GLE ++FIWV+R + +D F+
 Sbjct: 255
 DWLNKQPNESVLYISFGSGGSLTAQQLTELAWGLEESQQRFIWVVRPPVDG
 10 SSCSDYFSA 314Query: 183 ADKVKK---PQLLAD-
 YEERVKDRGIIVRDWAPQLEILAHPSVGGFMSHCGWN 329
 V K P+ L + + R DRG ++ WAPQ EILAH +VGGF++HCGW+
 Sbjct: 315
 KGGVTKDNTPEYLPGEFVTRTCDRGFMIPSWAPQAEILAHQAVGGFLTHCG
 15 WS 367
- RANK 7 ITERATION 0>gb|AAF17551.1| AF198453 UDP-glycose:flavonoid
 glycosyltransferase
 [Glycine max]
 20 Length = 244
- Score = 100 bits (247), Expect = 5e-021
 Identities = 49/105 (46%), Positives = 72/105 (67%), Gaps = 4/105 (3%)
 Frame = +3Query: 15
 25 NWXDKQGKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLRRADPND
 IFTEADKV 194
 +W D Q SV+++SFGS + Q+ E+A GLE+ ++F+WV+R F D V
 Sbjct: 140
 SWLDSQPSHSVLFSLFGSMGRFSRTQLGEIAIGLEKSEQRFLWVVRSE-----
 30 FENGDSV 194Query: 195 KKP---QLLAD-
 YEERVKDRGIIVRDWAPQLEILAHPSVGGFMSHCGWN 329
 + P +LL + + ER K++G++VRDWAPQ IL+H SVGGF++HCGWN
 Sbjct: 195
 EPPSLDELLPEGFLERTKEKGMVVRDWAPQAAILSHDSVGGFVTHCGWN
 35 243
- RANK 8 ITERATION 0>dbj|BAB17059.1| AP002523 putative glucosyl
 transferase [Oryza
 sativa]
 40 Length = 498
- Score = 100 bits (247), Expect = 5e-021
 Identities = 52/104 (50%), Positives = 67/104 (64%), Gaps = 1/104 (0%)
 Frame = +3Query: 18
 45 WXDQKQGKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLRRADPNDIF
 TEADKVK 197

W D + SVI+VSFGS S Q+ EL GLE + FIWV++ F E +
 Sbjct: 285
 WLDSKKPGSVIFVSFGSLSTDPQQLVELGLGLEASKKPFIWVIKAGKK---
 FPEVE--- 338Query: 198 KPQLLAD-

5 YEERVKDRGIIVRDWAPQLEILAHPSVGGFMSHCGWN 329
 + LAD +EERVKDRG+I+R WAPQ+ IL H ++GGFM+HCGWN

Sbjct: 339 --
 EWLADGFEERVKDRGMIIRGWAPQMMILWHQAIGGFMTHCGWN 381

10 RANK 9 ITERATION 0>emb|CAB16822.1| Z99708 glucosyltransferase-like
 protein

[Arabidopsis thaliana] >gi|7270626|emb|CAB80343.1|
 (AL161590) glucosyltransferase-like protein [Arabidopsis
 thaliana]

15 Length = 457

Score = 100 bits (246), Expect = 7e-021
 Identities = 52/105 (49%), Positives = 69/105 (65%), Gaps = 6/105 (5%)
 Frame = +3Query: 15

20 NWXDKQGKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLRR-
 ADPNDFTEADK 191

+W D Q K+SV+YV G +LT+Q ELA GLE G +F+WV+R A+ + + DK

Sbjct: 255

DWLDLQPKESVYVLLGVVGALTFEQTNELAYGLELTGHRFVWVVRPPAE
 25 DDPSASMFDK 314Query: 192 VKKPQLLADYE-----
 ERVKDRGIIVRDWAPQLEILAHPSVGGFMSHCGWN 329

K D+ +R KD G++VR WAPQ EILAH S GGF++HCGWN

Sbjct: 315

TKNETEPLDFLPNGFLDRTKDIGLVVRTWAPQEEILAHKSTGGFVTHCGWN
 30 365

RANK 10 ITERATION 0>pir|T03747 glucosyltransferase IS5a (EC 2.4.1.-),
 salicylate-induced

35 - common tobacco >gi|1685005|gb|AAB36653.1| (U32644)
 immediate-early salicylate-induced glucosyltransferase
 [Nicotiana tabacum]
 Length = 476

Score = 99.8 bits (245), Expect = 9e-021
 40 Identities = 48/104 (46%), Positives = 66/104 (63%)
 Frame = +3Query: 18

WXDKQGKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLRRADPNDF
 TEADKVK 197

W D + SV+Y+ FGS + T Q+ ELA G+E G++FIWV+R TE D

45 Sbjct: 271

WLDSKKPSSVYICFGSVANFTASQLHELAMGVEASGQEFIWVVR-----

TELDN-- 320Query: 198
 KPQLLADYEERVKDRGIIVRDWAPQLEILAHPSVGGFMSHCGWN 329
 + L +EER K++G+I+R WAPQ+ IL H SVG F++HCGWN
 Sbjct: 321 EDWLPEGFEERTKEKGLIIRGWAPQVLILDHESVGAFVTHCGWN
 364

RANK 11 ITERATION 0>emb|CAB88666.1| AJ400861 putative UDP-glycose
 [Cicer arietinum]
 Length = 438

Score = 99.5 bits (244), Expect = 1e-020
 Identities = 46/104 (44%), Positives = 69/104 (66%), Gaps = 2/104 (1%)
 Frame = +3Query: 18
 WXDKQGKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLRRADPN
 TEADKVK 197

W D + SV+Y+SFGS SL++DQ+ ELA G+E +F+WV+ R +D D
 Sbjct: 217
 WLDTKPSSVYISFGSLCSLSNDQLELAKGIEASKHQFLWVVRKGD
 ----DDDD 271Query: 198 KPQLLADYEERVKD--
 RGIIVRDWAPQLEILAHPSVGGFMSHCGWN 329
 + L ++ER+K+ RG++++ W PQ IL HPS+GGF++HCGWN
 Sbjct: 272
 ENWLPGKFKERMKEENRGMLIKGWVPQPLILDHPSIGGFLTHCGWN 317

RANK 12 ITERATION 0>pir|T03745 glucosyltransferase IS10a (EC 2.4.1.-),
 salicylate-induced - common tobacco
 >gi|1685003|gb|AAB36652.1| (U32643) immediate-early
 salicylate-induced glucosyltransferase [Nicotiana
 tabacum]
 Length = 476

Score = 99.1 bits (243), Expect = 2e-020
 Identities = 49/104 (47%), Positives = 65/104 (62%)
 Frame = +3Query: 18
 WXDKQGKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLRRADPN
 TEADKVK 197

W D + SV+YV FGS + T Q+ ELA G+E G++FIWV+R TE D
 Sbjct: 271
 WLDSKKPSSVYVCFGSVANFTASQLHELAMGIEASGQEFIWVVR-----
 TELDN-- 320Query: 198
 KPQLLADYEERVKDRGIIVRDWAPQLEILAHPSVGGFMSHCGWN 329
 + L EER K++G+I+R WAPQ+ IL H SVG F++HCGWN
 Sbjct: 321 EDWLPEGLEERTKEKGLIIRGWAPQVLILDHESVGAFVTHCGWN
 364

RANK 13 ITERATION 0>gb|AAD20154.1| AC006282 putative glucosyl
transferase [Arabidopsis
thaliana]
Length = 496

5 Score = 99.1 bits (243), Expect = 2e-020
Identities = 45/104 (43%), Positives = 69/104 (66%)
Frame = +3Query: 18
WXDKQGKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLRADPNDIF
10 TEADKVK 197
W D ++ SV+YV GS +L Q+ EL GLE FIWV+R ++ + ++
Sbjct: 281
WLDSKEEGSVLYVCLGSICNLPLSQLKELGLGLEESRRSFIWVIRGSE-----
KYKELF 334Query: 198
15 KPQLLADYEERVKDRGIIVRDWAPQLEILAHPSVGGFMSHCGWN 329
+ L ++EER+K+RG++++ WAPQ+ IL+HPSVGGF++HCGWN
Sbjct: 335 EWMLESGFEERIKERGLLIKGWAPQVLILSHPSVGGFLTHCGWN
378

20 RANK 14 ITERATION 0>sp|Q40287|UFO5_MANES FLAVONOL 3-O-
GLUCOSYLTRANSFERASE 5 (UDP-GLUCOSE
FLAVONOID 3-O-GLUCOSYLTRANSFERASE 5)
>gi|542015|pir||S41951 UTP-glucose glucosyltransferase -
cassava >gi|453249|emb|CAA54612.1| (X77462) UTP-glucose
25 glucosyltransferase [Manihot esculenta]
Length = 487
Score = 98.7 bits (242), Expect = 2e-020
Identities = 49/107 (45%), Positives = 73/107 (67%), Gaps = 6/107 (5%)
30 Frame = +3Query: 9
LSNWDXDKQGKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLR----
RADPNDIF 176
L +W D+Q K+SV+YVSFGS +L++Q+ ELA GLER ++FIWV+R + F
Sbjct: 261
35 LLDWLDQQPKESVYVSFGSGGTLSELMIELAWGLERSQQRFIWVVRQPT
VKTGDAAFF 320Query: 177 TEADKV--
KKPQLLADYEERVKDRGIIVRDWAPQLEILAHPSVGGFMSHCGWN 329
T+ D + R+++ G++V W+PQ+ I++HPSVG F+SHCGWN
Sbjct: 321
40 TQGDGADDMSGYFPEGFLTRIQNVGLVVPQWSPQIHIMSHPSVGVFLSHCG
WN 373

RANK 15 ITERATION 0>pir|T05423 probable glucosyltransferase F28A23.110
(EC 2.4.1.-) -
45 Arabidopsis thaliana >gi|2911049|emb|CAA17559.1|
(AL021961) glucosyltransferase-like protein [Arabidopsis

thaliana] >gi|7270362|emb|CAB80130.1| (AL161584)
glucosyltransferase-like protein [Arabidopsis thaliana]
Length = 478

5 Score = 98.7 bits (242), Expect = 2e-020
Identities = 48/104 (46%), Positives = 65/104 (62%)
Frame = +3Query: 18
WXDKQGKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLRRADPNDIF
TEADKVK 197

10 W D + +SVIYVSFGS ++Q+ E+A GLE G FIWV+R+ K K
Sbjct: 280
WLDSKKPNSVIYVSFGSVAFFKNEQLFEIAAGLEASGTSFIWVVRKT-----
KEK 329Query: 198
KPQLLADYEERVKDRGIIVRDWAPQLEILAHPSVGGFMSHCGWN 329
15 + L +EERVK +G+I+R WAPQ+ IL H + GF++HCGWN
Sbjct: 330 EEWLPEGFEERVKGKGMIRGWAPQVLILDHQATCGFVTHCGWN
373

RANK 16 ITERATION 0>gb|AAD12210.1| AC006135 putative flavonol 3-O-
20 glucosyltransferase
[Arabidopsis thaliana]
Length = 470

Score = 98.7 bits (242), Expect = 2e-020
25 Identities = 48/104 (46%), Positives = 68/104 (65%), Gaps = 1/104 (0%)
Frame = +3Query: 18
WXDKQGKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLRR-
ADPNDIFTEADKV 194
W D+Q + SV++V GS +LT+Q ELA GLE G++F+WVLRR A + D+
30 Sbjct: 260
WLDEQRERSVVFVCLGSGGTLTFEQTVELALGLELSGQRFVWVLRRPASYL
GAISSDDEQ 319Query: 195
KKPQLLADYEERVKDRGIIVRDWAPQLEILAHPSVGGFMSHCGWN 329
L ++R + GI+V WAPQ+EIL+H S+GGF+SHCGW+
35 Sbjct: 320 VSASLPEGFLDRTRGVGIVVTQWAPQVEILSHRSIGGFLSHCGWS
364

RANK 17 ITERATION 0>dbj|BAB17060.1| AP002523 putative glucosyl
40 transferase [Oryza
sativa]
Length = 501

Score = 98.7 bits (242), Expect = 2e-020
Identities = 50/104 (48%), Positives = 67/104 (64%), Gaps = 1/104 (0%)

Frame = +3Query: 18
 WXD KQGKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLRRADPN DIF
 TEADKVK 197

W D + S V I + V S F G + + S Q + E L G L E + F I W V + + + F + K

5 Sbjct: 288
 WLDSKKPGSVIFVSFGTLVSTAPQQLVELGLGLEASNKPFIWVIKAGNK---
 F P V V E K -- 342Query: 198 K P Q L L A D -
 Y E E R V K D R G I I V R D W A P Q L E I L A H P S V G G F M S H C G W N 329
 L A D + E E R V D R G + I + R W A P Q + I L H + + G G F M + H C G W N

10 Sbjct: 343 ---
 W L A D G F E E R V I D R G M I I R G W A P Q M M I L W H Q A I G G F M T H C G W N 384

RANK 18 ITERATION 0>gb|AAD17393.1| AC006248 putative
 glucosyltransferase [Arabidopsis

15 thaliana]
 Length = 460

Score = 98.3 bits (241), Expect = 3e-020
 Identities = 46/104 (44%), Positives = 70/104 (67%)

20 Frame = +3Query: 18
 WXD KQGKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLRRADPN DIF
 TEADKVK 197

W D + S V + Y + S F G S L + + Q + E + A G L E G + F I W V + + + N + T + +

Sbjct: 254
 25 WLDSKTPGSVVYLSFGSGTGLPNEQLLEIAFGLEGSGQNFIWVVSKNE-
 N Q V G T G E N E D W 312Query: 198
 K P Q L L A D Y E E R V K D R G I I V R D W A P Q L E I L A H P S V G G F M S H C G W N 329
 P + + E E R K + G + I + R W A P Q + I L H + + G G F + + H C G W N

Sbjct: 313 L P K --- G F E E R N K G K G L I I R G W A P Q V L I L D H K A I G G F V T H C G W N
 30 353

RANK 19 ITERATION 0>dbj|BAA98157.1| AB025613 anthocyanidin-3-glucoside
 rhamnosyltransferase-like [Arabidopsis thaliana]
 Length = 460

35 Score = 97.9 bits (240), Expect = 4e-020
 Identities = 46/107 (42%), Positives = 66/107 (60%)
 Frame = +3Query: 9

40 L S N W X D K Q G K D S V I Y V S F G S T I S L T D D Q I T E L A N G L E R C G E K F I W V L R R A D P
 N D I F T E A D 188

+ W D K Q + S V + Y V S G + S L + + + T E L A G L E + F W V L R

Sbjct: 264
 I K K W L D K Q R L N S V V Y V S L G T E A S L R H E E V T E L A L G L E K S E T P F F W V L R N -----
 ----- 312Query: 189

45 K V K K P Q L L A D Y E E R V K D R G I I V R D W A P Q L E I L A H P S V G G F M S H C G W N 329
 + P + + + R V K R G + + W P Q + + I L + H S V G G F + + H C G W N

Sbjct: 313 ---
EPKIPDGFKTRVKGRGMVHVGWVPQVKILSHESVGGFLTHCGWN 356

RANK 20 ITERATION 0>gb|AAF97321.1|AC023628_2 AC023628 Similar to

5 UTP-glucose

glucosyltransferases [Arabidopsis thaliana]

Length = 481

Score = 97.9 bits (240), Expect = 4e-020

10 Identities = 50/105 (47%), Positives = 70/105 (66%), Gaps = 8/105 (7%)

Frame = +3Query: 15

NWXDKQGKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLRADPND

IFTEADKV 194

NW D Q SV+YVSFGS +LT +Q ELA GL G++F+WV+R P+I++

15 Sbjct: 260

NWLDNQPFGSVLYVSFGSGGTLTFEQFIELALGLAESGKRFLWVIR--

SPSGIASSS--Y 315Query: 195 KKPQLLAD-----

YEERVKDRGIIVRDWAPQLEILAHPSVGGFMSHCGWN 329

PQ D ++R K++G++V WAPQ +IL H S+GGF++HCGWN

20 Sbjct: 316

FNPQSRNDPFSFLPQGFLDRTKEKGLVVGSWAPQAQILTHTSIGGFLTHCGW

N 368

[END

ALIGNMENTS]

25

Job DetailsReturn to top

[BEGIN JOB STATUS][BEGIN SEARCH TIME]

[END SEARCH TIME]

30

[VERSION]

[SEARCH ID]

[EOL] CRLF

[COMMENT] /Comment=NCBI BLASTX Translated Search

[COMMENT]

35

[ALGORITHM] BLASTX

[MATRIX] D:\DECYPHER\MATRIX\BLOSUM62.MAA

[QUERY FORMAT] FASTA/PEARSON

[QUERY TYPE] NT

[QUERY FILTER] T

40

[QUERY SEARCH] -1 -2 -3 1 2 3

[QUERY PATH] d:\decypher\query

[QUERY SET]

[TARGET TYPE] AA

[TARGET FRAMES] 1

45

[TARGET PATH] d:\decypher\target\blast

[TARGET SET] nr

[MAX SCORES] 30

[MAX ALIGNMENTS] 20
 [THRESHOLD] 1
 [RESULT PATH] d:\decypher\output
 [OUTPUT FORMAT] TEXT EXTRACTALIGNED[SHOW GI] F
 5 [EXPECTATION] 10
 [GAPPED ALIGNMENT] TBLASTX
 BLASTX
 Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
 Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
 10 "Gapped BLAST and PSI-BLAST: a new generation of protein database search
 programs", Nucleic Acids Res. 25:3389-3402. Query= Your_Query starting with:
 GATGAGTCCTGAGTAATTGG /QuerySize=342
 (342 letters) Database: Nonredundant Proteins
 598,029 sequences; 189,012,571 total letters Database: Nonredundant
 15 Proteins
 Posted date:
 Number of letters in database: 189,012,571
 Number of sequences in database: 598,029
 20 Lambda K H
 0.318 0.135 0.401 Gapped
 Lambda K H
 0.270 0.0470 0.230
 Matrix: BLOSUM62.MAA
 25 Gap Penalties: Existence: 11, Extension: 1
 Number of Hits to DB: 108516388
 Number of Sequences: 598029
 Number of extensions: 1761413
 Number of successful extensions: 7929
 30 Number of sequences better than 10.0: 384
 Number of HSP's better than 10.0 without gapping: 246
 Number of HSP's successfully gapped in prelim test: 108
 Number of HSP's that attempted gapping in prelim test: 7495
 Number of HSP's gapped (non-prelim): 362
 35 length of query: 114
 length of database: 189,012,571
 effective HSP length: 52
 effective length of query: 61
 effective length of database: 157,915,063
 40 effective search space: 9632818843
 effective search space used: 9632818843
 frameshift window, decay const: 50, 0.1
 T: 12
 A: 40
 45 X1: 16 (7.3 bits)
 X2: 38 (14.8 bits)

X3: 64 (24.9 bits)
 S1: 41 (21.7 bits)
 S2: 66 (30.1 bits)[JOB MESSAGES] [END JOB STATUS]

5 (342 letters)Database:
 154,797 sequences; 359,911,985 total
 lettersSearching.....done
 Score E
 Sequences producing significant alignments: (bits)

10	Value	CL037192.151	132 1e-30
		CL000385.121	129 9e-30
		CL008584.95	72 3e-26
		CL000385.124	75 4e-25
		CL006405.125	68 2e-24
15		CL024122.156	77 1e-23
		CL030297.22	107 3e-23
		CL005484.231	71 7e-23
		CL023819.77	64 2e-22
		CL041904.109.91	71 2e-22
20		CL010190.99	62 3e-22
		CL027779.406	63 6e-22
		CL027779.404	71 2e-21
		CL002034.493.126	68 2e-21
		CL005001.69	67 2e-21
25		CL004796.126	70 3e-21
		CL024122.154	72 3e-21
		CL034968.143	61 5e-21
		CL004815.98	71 1e-20
		CL010564.220	63 2e-20
30		CL021506.53	62 2e-20
		CL026058.234	66 2e-20
		CL027779.401	68 2e-20
		CL005185.85.92	61 3e-20
		CL046172.67.78	73 3e-20
35		CL021585.37	61 3e-20
		CL017888.77	63 4e-20
		CL009535.107.65	59 7e-20
		CL027779.355	64 7e-20
		CL008587.124	61 2e-19
40		CL002636.139	58 2e-19
		CL021570.172	61 2e-19
		CL023193.102	58 2e-19
		CL008830.31	73 3e-19
		CL020805.80	61 3e-19
45		CL016528.75.11	59 3e-19
		CL002440.161	73 4e-19

	CL002015.133.77	65 6e-19
	CL006613.15	57 1e-18
	CL004815.97	68 1e-18
	CL006813.89	59 1e-18
5	CL039915.41.49	57 1e-18
	CL038334.38	92 2e-18
	CL007873.113	62 2e-18
	CL007873.106	62 2e-18
	CL037701.143	71 2e-18
10	CL008587.125	61 4e-18
	CL018723.139.47	57 1e-17
	CL009812.347	58 1e-17
	CL009812.361	60 1e-17
	CL020036.38	61 1e-17
15	CL037972.43	57 1e-17
	CL034535.85	56 2e-17
	CL030368.81.82	57 2e-17
	CL011484.95	54 2e-17
	CL008051.83	55 3e-17
20	CL024242.128	58 6e-17
	CL034968.144	63 7e-17
	CL021644.104	54 9e-17
	CL014976.74	53 9e-17
	HTC046833-A01.74.76	57 1e-16
25	CL024242.141	55 1e-16
	CL017811.54	54 1e-16
	CL051859.93.94	53 2e-16
	CL031869.74	57 2e-16
	CL005175.139.58	57 2e-16
30	CL037983.71	62 2e-16
	CL008073.540	61 2e-16
	CL012878.80	56 4e-16
	CL016409.121	56 7e-16
	CL010277.55	53 8e-16
35	CL024122.163	83 8e-16
	CL005694.182	54 1e-15
	CL011220.184	56 1e-15
	CL001522.667	61 2e-15
	HTC018155-A01.R.38.95	52 2e-15
40	CL023620.124.51	53 2e-15
	CL039431.43	56 3e-15
	CL021720.29	54 3e-15
	CL009267.89	51 4e-15
	CL006514.229.168	55 5e-15
45	CL024324.140	51 5e-15
	CL035336.97	51 5e-15

	CL038292.23	65 5e-15
	CL008073.542	60 5e-15
	CL037422.178	56 9e-15
	CL003181.199	63 9e-15
5	CL039340.19	51 9e-15
	CL026437.83	56 9e-15
	CL005944.12	54 9e-15
	CL027541.163.148	56 2e-14
	CL003181.168	52 2e-14
10	CL014046.2	78 3e-14
	CL007722.118	53 4e-14
	CL026661.50	59 4e-14
	CL014445.209	54 8e-14
	CL027525.91	55 8e-14
15	CL014445.211	54 8e-14
	CL018085.225.139	51 1e-13
	CL056271.83.103	53 1e-13
	CL012295.141	53 1e-13
	CL037891.52.70	52 1e-13
20	CL010173.141	53 2e-13
	CL017801.43	53 3e-13
	CL006712.198	55 3e-13
	CL011675.53	63 5e-13
	CL005939.33	50 5e-13
25	CL000663.406	47 7e-13
	CL033762.101	52 7e-13
	CL007660.29	49 7e-13
	CL001522.659	53 9e-13
	CL002484.4	52 1e-12
30	CL002587.55.73	52 2e-12
	CL032230.57	52 2e-12
	CL011181.132	51 2e-12
	CL009819.69	48 3e-12
	CL003318.273	54 3e-12
35	CL041904.109.89	62 3e-12
	CL023246.106.114	59 1e-11
	CL015903.55	45 2e-11
	CL001632.293	46 2e-11
	CL014413.56.69	54 5e-11
40	CL036169.42	66 1e-10
	CL022193.143	66 1e-10
	CL019829.73	57 1e-10
	CL008718.5	43 2e-10
	CL002954.21	65 2e-10
45	CL038203.17	60 3e-10
	CL035030.166.173	47 5e-10

	CL013048.66	47 5e-10
	CL008671.33	54 9e-10
	CL037496.141	52 1e-09
	CL000509.218.7	62 1e-09
5	CL026417.121	57 1e-09
	CL006249.99	54 2e-09
	CL045993.22.1	47 2e-09
	CL006249.97	54 2e-09
	CL047792.34.5	54 2e-09
10	CL018971.79	54 4e-09
	CL020290.113.89	31 4e-09
	CL026049.88	52 4e-09
	CL025248.34.28	50 5e-09
	CL017286.114	59 8e-09
15	CL006073.199	60 8e-09
	CL037606.41	58 2e-08
	CL000445.107	48 3e-08
	CL017286.113	57 5e-08
	CL004019.70	57 8e-08
20	CL001229.56	57 8e-08
	CL038203.11	56 1e-07
	CL018910.18	50 2e-07
	CL004311.41	55 2e-07
	CL006249.98	49 3e-07
25	CL006250.59	49 3e-07
	CL037496.143	52 6e-07
	CL007311.64	48 1e-06
	CL040803.156.106	51 2e-06
	CL003045.38	51 2e-06
30	CL000021.522	51 2e-06
	CL023139.137	51 3e-06
	CL022070.105.37	51 3e-06
	CL027488.1.1	51 3e-06
	CL009267.94	51 5e-06
35	CL004109.192.131	50 6e-06
	CL002854.142	48 2e-05
	CL020732.41	48 3e-05
	CL047288.95.94	48 3e-05
	CL001395.104	46 1e-04
40	CL046651.78.92	43 1e-04
	CL012879.91	44 4e-04
	CL037422.184	44 4e-04
	CL024561.203	41 0.004
	CL031911.221	39 0.018
45	CL009894.82	39 0.018
	CL017435.41	35 0.32

CL025804.138 33 0.82
CL016357.110 33 1.1
CL016373.76 32 2.1
CL006799.122 32 2.1
5 CL021508.93 31 4.0
CL021508.96 31 4.0
CL040417.30.45 30 5.5
CL003447.129 30 5.5
CL018287.77.89 30 5.5
10 CL004077.196 30 5.5
CL002787.44 30 5.5
HTC170138-B01.1.56 30 7.6
CL000396.374 30 7.6
CL032065.41 30 7.6
15 CL003934.253 30 7.6
CL036158.8 30 7.6
CL044924.114.138 30 7.6>CL037192.151
Length = 3506

20 Score = 132 bits (282), Expect = 1e-30
Identities = 52/105 (49%), Positives = 71/105 (67%)
Frame = +3 / +2
Query: 15
NWXXDKQGKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLRADPND
25 IFTEADKV 194
+W DKQ SV+YVSFG+T SL DQ+ ELA L+ ++FIWVLR AD DIF +++
Sbjct: 1973
DWLDKQPAASVLYVSFGTTSSLRGDQVAELAAALKGSKQRFIWVLRDADR
ADIFADSGES 2152
30 Query: 195
KKPQLLADYEERVKDRGHIIVRDWAPQLEILAHPSVGGFMSHCGWN 329
+ +LL++ + G+++ WAPQLEILAH + FMSHCGWN
Sbjct: 2153
RHAELLSRFTAETEGVGLVITGWAPQLEILAHGATAAFMSHCGWN 2287
35 Score = 30.8 bits (61), Expect(2) = 0.90
Identities = 14/30 (46%), Positives = 17/30 (56%)
Frame = -3 / -3
Query: 331 QFHPQ*LMNPPTDG*AKISSCGAQSLTIIP 242
+F PQ LMN A+ISSCGA + P
40 Sbjct: 2289 EFQPQWLMNAAVAPCARISSCGAHPVITSP 2200
Score = 20.8 bits (39), Expect(2) = 0.90
Identities = 10/22 (45%), Positives = 14/22 (63%)
Frame = -2 / -2
Query: 152 SKHPYKLLPASFPVSQLCDLI 87
45 +KHP + L A+ Q +L DLI
Sbjct: 2110 AKHPDEPLLAALQRRGELRDLI 2045

>CL000385.121

Length = 6118

Score = 129 bits (276), Expect = 9e-30

5 Identities = 51/105 (48%), Positives = 71/105 (67%)

Frame = +3 / +3

Query: 15

NWXDKQGKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLRRADPND
IFTEADKV 194

10 +W DKQ SV+YVSFG+T SL DQ+ ELA L+ ++FIWVLR AD +IF ++ +

Sbjct: 2088

DWLDKQPLASVLYVSFGTTSSLRGDQVAELAAALKGSKQRFIWVLRDADR
ANIFADSGES 2267

Query: 195

15 KKPQLLADYEERVKDRGIIVRDWAPQLEILAHPSVGGFMSHCGWN 329

+ +LL++ + G+++ WAPQLEILAH + FMSHCGWN

Sbjct: 2268

RHAELLSRFTAETEGVGLVITGWAPQLEILAHGATAAFMSHCGWN 2402

Score = 30.4 bits (60), Expect(2) = 1.2

20 Identities = 14/30 (46%), Positives = 17/30 (56%)

Frame = -3 / -1

Query: 331 QFHPQ*LMNPPTDG*AKISSCGAQSLTIIP 242

+F PQ LMN A+ISSCGA + P

Sbjct: 2404 EFQPQWLMNAAVAPCARISSCGAHPVITNP 2315

25 Score = 20.8 bits (39), Expect(2) = 1.2

Identities = 10/22 (45%), Positives = 14/22 (63%)

Frame = -2 / -3

Query: 152 SKHPYKLLPASFPVSQLCDLI 87

+KHP + L A+ Q +L DLI

30 Sbjct: 2225 AKHPDEPLLAALQRRGELRDLI 2160

>CL008584.95

Length = 6651

Score = 72.1 bits (151), Expect(2) = 3e-26

35 Identities = 29/56 (51%), Positives = 40/56 (70%)

Frame = +3 / -3

Query: 15

NWXDKQGKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLRRADPND
IFTE 182

40 +W D+Q DSV+YVSFG+T SL +Q+ ELA L ++FIWV+R AD +IFT+

Sbjct: 5035

DWLDRQPPDSVLYVSFGTTCSLRVEQVAELAATLRGSKQRFIWVMRDADR
GNIFTD 4868

Score = 66.6 bits (139), Expect(2) = 3e-26

45 Identities = 22/51 (43%), Positives = 35/51 (68%)

Frame = +3 / -3

- Frame = +3 / -1
 Query: 213 ADYEERVKDRGIIVRDWAPQLEILAHPSVGGFMSHCGWN 329
 A +EERV DRG++VRDW PQ ILAH + F++HCGWN
 Sbjct: 5239 AGWEERVGDRGLLVRDWVPQTALAHSATAAFLTHCGWN 5123
- 5 Score = 49.6 bits (102), Expect(2) = 7e-21
 Identities = 19/46 (41%), Positives = 29/46 (62%)
 Frame = +3 / -2
 Query: 15
 NWXDKQGKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLR 152
 10 +W + SV+Y+ FGS ++D Q+ ELA GL G+ F+WV+R
 Sbjct: 999
 DWLSSKPSRSVVYLCFGLTHVSDTQLDELALGL*AAGKPFLWVVR 862
 Score = 70.7 bits (148), Expect(2) = 7e-21
 Identities = 24/37 (64%), Positives = 31/37 (82%)
- 15 Frame = +3 / -2
 Query: 219 YEERVKDRGIIVRDWAPQLEILAHPSVGGFMSHCGWN 329
 ++ERV DRG+++R WAPQ ILAHPSVG F++ CGWN
 Sbjct: 834 WKERVGDRGMVIRGWAPQKAILAHPSVGAFVTQCGWN 724
 Score = 46.0 bits (94), Expect(2) = 1e-04
- 20 Identities = 20/35 (57%), Positives = 23/35 (65%)
 Frame = -3 / +2
 Query: 331 QFHPQ*LMNPPTDG*AKISSCGAQSLTIPLSFTL 227
 +FHP + PTDG A I+ CGAQ L IPLS TL
 Sbjct: 722 EFHPHCVTKAPTGWASIAFCGAQPLMTIPLSPTL 826
- 25 Score = 19.4 bits (36), Expect(2) = 1e-04
 Identities = 13/51 (25%), Positives = 20/51 (38%)
 Frame = -3 / +2
 Query: 193
 TLSASVKMSFGSALLSTHINFSPHLSNPLANXXXXXXXXXXXXDPKETYITE
- 30 41
 TLS ++L+TH N P +P A+ PK+ T+
 Sbjct: 821
 TLSFQPSGGAHMSVLTTTHRNGFPAAYSPKASSSS*VSDTWVRLPKQR*TTD
 973
- 35 Score = 31.8 bits (63), Expect(2) = 0.080
 Identities = 16/34 (47%), Positives = 19/34 (55%)
 Frame = -3 / +3
 Query: 331 QFHPQ*LMNPPTDG*AKISSCGAQSLTIPLSFT 230
 +F PQ + N A I+ CG QSLT PLS T
- 40 Sbjct: 5121 EFQPQCVKNAAVAWEASIAVCGTQSLTSNPLSPT 5222
 Score = 23.5 bits (45), Expect(2) = 0.080
 Identities = 9/20 (45%), Positives = 13/20 (65%)
 Frame = -2 / +2
 Query: 143 PYKLLPASFQPVSQLCDLII 84
- 45 P + L FQP SQL +L++
 Sbjct: 5273 PKERLAGGFQPESQLMELLL 5332

>CL023819.77

Length = 4766

Score = 61.1 bits (127), Expect(2) = 2e-22

5 Identities = 24/45 (53%), Positives = 30/45 (66%)

Frame = +3 / -2

Query: 18 WDXKQGKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLR
152

W DKQ + SVIYV+ GS LT+D + ELA GLE +F+W LR

10 Sbjct: 2620

WLDKQSEKSVIYVALGSEAPLTEDHVRELALGLELANVRFLWALR 2486

Score = 64.3 bits (134), Expect(2) = 2e-22

Identities = 21/36 (58%), Positives = 27/36 (74%)

Frame = +3 / -2

15 Query: 219 YEERVKDRGIIVRDWAPQLEILAHPSVGGFMSHCGW 326

+E RV RGI+ W PQL +LAH +VGGF++HCGW

Sbjct: 2425 FESRVAARGIVCTQWVPQLRVLAHRAVGGFLTHCGW 2318

>CL041904.109.91

Length = 1742

20

Score = 54.7 bits (113), Expect(2) = 2e-22

Identities = 21/52 (40%), Positives = 32/52 (61%)

Frame = +3 / +2

Query: 6

25 VLSNWDXKQGKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLRAD
161

V++ W D DSVIYV+FGS + E+ +GLE G+ FIWV++ ++

Sbjct: 314

VVTTWLDAMDTDSVIYVNFGSLARKVPKYLFEVGHGLEDSGKPFIVVVKES

30 E 469

Score = 70.7 bits (148), Expect(2) = 2e-22

Identities = 25/40 (62%), Positives = 32/40 (79%)

Frame = +3 / +2

Query: 210 LADYEERVKDRGIIVRDWAPQLEILAHPSVGGFMSHCGWN 329

35 L+ E RV RG++VR WAPQL IL+H +VGGF++HCGWN

Sbjct: 497 LSALEARVAGRGVVVRGWAPQLAILSHRAVGGFVTHCGWN 616

Score = 29.9 bits (59), Expect = 7.6

Identities = 12/30 (40%), Positives = 17/30 (56%)

Frame = -3 / -3

40 Query: 331 QFHPQ*LMNPPTDG*AKISSCGAQSLTIIP 242

+F PQ+ PPT +++SCGA T P

Sbjct: 618 EFQPQWVTKPPTARCDRMASCGAHPRTTTP 529

>CL010190.99

Length = 7963

45

Score = 62.5 bits (130), Expect(2) = 3e-22

Identities = 24/51 (47%), Positives = 33/51 (64%)

Frame = +3 / -1

Query: 18

WXDKQGKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLRRADPND

5 170

W D+Q SV+Y+SFGS +T Q+ ELA GLE+ +F+WV+R ND

Sbjct: 6244

WLDEQPPGSVLYISFGSLYRITAPQMMELARGLEQSSHRFVWVIRPPAGND
6092

10 Score = 62.5 bits (130), Expect(2) = 3e-22

Identities = 20/30 (66%), Positives = 26/30 (86%)

Frame = +3 / -1

Query: 240 RGIIVRDWAPQLEILAHPSVGGFMSHCGWN 329

RG++VR WAPQ+EILAH + G F++HCGWN

15 Sbjct: 6025 RGLVVRCWAPQVEILAHTATGAFLTHCGWN 5936

Score = 32.2 bits (64), Expect = 1.5

Identities = 14/30 (46%), Positives = 18/30 (59%)

Frame = -3 / +3

Query: 331 QFHPQ*LMNPPTDG*AKISSCGAQSITIIP 242

20 +F PQ + N P A+IS+CGAQ T P

Sbjct: 5934 EFQPQCVRNAPVAVCARISTCGAQHRTTSP 6023

>CL027779.406

Length = 2591

25 Score = 62.9 bits (131), Expect(2) = 6e-22

Identities = 23/51 (45%), Positives = 35/51 (68%)

Frame = +3 / +2

Query: 18

WXDKQGKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLRRADPND

30 170

W D Q + SV++VSFGS +++ +Q+ E+A GLE G +F+WV+R P D

Sbjct: 1622

WLDAQPERSVVFVSFGSMGAVSAEQLKEIARGLENSGHRFLWVVRSPPPED
1774

35 Score = 61.1 bits (127), Expect(2) = 6e-22

Identities = 18/35 (51%), Positives = 27/35 (76%)

Frame = +3 / +2

Query: 225 ERVKDRGIIVRDWAPQLEILAHPSVGGFMSHCGWN 329

ER ++RG++V WAPQ+E+L H + F++HCGWN

40 Sbjct: 1841 ERTREGRMVMSWAPQVEVLRHAATAAFVTHCGWN 1945

Score = 36.3 bits (73), Expect = 0.089

Identities = 15/35 (42%), Positives = 19/35 (53%)

Frame = -3 / -3

Query: 331 QFHPQ*LMNPPTDG*AKISSCGAQSITIPLSFTL 227

45 +FHPQ + N S+CGA +T IPLS L

Sbjct: 1947 EFHPQCVTNAAVAACRSTSTCGAHDITTIPLSLVL 1843

Identities = 22/41 (53%), Positives = 30/41 (72%)

Frame = +3 / -3

Query: 207 LLADYEERVKDRGIIVRDWAPQLEILAHPSVGGFMSHCGWN 329
L A +EER + RG++ W PQ+ ILAH +VG F++HCGWN

5 Sbjct: 1308 LPAGFEERTRGRGVVATRWVPQMSILAHAAVGAFLTHCGWN
1186

>CL005001.69

Length = 3014

10 Score = 55.6 bits (115), Expect(2) = 2e-21
Identities = 20/51 (39%), Positives = 33/51 (64%)
Frame = +3 / +3

Query: 9

LSNWDXDKQGKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLRRAD

15 161

++ W D+Q SV+YVSFGS + + E+ NGL E G+ F+WV++ ++

Sbjct: 1251

ITAWLDEQVTGSSVYVSFGSVLRKLPKHLFEVGNGLSDSGKPFLWVVKES
1403

20 Score = 66.6 bits (139), Expect(2) = 2e-21
Identities = 22/40 (55%), Positives = 31/40 (77%)
Frame = +3 / +3

Query: 210 LADYEERVKDRGIIVRDWAPQLEILAHPSVGGFMSHCGWN 329
L ++ R RG++VR WAPQ+ IL+H +VGGF++HCGWN

25 Sbjct: 1437 LDEFMARTATRGLVVRGWAPQVTILSHRAVGGFLTHCGWN
1556

Score = 29.9 bits (59), Expect = 7.6
Identities = 12/30 (40%), Positives = 17/30 (56%)
Frame = -3 / -2

30 Query: 331 QFHPQ*LMNPPTDG*AKISSCGAQSLTIIP 242
+FHPQ + PPT ++ +CGA T P

Sbjct: 1558 EFHPQCVRKPPTARCDRMVTCGAHPRTTRP 1469
>CL004796.126

Length = 6003

35

Score = 51.9 bits (107), Expect(2) = 3e-21
Identities = 20/48 (41%), Positives = 29/48 (59%)
Frame = +3 / +3

Query: 9

40 LSNWDXDKQGKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLR 152
++ W D DSVIYV+FGS + E+ +GLE G+ FIWV++

Sbjct: 468

ITTWLDAMDTDSVIYVNFGSLARKVPKYLFEVGHGLEDSGKPFIVVVK 611

Score = 69.8 bits (146), Expect(2) = 3e-21
45 Identities = 25/40 (62%), Positives = 32/40 (79%)
Frame = +3 / +3

Sbjct: 772
 LMSSWLDRQPPKSVVYVALGSXAPLTAEQRRXLALGLELSGAPFLWALRKP
 HGGD 608
 Score = 59.3 bits (123), Expect(2) = 7e-20
 5 Identities = 19/35 (54%), Positives = 28/35 (79%)
 Frame = +3 / -3
 Query: 219 YEERVKDRGIIVRDWAPQLEILAHPSVGGFMSHCG 323
 +EER + RG++ +W PQL+ILAH +VG F++HCG
 Sbjct: 580 FEERTRGRGMVKTEWVPQLKILAHAAVGAFLTHCG 476
 10 >CL027779.355
 Length = 2607

 Score = 53.3 bits (110), Expect(2) = 7e-20
 Identities = 19/46 (41%), Positives = 32/46 (69%)
 15 Frame = +3 / +2
 Query: 15
 NWXDKQGKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLR 152
 +W D Q + SV+++ FGS +++ Q+ E+A GLE G +F+WV+R
 Sbjct: 1868
 20 SWLDAQPERSVVFLCFGSLGAVSVKQLKEIARGLENSGHRFLWVVR 2005
 Score = 63.8 bits (133), Expect(2) = 7e-20
 Identities = 19/37 (51%), Positives = 28/37 (75%)
 Frame = +3 / +2
 Query: 219 YEERVKDRGIIVRDWAPQLEILAHPSVGGFMSHCGWN 329
 25 + ER +DRG++V WAPQ+E+L H + F++HCGWN
 Sbjct: 2081 FTERTRDRGMVVTSWAPQVEVLRHAATAAFVTHCGWN 2191
 Score = 34.5 bits (69), Expect = 0.32
 Identities = 15/35 (42%), Positives = 19/35 (53%)
 Frame = -3 / -1
 30 Query: 331 QFHPQ*LMNPPTDG*AKISSCGAQSLTIPLSFTL 227
 +FHPQ + N S+CGA +T IPLS L
 Sbjct: 2193 EFHPQCVTNAAVAACRSTSTCGAHDVTTIPLSRVL 2089
 >CL008587.124
 Length = 5621
 35
 Score = 55.1 bits (114), Expect(2) = 2e-19
 Identities = 18/45 (40%), Positives = 31/45 (68%)
 Frame = +3 / +3
 Query: 18 WXDKQGKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLR
 40 152
 W D+Q K SV+++ FGS ++ Q++E+A G+E G +F+W +R
 Sbjct: 3210
 WLDRQPKQSVVFLCFGSRGTFSVSQLSEMARGIENSGHRFLWAVR 3344
 Score = 60.6 bits (126), Expect(2) = 2e-19
 45 Identities = 19/35 (54%), Positives = 27/35 (76%)
 Frame = +3 / +3

Frame = -3 / -3
 Query: 337 AYQFHPQ*LMNPPTDG*AKISSCGAQSLTHIPLS 236
 A FHPQ + NPPT G ++S CGAQ + P S
 Sbjct: 4572 ASSFHPQCVTNPPTAGWFRMSICGAQPRMVRPRS 4471
 5 >CL023193.102
 Length = 1884

 Score = 57.9 bits (120), Expect(2) = 2e-19
 Identities = 21/47 (44%), Positives = 33/47 (69%)
 10 Frame = +3 / +1
 Query: 15
 NWXDKQGKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLRR 155
 +W D Q + SV+++ FGS S +Q+ E+A GLE G++F+WV+RR
 Sbjct: 853
 15 SWLDAQPEKSVVFLCFGSMGSFPKEQLAEIAIGLEXSGQRFLWVVRR 993
 Score = 57.4 bits (119), Expect(2) = 2e-19
 Identities = 18/35 (51%), Positives = 24/35 (68%)
 Frame = +3 / +1
 Query: 225 ERVKDRGIIVRDWAPQLEILAHPSVGGFMSHCGWN 329
 20 ER K RG+ WAPQ ++L H + G F++HCGWN
 Sbjct: 1093 ERTKGRGLAAGSWAPQADVLRHRATGAFVTHCGWN 1197
 Score = 28.6 bits (56), Expect(2) = 0.94
 Identities = 13/35 (37%), Positives = 16/35 (45%)
 Frame = -3 / -2
 25 Query: 331 QFHPQ*LMNPPTDG*AKISSCGAQSLTHIPLSFTL 227
 +FHPQ + N P S+CGA PL L
 Sbjct: 1199 EFHPQCVTNAPVALCRSTSACGAHDPAASPLPLVL 1095
 Score = 23.1 bits (44), Expect(2) = 0.94
 Identities = 12/42 (28%), Positives = 16/42 (37%)
 30 Frame = -3 / -2
 Query: 148 STHINFSPHLSNPLANXXXXXXXXXXXXDPKETYITESFPCLS 23
 +TH N P S+P+A PK+ T C S
 Sbjct: 986 TTHRNLCPDXSSPMAISASCSLGNEPMLPKQRNTTLFSGCAS 861
 35 >CL008830.31
 Length = 3276

 Score = 41.4 bits (84), Expect(2) = 3e-19
 Identities = 14/36 (38%), Positives = 25/36 (68%)
 Frame = +3 / +2
 40 Query: 45 VIYVSFGSTISLTDDQITELANGLERCGEKFIWVLRR 152
 V+Y++ G+ ++ + Q+ E+A+GLER FIW +R
 Sbjct: 974 VLYIALGTLAAIPEVQLKEVADGLERADVNFIVAVR 1081
 Score = 73.5 bits (154), Expect(2) = 3e-19
 Identities = 29/52 (55%), Positives = 36/52 (68%)
 45 Frame = +3 / +2

>CL002440.161

Length = 3854

Score = 40.9 bits (83), Expect(2) = 4e-19

5 Identities = 17/45 (37%), Positives = 23/45 (50%)

Frame = +3 / -3

Query: 18 WXD KQGKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLR
152

W + SV+Y GS + Q ELA GLE + F+WV+R

10 Sbjct: 3795

WLSTKPSQSVVYXCXGSWXHFSVTQTRELALGLEASNQPFLWVIR 3661

Score = 73.5 bits (154), Expect(2) = 4e-19

Identities = 24/37 (64%), Positives = 32/37 (85%)

Frame = +3 / -3

15 Query: 219 YEERVKDRGIIVRDWAPQLEILAHPSVGGFMSHCGWN 329

+E R++ RG++VR WAPQL +LAHPSVG F++HCGWN

Sbjct: 3615 WERRMEGRGMVVRGWAPQLAVLAHPSVGAFVTHCGWN 3505

Score = 41.8 bits (85), Expect = 0.002

Identities = 16/30 (53%), Positives = 20/30 (66%)

20 Frame = -3 / +2

Query: 331 QFHPQ*LMNPPTDG*AKISSCGAQSLTIIP 242

+FHPQ + N PTDG A +SCGA T +P

Sbjct: 3503 EFHPQWVTNAPT D GWASTASCGAHPRTTMP 3592

>CL002015.133.77

25 Length = 5794

Score = 48.7 bits (100), Expect(2) = 6e-19

Identities = 18/45 (40%), Positives = 30/45 (66%)

Frame = +3 / +1

30 Query: 18 WXD KQGKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLR
152

W D Q + SV+++ FGS + +Q+ E+A GLE ++F+WV+R

Sbjct: 2398

WLDAQPEHSVFLCFGSKGVFSAEQLKEIAVGLENSRQRFMWVVR 2532

35 Score = 65.2 bits (136), Expect(2) = 6e-19

Identities = 21/37 (56%), Positives = 28/37 (74%)

Frame = +3 / +1

Query: 219 YEERVKDRGIIVRDWAPQLEILAHPSVGGFMSHCGWN 329

+ ER KDRG IV WAPQ+++L H + G F++HCGWN

40 Sbjct: 2617 FVERTKDRGFIVTTWAPQVDVLRHRATGAFVTHCGWN 2727

Score = 30.8 bits (61), Expect = 4.0

Identities = 13/32 (40%), Positives = 18/32 (55%)

Frame = -3 / -3

Query: 331 QFHPQ*LMNPPTDG*AKISSCGAQSLTIIPLS 236

45 +FHPQ + N P S+CGA +T+ P S

Sbjct: 2729 EFHPQCVTNAPVARWRSTSTCGAHVVTMKPRS 2634

>CL006813.89

Length = 5431

Score = 58.8 bits (122), Expect(2) = 1e-18

5 Identities = 22/45 (48%), Positives = 32/45 (70%)

Frame = +3 / -1

Query: 18 W X D K Q G K D S V I Y V S F G S T I S L T D D Q I T E L A N G L E R C G E K F I W V L R
152

W D Q S V + Y V S F G S + + + + Q + E L A G L E G + F + W V + +

10 Sbjct: 1135

W L D A Q P A R S V V Y V S F G S R K A I S G E Q L R E L A A G L E T S G H R F L W V V K 1001

Score = 53.8 bits (111), Expect(2) = 1e-18

Identities = 18/35 (51%), Positives = 25/35 (71%)

Frame = +3 / -1

15 Query: 225 E R V K D R G I I V R D W A P Q L E I L A H P S V G G F M S H C G W N 329

+ R V + R G + + + W Q E + L H S V F + S H C G W N

Sbjct: 937 K R V E K R G L V T K A W V D Q E E V L K H E S V A L F V S H C G W N 833

>CL039915.41.49

Length = 4304

20

Score = 56.5 bits (117), Expect(2) = 1e-18

Identities = 23/45 (51%), Positives = 31/45 (68%)

Frame = +3 / -3

Query: 18 W X D K Q G K D S V I Y V S F G S T I S L T D D Q I T E L A N G L E R C G E K F I W V L R
25 152

W D + Q S V + + V S F G S L + + Q E L A G L E G + F + W V + R

Sbjct: 1980

W L D R Q P A G S V V F V S F G S G G I L S V E Q T R E L A A G L E M S G H R F L W V V R 1846

Score = 56.0 bits (116), Expect(2) = 1e-18

30 Identities = 18/35 (51%), Positives = 26/35 (73%)

Frame = +3 / -3

Query: 225 E R V K D R G I I V R D W A P Q L E I L A H P S V G G F M S H C G W N 329

E R + R G + V W A P Q + + L + H P + + F + S H G W N

Sbjct: 1749 E R T R G R G L A V A S W A P Q V R V L S H P A M V A F V S H Y G W N 1645

35 >CL038334.38

Length = 811

Score = 91.8 bits (194), Expect = 2e-18

Identities = 40/96 (41%), Positives = 53/96 (54%)

40 Frame = +3 / -3

Query: 42

S V I Y V S F G S T I S L T D D Q I T E L A N G L E R C G E K F I W V L R R A D P N D I F T E A D K V K K
P Q L L A D Y 221

S V + + + F G S L Q + E L A G L E R G + F + W V L R A + D L +

Sbjct: 794
SVVFLCFGSIGFLEAAQVRELAAGLERSGHRFLWVLRGAPAGGVRYPTDAD
PGELLPEGF 615

Query: 222 EERVKDRGHIIVRDWAPQLEILAHPSVGGFMSHCGWN 329

5 E R + WAPQ +IL H + GGF++HCGWN

Sbjct: 614 LEATAGRXXVWPXWAPQKDILGHAAXGGFVTHCGWN 507

>CL007873.113

Length = 4434

10 Score = 49.6 bits (102), Expect(2) = 2e-18

Identities = 18/37 (48%), Positives = 26/37 (69%)

Frame = +3 / +3

Query: 42 SVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLR 152

SV+YVSFG+ +D+Q+ ELA GL + G F+W +R

15 Sbjct: 420 SVVYVSFGTQAHVADEQLDELARGLVQSGHPFLWAVR 530

Score = 62.5 bits (130), Expect(2) = 2e-18

Identities = 22/31 (70%), Positives = 25/31 (79%)

Frame = +3 / +3

Query: 237 DRGHIIVRDWAPQLEILAHPSVGGFMSHCGWN 329

20 D+G IVR W PQ +LAH SVGGF+SHCGWN

Sbjct: 567 DQGRIVRGWVPQRGVLAHESVGGFVSHCGWN 659

Score = 42.8 bits (87), Expect = 0.001

Identities = 17/32 (53%), Positives = 20/32 (62%)

Frame = -3 / -3

25 Query: 331 QFHPQ*LMNPPTDG*AKISSCGAQSLTIPLS 236

+FHPQ L NPPTD A+ CG LT+ P S

Sbjct: 661 EFHPQWLTNPPTDSWARTPRCGTHPLTMRPWS 566

>CL007873.106

Length = 3267

30

Score = 49.6 bits (102), Expect(2) = 2e-18

Identities = 18/37 (48%), Positives = 26/37 (69%)

Frame = +3 / +1

Query: 42 SVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLR 152

35 SV+YVSFG+ +D+Q+ ELA GL + G F+W +R

Sbjct: 1321 SVVYVSFGTQAHVADEQLDELARGLVQSGHPFLWAVR 1431

Score = 62.5 bits (130), Expect(2) = 2e-18

Identities = 22/31 (70%), Positives = 25/31 (79%)

Frame = +3 / +1

40 Query: 237 DRGHIIVRDWAPQLEILAHPSVGGFMSHCGWN 329

D+G IVR W PQ +LAH SVGGF+SHCGWN

Sbjct: 1468 DQGRIVRGWVPQRGVLAHESVGGFVSHCGWN 1560

Score = 42.8 bits (87), Expect = 0.001

Identities = 17/32 (53%), Positives = 20/32 (62%)

45 Frame = -3 / -2

Query: 331 QFHPQ*LMNPPTDG*AKISSCGAQSLTIPLS 236

+FHPQ L NPPTD A+ CG LT+ P S
 Sbjct: 1562 EFHPQWLTNPPTDSWARTPRCGTHPLTMPWS 1467
 >CL037701.143
 Length = 1153

5
 Score = 40.9 bits (83), Expect(2) = 2e-18
 Identities = 16/40 (40%), Positives = 25/40 (62%)
 Frame = +3 / +2
 Query: 42 SVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLRRAD 161
 10 SV+Y++ G+ + + Q+ E+A GLER FIWV+ D
 Sbjct: 419 SVLYIALGTLAVIPEVQLKEVAKGLERAEVDFIWVVSPKD 538
 Score = 71.2 bits (149), Expect(2) = 2e-18
 Identities = 25/37 (67%), Positives = 30/37 (80%)
 Frame = +3 / +2

15 Query: 219 YEERVKDRGIIVRDWAPQLEILAHPSVGGFMSHCGWN 329
 +EERVK +GI+VRDW Q +IL H SV GF+SHCGWN
 Sbjct: 557 FEERVKKGKIVVRDWVDQSQILQHKSVRGFLSHCGWN 667
 Score = 32.2 bits (64), Expect(2) = 0.004
 Identities = 17/34 (50%), Positives = 18/34 (52%)

20 Frame = -3 / -2
 Query: 331 QFHPQ*LMNPPTDG*AKISSCGAQSLTIIPLSFT 230
 +FHPQ*L P T KI QSLT IP T
 Sbjct: 669 EFHPQ*LRKPRTLLCCKIWD*STQSLTTIPFPLT 568
 Score = 27.6 bits (54), Expect(2) = 0.004
 25 Identities = 12/37 (32%), Positives = 16/37 (42%)
 Frame = -3 / -2

Query: 151 LSTHINFSPHLSNPLANXXXXXXXXXXXXDPKETYITE 41
 L+TH+ + LSNPLA P Y T+
 Sbjct: 528 LTTHMKSTSALS NPLATSLSCTSGITARVPSAMYSTD 418
 30 >CL008587.125
 Length = 3850

Score = 50.1 bits (103), Expect(2) = 4e-18
 Identities = 19/45 (42%), Positives = 28/45 (62%)
 35 Frame = +3 / +1
 Query: 18 WXDQKQKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLR
 152

W D Q SV+++ FGS S+ +Q+ E+A GLER F+W +R
 Sbjct: 2473
 40 WLDAQPPRSVVFLCFGSASSVPAEQLKEIAVGLERSKHSFLWAVR 2607
 Score = 61.1 bits (127), Expect(2) = 4e-18
 Identities = 18/35 (51%), Positives = 27/35 (76%)
 Frame = +3 / +1
 Query: 225 ERVKDRGIIVRDWAPQLEILAHPSVGGFMSHCGWN 329
 45 +R RG+++ WAPQ+E+L HP+ G F++HCGWN
 Sbjct: 2698 DRTWGRGLVLPSWAPQVEVLRHPATGAFVTHCGWN 2802

Score = 30.4 bits (60), Expect = 5.5

Identities = 12/33 (36%), Positives = 18/33 (54%)

Frame = -3 / -3

Query: 340 TAYQFHPQ*LMNPPTDG*AKISSCGAQSLTIIP 242

5 ++ +FHPQ + N P G S+CGA + P

Sbjct: 2813 SSVEFHPQCVTNAPVAGCRSTSTCGAHDGSTSP 2715

>CL018723.139.47

Length = 4633

10 Score = 53.3 bits (110), Expect(2) = 1e-17

Identities = 21/44 (47%), Positives = 26/44 (58%)

Frame = +3 / +2

Query: 18 WXDQKQGKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVL

149

15 W D Q SV+Y FGST + Q+TELA GL G F+WV+

Sbjct: 3392

WLDGQPAGSVLYACFGSTCGMGASQLTELAAGLRASGRPFLWVI 3523

Score = 56.5 bits (117), Expect(2) = 1e-17

Identities = 18/28 (64%), Positives = 23/28 (81%)

20 Frame = +3 / +2

Query: 246 IIVRDWAPQLEILAHPSVGGFMSHCGWN 329

++ WAPQ +ILAH +VGGF+SHCGWN

Sbjct: 3581 VVAGRWAPQADILAHRAVGGFSLSHCGWN 3664

Score = 35.0 bits (70), Expect = 0.23

25 Identities = 13/26 (50%), Positives = 19/26 (73%)

Frame = -3 / -2

Query: 340 TAYQFHPQ*LMNPPTDG*AKISSCGA 263

++ +FHPQ L PPT A++S+CGA

Sbjct: 3675 SSIEFHPQWLRKPPTARCARMSACGA 3598

30 >CL009812.347

Length = 1258

Score = 51.5 bits (106), Expect(2) = 1e-17

Identities = 21/48 (43%), Positives = 28/48 (57%)

35 Frame = +3 / +1

Query: 18

WXDKQKGKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLRRAD 161

W D + SV+YVSFG+ S + + ELA GL+ G F WV+ AD

Sbjct: 343

40 WLDTKPDGSSVYVSFGTVSSFSPAETRELARGLDLSGMNFAWVISGAD 486

Score = 58.3 bits (121), Expect(2) = 1e-17

Identities = 19/31 (61%), Positives = 25/31 (80%)

Frame = +3 / +1

Query: 237 DRGIIVRDWAPQLEILAHPSVGGFMSHCGWN 329

45 DRG +R WAPQ+ +L HP+VG F++HCGWN

Sbjct: 544 DRGRTIRGWAPQVLVLNHPAVGVFVTHCGWN 636

Score = 35.0 bits (70), Expect = 0.23
 Identities = 14/35 (40%), Positives = 21/35 (60%)
 Frame = -3 / -3
 Query: 340 TAYQFHPQ*LMNPPTDG*AKISSCGAQSLTIIPLS 236
 5 ++ +FHPQ + N PT G + S+CGA + P S
 Sbjct: 647 SSVEFHPQCVTNTPTAGWFRTSTCGAHPRMVRPRS 543
 >CL009812.361
 Length = 5666

10 Score = 49.6 bits (102), Expect(2) = 1e-17
 Identities = 20/47 (42%), Positives = 28/47 (59%)
 Frame = +3 / +1
 Query: 18
 WXD KQ GKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLRRA 158
 15 W D + SV YVSFG+ S + ++ ELA GL+ G F+WV+ A
 Sbjct: 2179
 WLD AKPHGSVAYVSFGTLSSFSPAEMRELARGLDLSGMNFVWVINGA 2319
 Score = 59.7 bits (124), Expect(2) = 1e-17
 Identities = 20/31 (64%), Positives = 26/31 (83%)
 20 Frame = +3 / +1
 Query: 237 DRGIIVRDWAPQLEILAHPSVGGFMSHCGWN 329
 DRG+ +R APQ+ IL HP+VGGF++HCGWN
 Sbjct: 2389 DRGLTIRGXAPQMLILNHPAVGGFVTHCGWN 2481
 Score = 37.7 bits (76), Expect = 0.034
 25 Identities = 15/35 (42%), Positives = 22/35 (62%)
 Frame = -3 / -1
 Query: 340 TAYQFHPQ*LMNPPTDG*AKISSCGAQSLTIIPLS 236
 ++ +FHPQ + NPPT G ++S CGA + P S
 Sbjct: 2492 SSXEFHPQCVTNPPTAGWFRMSICGAXPRMVRPRS 2388
 30 >CL020036.38
 Length = 3141

Score = 48.7 bits (100), Expect(2) = 1e-17
 Identities = 20/49 (40%), Positives = 27/49 (54%)
 35 Frame = +3 / +3
 Query: 18
 WXD KQ GKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLRRADP 164
 W D Q SV+++ FGS Q+ E+ LER G +F+WVLR P
 Sbjct: 2304
 40 WLDGQPPASVFLCFGSMGWFEAAQVVEITAALERSGHRFLWVLRGPPP
 2450
 Score = 60.6 bits (126), Expect(2) = 1e-17
 Identities = 21/35 (60%), Positives = 27/35 (77%)
 Frame = +3 / +3
 45 Query: 225 ERVKDRGIIVRDWAPQLEILAHPSVGGFMSHCGWN 329
 ER K G++ WAPQ EILAH++GGF++H GWN

Sbjct: 2538 ERTKGXGMVWPTWAPQKEILAHPAIGGFVTHGGWN 2642

Score = 31.8 bits (63), Expect = 2.1

Identities = 14/35 (40%), Positives = 18/35 (51%)

Frame = -3 / -3

5 Query: 331 QFHPQ*LMNPPTDG*AKISSCGAQSLTIPLSFTL 227

+FHP + PP G A+IS CGA +P L

Sbjct: 2644 EFHPPCVTKPPMAGWARISFCGAHVGH TMPXPLVL 2540

>CL037972.43

Length = 1471

10

Score = 56.5 bits (117), Expect(2) = 1e-17

Identities = 22/46 (47%), Positives = 30/46 (64%)

Frame = +3 / -3

Query: 18

15 WXDKQGKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLR 155

W D Q SV+YV+ GS + L +Q+ ELA GLE G +F+W LR+

Sbjct: 1049

WLDAQPAKSVVYVALGSEVPLRLEQVHELALGLELAGTRFLWALRK 912

Score = 52.8 bits (109), Expect(2) = 1e-17

20 Identities = 18/37 (48%), Positives = 23/37 (61%)

Frame = +3 / -3

Query: 219 YEERVKDRGIIVRDWAPQLEILAHPSVGGFMSHCGWN 329

Y ER G + W PQ+ ILAH +VG F++HCG N

Sbjct: 869 YRERTNGHGHVAMGWVPQIAILAHAAVGAFLTHCGRN 759

25 Score = 35.9 bits (72), Expect = 0.12

Identities = 16/45 (35%), Positives = 25/45 (55%)

Frame = -2 / +3

Query: 149 KHPYKLLPASFPVSQLCDLIICQ*YCRPKRNIYH*IFPLFVXPI 15

+ P K P QP SQL L+ Q + P+R+++H + L V P+

30 Sbjct: 918

QRPQKPCPGELQPESQLVHLLQSQRHLAPQRHVHHRLRRLRVQPL 1052

>CL034535.85

Length = 6166

35 Score = 55.6 bits (115), Expect(2) = 2e-17

Identities = 21/45 (46%), Positives = 31/45 (68%)

Frame = +3 / +3

Query: 18 WXDKQGKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLR

152

40 W D Q + SV+++SFGS +L Q+ E+A GLE G +F+WV+R

Sbjct: 2157

WLDAQPRRSVVFLSFGSQGALPAAQLKEIARGLESSGHRFLWVVR 2291

Score = 53.3 bits (110), Expect(2) = 2e-17

Identities = 15/29 (51%), Positives = 24/29 (82%)

45 Frame = +3 / +1

Query: 243 GIIVRDWAPQLEILAHPSVGGFMSHCGWN 329

G++ ++WAPQ E++ H +VG F++HCGWN
 Sbjct: 2380 GMVAKNWAPQAEVVQHEAVGVFVTHCGWN 2466
 Score = 35.9 bits (72), Expect(2) = 0.007
 Identities = 14/33 (42%), Positives = 20/33 (60%)
 5 Frame = -3 / -3
 Query: 340 TAYQFHPQ*LMNPPTDG*AKISSCGAQLTIIP 242
 ++ +FHPQ + N PT S+CGAQ L +P
 Sbjct: 2477 SSVEFHPQCVTNTPTASCCTTSACGAQFLATMP 2379
 Score = 23.1 bits (44), Expect(2) = 0.007
 10 Identities = 13/37 (35%), Positives = 15/37 (40%)
 Frame = -3 / -1
 Query: 154 LLSTHINFSPHLSNPLANXXXXXXXXXXXXDPKETIIT 44
 LL+TH P LS+P A PKE T
 Sbjct: 2293 LLTTHRKRWPPELSSPRAISFSCAAGSAPWLPKERNTT 2183
 15 >CL030368.81.82
 Length = 6862

 Score = 51.5 bits (106), Expect(2) = 2e-17
 Identities = 20/55 (36%), Positives = 33/55 (59%)
 20 Frame = +3 / -3
 Query: 9
 LSNWXDKQGKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLRRADP
 NDI 173
 ++++ D SV+YVSFGS S+ ++ ELA LE G F+W ++ D ++I
 25 Sbjct: 6413
 ITSFLDSHPPSSVLYVSFGSQFSIQAEHMAELAAALEATGRPFVWAVKPPDG
 HNI 6249
 Score = 57.0 bits (118), Expect(2) = 2e-17
 Identities = 18/30 (60%), Positives = 24/30 (80%)
 30 Frame = +3 / -3
 Query: 240 RGIIVRDWAPQLEILAHPSVGGFMSHCGWN 329
 +G+++ WAPQ+ ILAH S G F+SHCGWN
 Sbjct: 6185 KGLLLHGWAPQVGILAHHSTGAFLSHCGWN 6096
 Score = 31.3 bits (62), Expect = 2.9
 35 Identities = 12/23 (52%), Positives = 16/23 (69%)
 Frame = -3 / +1
 Query: 331 QFHPQ*LMNPPTDG*AKISSCGA 263
 +FHPQ L N P + A+I +CGA
 Sbjct: 6094 EFHPQWLRNAPVE*CARIPTCGA 6162
 40 >CL011484.95
 Length = 3582

 Score = 54.2 bits (112), Expect(2) = 2e-17
 Identities = 19/49 (38%), Positives = 31/49 (62%)
 45 Frame = +3 / -3

Query: 9
LSNWDXDKQGKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLRR 155
+ W D Q SV+YV+ GS ++ D + ELA+GL+ G +F+W +R+
Sbjct: 3388
5 IMQWLDAQPAKSVVYVALGSEAPMSADLLRELAHGLDLAGTRFLWAMRK
3242
Score = 54.2 bits (112), Expect(2) = 2e-17
Identities = 19/40 (47%), Positives = 27/40 (67%)
Frame = +3 / -3
10 Query: 207 LLADYEERVKDRGIIVRDWAPQLEILAHPSVGGFMSHCGW 326
L A + R +RG++ WAPQ+ ILAH +V F++HCGW
Sbjct: 3214 LPAGFLGRTGERGLVTTRWAPQVSILAHAAVCAFLTHCGW 3095
>CL008051.83
Length = 4853
15
Score = 55.1 bits (114), Expect(2) = 3e-17
Identities = 23/45 (51%), Positives = 29/45 (64%)
Frame = +3 / -2
Query: 18 WDXDKQGKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLRR
20 152
W D+Q + SVIYV+ GS LT + ELA GLE G +F+W LR
Sbjct: 577
WLDEQPERSVIYVALGSEAPLTVGHVRELALGLELAGVRFLWALR 443
Score = 52.8 bits (109), Expect(2) = 3e-17
25 Identities = 16/29 (55%), Positives = 22/29 (75%)
Frame = +3 / -2
Query: 243 GIIVRDWAPQLEILAHPSVGGFMSHCGWN 329
G++ W PQL ILAH + GGF++HCGW+
Sbjct: 340 GLVCARWVPQLRILAHRAATGGFLTHCGWS 254
30 >CL024242.128
Length = 7186
Score = 58.3 bits (121), Expect(2) = 6e-17
Identities = 23/45 (51%), Positives = 30/45 (66%)
35 Frame = +3 / -1
Query: 18 WDXDKQGKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLRR
152
W D Q SV+YVSFGS SL ++ E+A GLE G+ F+WV+R
Sbjct: 4618
40 WLDTQATGSVLYVSFGSLASLDSNEFLEVAWGLESSGQPFLWVVR 4484
Score = 48.7 bits (100), Expect(2) = 6e-17
Identities = 21/40 (52%), Positives = 25/40 (62%)
Frame = +3 / -1
Query: 210 LADYEERVKDRGIIVRDWAPQLEILAHPSVGGFMSHCGWN 329
45 L D ER + V WAPQ E+LAH +VGGF +H GWN

Sbjct: 4450 LPDGFERAVEGRGKVIKWAPQQEVLAAHHA VGGFWTHNGWN
4331
Score = 56.0 bits (116), Expect(2) = 9e-15
Identities = 22/43 (51%), Positives = 29/43 (67%)
5 Frame = +3 / -1
Query: 24 DKQGKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLR 152
D Q SV+YVSFGS S+ D+ E+A GLE+ G F+WV+R
Sbjct: 1324 DTQATGSVLVVSFGSLASMDSDDEFMEVAFGLEKSGHPFLWVVR
1196
10 Score = 43.7 bits (89), Expect(2) = 9e-15
Identities = 15/23 (65%), Positives = 18/23 (78%)
Frame = +3 / -1
Query: 261 WAPQLEILAHPSVGGFMSHCGWN 329
WAPQ E+LAH +VG F +H GWN
15 Sbjct: 1111 WAPQQEVLAAHCAVGWFWTHGGWN 1043
Score = 34.1 bits (68), Expect(2) = 2e-04
Identities = 13/31 (41%), Positives = 19/31 (60%)
Frame = -3 / +3
Query: 340 TAYQFHPQ*LMNPPTDG*AKISSCGAQSLTI 248
++ +FHP +NPPT A S CGA +T+
20 Sbjct: 4320 SSVEFHPLCVQNPPTAWCASTSCCGAHLITL 4412
Score = 30.4 bits (60), Expect(2) = 2e-04
Identities = 15/47 (31%), Positives = 20/47 (41%)
Frame = -3 / +3
25 Query: 148
STHINFSPHLSNPLANXXXXXXXXXXXXDPKETYITESFPCLSXQLLR 8
+TH P LSNP A PK TY T+ C+S ++
Sbjct: 4488
TTHRKGWPLLSNPHATSKNSLESNDAKLPKLTYNTDPVACVSSHSMQ 4628
30 Score = 30.4 bits (60), Expect(2) = 0.007
Identities = 12/28 (42%), Positives = 16/28 (56%)
Frame = -3 / +3
Query: 331 QFHPQ*LMNPPTDG*AKISSCGAQSLTI 248
+FHP +N PT A S CGA +T+
35 Sbjct: 1041 EFHPPCVQNQPTAQCASTSCCGAHLITL 1124
Score = 28.6 bits (56), Expect(2) = 0.007
Identities = 14/42 (33%), Positives = 17/42 (40%)
Frame = -3 / +3
Query: 148 STHINFSPHLSNPLANXXXXXXXXXXXXDPKETYITESFPCLS 23
+TH P SNP A PK TY T+ C+S
40 Sbjct: 1200 TTHRKGWPLFSNP NATSMNSSESMDAKLPKLTYNTDPVACVS
1325
>CL034968.144
Length = 5274
45 Score = 38.6 bits (78), Expect(3) = 7e-17

Identities = 17/32 (53%), Positives = 21/32 (65%)

Frame = +3 / +3

Query: 18 WXDKQGKDSVIYVSFGSTISLTDDQITELANG 113

W D Q SV+YVSFGS +L+ +Q ELA G

5 Sbjet: 1458 WLDHQAGSVVYVSFGSGGALSVEQTAELAAG 1553

Score = 24.9 bits (48), Expect(3) = 7e-17

Identities = 8/14 (57%), Positives = 10/14 (71%)

Frame = +3 / +1

Query: 111 GLERCGEKFIWVLR 152

10 GLE G F+WV+R

Sbjet: 1552 GLEMSGHNFLWVVR 1593

Score = 62.9 bits (131), Expect(3) = 7e-17

Identities = 20/37 (54%), Positives = 26/37 (70%)

Frame = +3 / +1

15 Query: 219 YEERVKDRGIIVRDWAPQLEILAHPSVGGFMSHCGWN 329

+ ER RG+ V WAPQ+ +LAHP+ F+SHCGWN

Sbjet: 1669 FVERTNGRGLAVASWAPQVRVLAHPATAAFVSHCGWN 1779

Score = 29.9 bits (59), Expect = 7.6

Identities = 14/35 (40%), Positives = 16/35 (45%)

20 Frame = -3 / -2

Query: 331 QFHPQ*LMNPPTDG*AKISSCGAQSLTIPLSFTL 227

+FHPQ N G A +CGA T P F L

Sbjet: 1781 EFHPQCDTNAAVAGCASTRTCGAHDATARPRPFVL 1677

>CL021644.104

25 Length = 1672

Score = 54.2 bits (112), Expect(2) = 9e-17

Identities = 21/48 (43%), Positives = 32/48 (65%)

Frame = +3 / +3

30 Query: 18

WXDKQGKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLRRAD 161

W D++ SV+YVSFGS ++ Q+ ELA+GL G F+WV+R ++

Sbjet: 180

WLDERAASSVVYVSFGSLATPSAVQMAELAHGLRDSGRFFLWVVRSSSE 323

35 Score = 52.4 bits (108), Expect(2) = 9e-17

Identities = 18/36 (50%), Positives = 25/36 (69%)

Frame = +3 / +3

Query: 222 EERVKDRGIIVRDWAPQLEILAHPSVGGFMSHCGWN 329

E K+ ++ W PQLE+LAH +VG F++HCGWN

40 Sbjet: 354 ETAAKNTTGLIVPWCPQLEVLAHGAVGCFVTHCGWN 461

>CL014976.74

Length = 952

Score = 53.3 bits (110), Expect(2) = 9e-17

45 Identities = 21/45 (46%), Positives = 29/45 (63%)

Frame = +3 / -1

Score = 50.1 bits (103), Expect(2) = 7e-15
Identities = 15/23 (65%), Positives = 19/23 (82%)
Frame = +3 / +2

Query: 261 WAPQLEILAHPSVGGFMSHCGWN 329

Sbjct: 1322 WAPQQSVLSHPSIACFVSHCGWN 1390

Score = 51.9 bits (107), Expect(2) = 2e-16
Identities = 24/52 (46%), Positives = 29/52 (55%)

10 Query: 18

Sbjct: 4565

Identities = 17/27 (62%), Positives = 21/27 (76%)
Frame = +3 / +2

Score = 20.8 bits (39), Expect(2) = 5.1
Identities = 10/27 (37%), Positives = 13/27 (48%)

Query: 331 QFHPQ*LMNPPTDG*AKISSCGAQSLT 251

Sbjct: 4851 EFHPQCDMKQAIEGCDSTRCWGAQLIT 4771

30 Identities = 15/45 (33%), Positives = 21/45 (46%)
Frame = -3 / -2

35 Sbjct: 4695

Length = 4032

Sbjct: 3240
 WLDAQPERSVVFLCFGSRGALSPEQVSEMATGLERSEQRFLWALR 3374
 Score = 48.3 bits (99), Expect(2) = 2e-16
 Identities = 13/28 (46%), Positives = 19/28 (67%)
 5 Frame = +3 / +3
 Query: 246 IIVRDWAPQLEILAHPSVGGFMSHCGWN 329
 ++ W PQ+ +L H S G F++HCGWN
 Sbjct: 3456 VVTASWVPQVAVLQHASTGAFVTHCGWN 3539
 Score = 30.4 bits (60), Expect = 5.5
 10 Identities = 10/27 (37%), Positives = 16/27 (59%)
 Frame = -3 / -3
 Query: 340 TAYQFHPQ*LMNPPTDG*AKISSCGAQ 260
 ++ +FHPQ + N P D ++CG Q
 Sbjct: 3550 SSVEFHPQCVTNAPVDACCSTATCGTQ 3470
 15 >CL005175.139.58
 Length = 3753

 Score = 57.0 bits (118), Expect(2) = 2e-16
 Identities = 20/45 (44%), Positives = 33/45 (72%)
 20 Frame = +3 / -2
 Query: 18 WXDQKQGKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLR
 152
 W D Q + SV+++ FGS +L+ +Q++E+A GLER ++F+W LR
 Sbjct: 3494
 25 WLDAQPERSVVFLCFGSRGALSPEQVSEMATGLERSEQRFLWALR 3360
 Score = 48.3 bits (99), Expect(2) = 2e-16
 Identities = 13/28 (46%), Positives = 19/28 (67%)
 Frame = +3 / -2
 Query: 246 IIVRDWAPQLEILAHPSVGGFMSHCGWN 329
 ++ W PQ+ +L H S G F++HCGWN
 30 Sbjct: 3278 VVTASWVPQVAVLQHASTGAFVTHCGWN 3195
 Score = 30.4 bits (60), Expect = 5.5
 Identities = 10/27 (37%), Positives = 16/27 (59%)
 Frame = -3 / +1
 35 Query: 340 TAYQFHPQ*LMNPPTDG*AKISSCGAQ 260
 ++ +FHPQ + N P D ++CG Q
 Sbjct: 3184 SSVEFHPQCVTNAPVDACCSTATCGTQ 3264
 >CL037983.71
 Length = 1692
 40
 Score = 43.7 bits (89), Expect(2) = 2e-16
 Identities = 18/38 (47%), Positives = 24/38 (62%)
 Frame = +3 / -2
 Query: 30 QGKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIW 143
 45 Q SVIYV+ GS +T + + ELA GLE G +F+W
 Sbjct: 1691 QPNGSVIYVALGSEAPITTNHVRELALGLELSGVRFLW 1578

Score = 61.5 bits (128), Expect(2) = 2e-16
Identities = 19/40 (47%), Positives = 29/40 (72%)
Frame = +3 / -3

5 Query: 207 LLADYEERVKDRGIIVRDWAPQLEILAHPSVGGFMSHCGW 326
L + +E RV RGI+ +W PQ+ +LAH ++G F++HCGW
Sbjct: 1531 LPSGFESRVATRGIVCTEWVPQVRVLAHGAIGAFLTHCGW 1412
>CL008073.540
Length = 9953

10 Score = 28.1 bits (55), Expect(3) = 2e-16
Identities = 9/18 (50%), Positives = 14/18 (77%)
Frame = +3 / -1

Query: 18 WDXKQGKDSVIYVSFGST 71
W D+Q + SV+++ FGST

15 Sbjct: 6995 WLDRQPERSVVFLCFGST 6942
Score = 35.4 bits (71), Expect(3) = 2e-16
Identities = 11/22 (50%), Positives = 19/22 (86%)
Frame = +3 / -1

Query: 87 DQITELANGLERCGEKFIWVLR 152
20 +Q+ E+A GLE+ G++F+WV+R
Sbjct: 6920 EQLREIAVGLEKSGQRFLWVVR 6855
Score = 61.1 bits (127), Expect(3) = 2e-16
Identities = 20/41 (48%), Positives = 30/41 (72%)
Frame = +3 / -1

25 Query: 207 LLADYEERVKDRGIIVRDWAPQLEILAHPSVGGFMSHCGWN 329
L A + ER RG++V+ WAPQ+++L H + G F++HCGWN
Sbjct: 6782 LPAGFLERTTGRGVVVKLWAPQVDVLYHRATGAFVTHCGWN
6660

Score = 32.7 bits (65), Expect = 1.1
30 Identities = 14/30 (46%), Positives = 17/30 (56%)
Frame = -3 / +1

Query: 331 QFHPQ*LMNPPTDG*AKISSCGAQSLTIIP 242
+FHPQ + N P S+CGA SLT P
Sbjct: 6658 EFHPQCVTNAPVARW*STSTCGAHS�TTTP 6747
35 >CL012878.80
Length = 5271

Score = 48.7 bits (100), Expect(2) = 4e-16
Identities = 19/52 (36%), Positives = 32/52 (61%)
40 Frame = +3 / +2

Query: 18
WDXKQGKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLRRADPNDI
173
W + + +V YVSFGS + + Q+ E+A GL G+ F+WV+R + + + I

- Query: 243 GIIVRDWAPQLEILAHPSVGGFMSHCGWN 329
 G +V +W Q+++L HP+VG F++HCGWN
 Sbjct: 4224 GGVVVEWCDQVKVLGHPAVGCFVTHCGWN 4310
 >CL024122.163
- 5 Length = 600
- Score = 83.1 bits (175), Expect = 8e-16
 Identities = 27/37 (72%), Positives = 34/37 (90%)
 Frame = +3 / +2
- 10 Query: 219 YEERVKDRGIIVRDWAPQLEILAHPSVGGFMSHCGWN 329
 YEERVKDRG++VR WAPQ+ IL+HP+ GGF++HCGWN
 Sbjct: 62 YEERVKDRGVLRGWAPQVSILSHPATGGFLTHCGWN 172
 Score = 39.1 bits (79), Expect = 0.013
 Identities = 16/33 (48%), Positives = 20/33 (60%)
- 15 Frame = -3 / -1
 Query: 328 FHPQ*LMNPPTDG*AKISSCGAQSLTIPLSFT 230
 FHPQ + NPP G ++ +CGA T PLS T
 Sbjct: 171 FHPQWVRNPPVAGCERMLTCGAXPRTRTPLSLT 73
 >CL005694.182
- 20 Length = 12971
- Score = 54.2 bits (112), Expect(2) = 1e-15
 Identities = 17/46 (36%), Positives = 31/46 (66%)
 Frame = +3 / +2
- 25 Query: 18
 WXD KQGKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLRR 155
 W D + SV+Y+SFGS ++ + Q+ E+ +G++ C F+WV+R+
 Sbjct: 7619
 WLDTHSERSVYISFGSILTYSKRQVDEILHGMQECEWPFLWVVRK 7756
- 30 Score = 48.3 bits (99), Expect(2) = 1e-15
 Identities = 15/27 (55%), Positives = 22/27 (80%)
 Frame = +3 / +2
 Query: 249 IVRDWAPQLEILAHPSVGGFMSHCGWN 329
 +V +W QL++L+HPSVG F++ CGWN
- 35 Sbjct: 7817 MVIEWCDQLDVLSHPSVGCFTQCGWN 7897
 >CL011220.184
 Length = 2561
- Score = 56.0 bits (116), Expect(2) = 1e-15
 Identities = 20/46 (43%), Positives = 31/46 (66%)
 Frame = +3 / +3
 Query: 18
 WXD KQGKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLRR 155
 W D + SV+YV+FGS +T++Q+ E A GL G +F+W++RR
- 45 Sbjct: 861
 WLDGKEAGSVVYVNFGSITVMTNEQLVEFAWGLANSGREFLWIVRR 998

0967706270

Sbjct: 4185 VLASWCPQELVLSHPSVGLFLTHCGWN 4105
Score = 37.3 bits (75), Expect = 0.047
Identities = 14/27 (51%), Positives = 19/27 (69%)
Frame = -3 / +2

5 Query: 340 TAYQFHPQ*LMNPPTDG*AKISSCGAQ 260
++ +FHPQ + N PTDG + SSCG Q
Sbjct: 4094 SSVEFHPQCVRNRPTDGCERTSSCGHQ 4174
>CL023620.124.51
Length = 3683

10 Score = 53.3 bits (110), Expect(2) = 2e-15
Identities = 20/45 (44%), Positives = 31/45 (68%)
Frame = +3 / -1
Query: 18 WXDQKQKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLR
15 152
W D Q ++SV+YVS GS +S++ Q+ E+A GL +F+W+LR
Sbjct: 1451 WLDCQPENSVLYVSLGSFVSVSSQLDEIALGLATSEVRFLWILR
1317
Score = 48.7 bits (100), Expect(2) = 2e-15
20 Identities = 15/27 (55%), Positives = 21/27 (77%)
Frame = +3 / -1
Query: 249 IVRDWAPQLEILAHPSVGGFMSHCGWN 329
++ W QL++L HPSVGGF++HCG N
Sbjct: 1268 MILPWCDQLKVLCHPSVGGFLTHCGMN 1188
25 >CL039431.43
Length = 3553

Score = 46.0 bits (94), Expect(2) = 3e-15
Identities = 20/45 (44%), Positives = 26/45 (57%)
30 Frame = +3 / -3
Query: 18 WXDQKQKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLR
152
W D Q SV+ V FGS L ++ E+A LER +F+WVLR
Sbjct: 1541
35 WLDAQPPASVLLVCFGSKGLLPPPKVREIAAALERSEHRFLWVLR 1407
Score = 55.6 bits (115), Expect(2) = 3e-15
Identities = 19/35 (54%), Positives = 27/35 (76%)
Frame = +3 / -3
Query: 225 ERVKDRGIIVRDWAPQLEILAHPSVGGFMSHCGWN 329
40 ++ K RG++ APQ +ILAH +VGGF++HCGWN
Sbjct: 1325 DKTKGRGLVWPTRAPQKDILAHAAVGGFVTHCGWN 1221
Score = 37.3 bits (75), Expect = 0.047
Identities = 16/35 (45%), Positives = 21/35 (59%)
Frame = -3 / +1
45 Query: 331 QFHPQ*LMNPPTDG*AKISSCGAQLTIPLSFTL 227
+FHPQ + NPPT A++S CGA+ PL L

Sbjct: 1219 EFHPQCVTNPPTAAWARMSCGARGHTSPLPLVL 1323
>CL021720.29
Length = 3000

5 Score = 47.8 bits (98), Expect(2) = 3e-15
Identities = 18/45 (40%), Positives = 29/45 (64%)
Frame = +3 / +2
Query: 18 WXDQKQKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLR
152

10 W + Q SV++VSFG+ +S+ D++ E+A GL F+WV+R
Sbjct: 1235
WLNTQLPGSVLFVSFGTLVSI DADELLEVAWGLAASNRPFLLWVVR 1369
Score = 53.8 bits (111), Expect(2) = 3e-15
Identities = 15/23 (65%), Positives = 21/23 (91%)

15 Frame = +3 / +2
Query: 261 WAPQLEILAHPSVGGFMSHCGWN 329
WAPQ E+L+HP++G F++HCGWN
Sbjct: 1454 WAPQEEVLSPHAI GAFLTHCGWN 1522
Score = 32.2 bits (64), Expect = 1.5
20 Identities = 12/31 (38%), Positives = 19/31 (60%)
Frame = -3 / -1
Query: 340 TAYQFHPQ*LMNPPTDG*AKISSCGAQS LTI 248
++ +FHPQ + N P G + SSCGA ++

Sbjct: 1533 SSVEFHPQCVKNAPIAGWLRTSSCGAHL MIL 1441
25 >CL009267.89
Length = 5165

Score = 50.5 bits (104), Expect(2) = 4e-15
Identities = 22/46 (47%), Positives = 27/46 (57%)
30 Frame = +3 / -3
Query: 15
NWXDQKQKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLR 152
+W D Q SV+YV+FGS Q ELA GLE G F+WV+R

Sbjct: 3549
35 SWLDAQPVRSVVYVAFGSFTVFDRRQFQELALGLELTGRPFLWVVR 3412
Score = 50.5 bits (104), Expect(2) = 4e-15
Identities = 16/23 (69%), Positives = 19/23 (82%)
Frame = +3 / -3

Query: 261 WAPQLEILAHPSVGGFMSHCGWN 329
WAPQ +LAHP+V F+SHCGWN
40 Sbjct: 3309 WAPQQRVLAHPAVACFVSHCGWN 3241
>CL006514.229.168
Length = 11174

45 Score = 46.0 bits (94), Expect(2) = 5e-15
Identities = 17/45 (37%), Positives = 26/45 (57%)

Frame = +3 / -3

Query: 18 WXDKQGKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLR
152

W D Q SV+Y+SFG+ + + + ELA LE G F+W ++

5 Sbjct: 4821

WMDTQPPGSVLYISFGTNSMIRPEHMLELAAALESSGRCFLWKIK 4687

Score = 54.7 bits (113), Expect(2) = 5e-15

Identities = 19/30 (63%), Positives = 24/30 (79%)

Frame = +3 / -3

10 Query: 240 RGIIVRDWAPQLEILAHPSVGGFMSHCGWN 329

RG++VR APQ+ ILAHPS F+SHCGW+

Sbjct: 4581 RGLLVRR*APQVRILAH PSTAAFLSHCGWS 4492

Score = 35.4 bits (71), Expect = 0.17

Identities = 15/31 (48%), Positives = 19/31 (60%)

15 Frame = -3 / +2

Query: 331 QFHPQ*LMNPPTDG*AKISSCGAQSLTIHPL 239

+ HPQ L N +G A+I +CGA LT PL

Sbjct: 4490 ELHPQWLKNAAVEGCARILTCGAHRLTSRPL 4582

>CL024324.140

20 Length = 9439

Score = 51.5 bits (106), Expect(2) = 5e-15

Identities = 19/47 (40%), Positives = 30/47 (63%)

Frame = +3 / -3

25 Query: 15

NWXDKQGKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLR 155

+W D + SV+YVSFG+ +S++ Q E+ GLE G ++WV R+

Sbjct: 7670

DWLDTKPARSVVYVSFGTLLSMSKRQEEEMRRGLEATGRPYLWVARQ

30 7530

Score = 49.2 bits (101), Expect(2) = 5e-15

Identities = 14/27 (51%), Positives = 23/27 (84%)

Frame = +3 / -3

Query: 249 IVRDWAPQLEILAHPSVGGFMSHCGWN 329

35 +V +W Q+++L+HP+VG F++HCGWN

Sbjct: 7439 MVVEWCDQMKVLSHPAVGCFVTHCGWN 7359

>CL035336.97

Length = 6982

40 Score = 50.1 bits (103), Expect(2) = 5e-15

Identities = 20/45 (44%), Positives = 27/45 (59%)

Frame = +3 / -3

Query: 18 WXDKQGKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLR
152

45 W D Q + SV+YVSFGS +S+ Q+ E+A L +F WV R

Sbjct: 2261
 WLDAQPERSVLYVSFGSVVSMWPSQLEEVAVALRDSAVRFFWVAR 2127
 Score = 50.5 bits (104), Expect(2) = 5e-15
 Identities = 17/27 (62%), Positives = 20/27 (73%)
 5 Frame = +3 / -3
 Query: 249 IVRDWAPQLEILAHPSVGGFMSHCGWN 329
 +V W QL +L H SVGGF+SHCGWN
 Sbjct: 2078 LVVPWCDQLGVLCCHRSVGGFSLSHCGWN 1998
 >CL038292.23
 10 Length = 2299

 Score = 35.4 bits (71), Expect(2) = 5e-15
 Identities = 17/36 (47%), Positives = 17/36 (47%)
 Frame = +3 / -1
 15 Query: 54 VSFGSTISLTDDQITELANGLERCGEKFIWVLRRAD 161
 VSFGS L Q ELA GLE F WV D
 Sbjct: 2299 VSFGSIARLXSPQAAELAAGLEASHRPFVWVTXDTD 2192
 Score = 65.2 bits (136), Expect(2) = 5e-15
 Identities = 21/33 (63%), Positives = 29/33 (87%)
 20 Frame = +3 / -1
 Query: 231 VKDRGIIVRDWAPQLEILAHPSVGGFMSHCGWN 329
 V DRG+++R APQ+ IL+HP+VGGF++HCGWN
 Sbjct: 2152 VADRGLVIRGLAPQVTILSHPAVGGFLTHCGWN 2054
 Score = 29.9 bits (59), Expect = 7.6
 25 Identities = 13/34 (38%), Positives = 18/34 (52%)
 Frame = -3 / +3
 Query: 331 QFHPQ*LMNPPTDG*AKISSCGAQSLTIPLSFT 230
 +F PQ + PPT G ++ +CGA P S T
 Sbjct: 2052 EFQPQWVRKPPTAGCDRMVTCGANPRMTSPRSAT 2153
 30 >CL008073.542
 Length = 4901

 Score = 25.8 bits (50), Expect(3) = 5e-15
 Identities = 8/18 (44%), Positives = 13/18 (71%)
 35 Frame = +3 / +1
 Query: 18 WXDQKQKDSVIYVSFGST 71
 W D+Q +V+++ FGST
 Sbjct: 2623 WLDROPDRTVVFLCFGST 2676
 Score = 34.5 bits (69), Expect(3) = 5e-15
 40 Identities = 11/22 (50%), Positives = 18/22 (81%)
 Frame = +3 / +1
 Query: 87 DQITELANGLERCGEKFIWVLR 152
 +Q+ E+A GLE+ G +F+WV+R
 Sbjct: 2698 EQLREIAVGLEKSGHRFLWVVR 2763
 45 Score = 59.7 bits (124), Expect(3) = 5e-15
 Identities = 19/41 (46%), Positives = 29/41 (70%)

Sbjct: 572
 WLDAQPRRSVVFVAFGSLVDIGHDEVVEIAEGLASTGRPFLWVLARRQPRA
 LF 730
 Score = 36.8 bits (74), Expect(2) = 9e-15
 5 Identities = 11/23 (47%), Positives = 15/23 (64%)
 Frame = +3 / +2
 Query: 261 WAPQLEILAHPSVGGFMSHCGWN 329
 W Q +L +VG F++HCGWN
 Sbjct: 785 WXXQRRVLVQAAVGCFVTHCGWN 853
 10 >CL039340.19
 Length = 2013

 Score = 49.2 bits (101), Expect(2) = 9e-15
 Identities = 21/46 (45%), Positives = 26/46 (55%)
 15 Frame = +3 / +3
 Query: 15
 NWXDKQGKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLR 152
 +W D Q SV+YV+FGS Q EL GLE G F+WV+R
 Sbjct: 105
 20 SWLDVQPARSVVYVAFGSFTVFXXRRQFQELXLGLELTGRPFLWVVR 242
 Score = 50.5 bits (104), Expect(2) = 9e-15
 Identities = 16/23 (69%), Positives = 19/23 (82%)
 Frame = +3 / +3
 Query: 261 WAPQLEILAHPSVGGFMSHCGWN 329
 25 WAPQ +LAHP+V F+SHCGWN
 Sbjct: 342 WAPQQRVLAHPAVACFVSHCGWN 410
 >CL026437.83
 Length = 2002

 30 Score = 44.1 bits (90), Expect(2) = 9e-15
 Identities = 19/45 (42%), Positives = 23/45 (50%)
 Frame = +3 / +2
 Query: 18 WXDKQGKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLR
 152
 35 W D SV+YVS GS + D E+A GL G F+WV R
 Sbjct: 773
 WLDAHPPRSVLYVSLGSVACIDHDMFDEMAWGLAASGVPFLWVNR 907
 Score = 55.6 bits (115), Expect(2) = 9e-15
 Identities = 16/23 (69%), Positives = 21/23 (90%)
 40 Frame = +3 / +2
 Query: 261 WAPQLEILAHPSVGGFMSHCGWN 329
 WAPQ ++LAHP++GGF +HCGWN
 Sbjct: 980 WAPQRDVLAHPAIGGFVTHCGWN 1048
 Score = 36.3 bits (73), Expect = 0.089
 45 Identities = 15/37 (40%), Positives = 22/37 (58%)
 Frame = -3 / -2

Query: 340 TAYQFHPQ*LMNPPTDG*AKISSCGAQSLTIPLSFT 230
 ++ +FHPQ + NPP G A+ S CGA + L+ T
 Sbjct: 1059 SSVEFHPQCVQNPPMAGCARTSLCGAHGTILPLLTST 949
 >CL005944.12

5 Length = 1030

Score = 54.2 bits (112), Expect(2) = 9e-15
 Identities = 22/46 (47%), Positives = 30/46 (64%)
 Frame = +3 / -2

10 Query: 18

WXDKQGKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLR 155
 WDKQ SV+YV+FGS L+ Q+ E+ + LE G F+WV+RR

Sbjct: 777

WLDKQRXASVVYVAFGSLAVLSRQLEEIRHCLEVTGRPFLWVVR 640

15 Score = 45.5 bits (93), Expect(2) = 9e-15
 Identities = 15/29 (51%), Positives = 21/29 (71%)
 Frame = +3 / -2

Query: 243 GIIVRDWAPQLEILAHPSVGGFMSHCGWN 329
 G +V +W Q +LAH +VG F++HCGWN

20 Sbjct: 582 GGMVVEWCSQARVLAHRAVGCFTVTHCGWN 496
 >CL027541.163.148
 Length = 9817

Score = 56.0 bits (116), Expect(2) = 2e-14
 Identities = 21/45 (46%), Positives = 28/45 (61%)
 Frame = +3 / -3

25 Query: 18 WXDKQGKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLR
 152

W D Q SV+YV+FGS ++ + E A GL RCG F+WV+R

30 Sbjct: 9503

WLDAQPGSVVYVNFGSITVMSPAHLAEFAWGLARCGRPFLWVIR 9369

Score = 42.3 bits (86), Expect(2) = 2e-14
 Identities = 13/27 (48%), Positives = 18/27 (66%)
 Frame = +3 / -3

35 Query: 249 IVRDWAPQLEILAHPSVGGFMSHCGWN 329
 I W PQ ++L HP+ G F++H GWN

Sbjct: 9299 IFLSWCPQEQVLEHPATGLFLTHSGWN 9219
 >CL003181.168

Length = 1451

40

Score = 51.9 bits (107), Expect(2) = 2e-14
 Identities = 19/45 (42%), Positives = 28/45 (62%)
 Frame = +3 / +3

45 Query: 18 WXDKQGKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLR
 152

W D Q SV++V+FGS ++ D+ E+A GL G F+WV+R

Sbjct: 132
WLDAQPPRSVVFVAFGSVVVIGRDETAEVAEGLASTGHPFLWVVR 266
Score = 46.4 bits (95), Expect(2) = 2e-14
Identities = 14/23 (60%), Positives = 18/23 (77%)

5 Frame = +3 / +3
Query: 261 WAPQLEILAHPSVGGFMSHCGWN 329
W Q +LAHP+VG F++HCGWN
Sbjct: 336 WCEQRRVLAHPAVGCFVTHCGWN 404
>CL014046.2

10 Length = 790

Score = 77.6 bits (163), Expect = 3e-14
Identities = 25/37 (67%), Positives = 32/37 (85%)
Frame = +3 / -2

15 Query: 219 YEERVKDRGIIVRDWAPQLEILAHPSVGGFMSHCGWN 329
YEER DRG++VR WAPQ+ IL+HP+ GGF++HCGWN
Sbjct: 693 YEERFSDRGLLVRGWAPQVTILSHPAAGGFLTHCGWN 583
Score = 32.2 bits (64), Expect = 1.5
Identities = 14/31 (45%), Positives = 18/31 (57%)

20 Frame = -3 / +2
Query: 328 FHPQ*LMNPPTDG*AKISSCGAQSLTIPLS 236
F PQ + NPP G ++ +CGA T PLS
Sbjct: 584 FQPQWVRNPPAAGWDRMVTCTGAHPRTTRRPLS 676
>CL007722.118

25 Length = 7966

Score = 52.8 bits (109), Expect(2) = 4e-14
Identities = 21/45 (46%), Positives = 29/45 (63%)
Frame = +3 / -1

30 Query: 18 WXDQKQKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLR
152

W ++ SV+YV+FGS + LT Q+ ELA GL G F+WV+R

Sbjct: 4321

WLGRKRPCSVLYVNFSGSIVYLTSTQLVELAWGLADSGHDFLWVIR 4187

35 Score = 44.6 bits (91), Expect(2) = 4e-14
Identities = 12/23 (52%), Positives = 17/23 (73%)
Frame = +3 / -1

Query: 261 WAPQLEILAHPSVGGFMSHCGWN 329
W PQ +L H ++G F++HCGWN

40 Sbjct: 4090 WCPQEAVLRHDAIGAFLTHCGWN 4022
>CL026661.50

Length = 5570

Score = 38.6 bits (78), Expect(2) = 4e-14
Identities = 14/38 (36%), Positives = 26/38 (67%)
Frame = +3 / -3

45

Frame = +3 / -1
Query: 222 EERVKDRGIIVRDWAPQLEILAHPSVGGFMSHCGWN 329
E RG ++R WAPQ+ L H +VG F++HCGWN
Sbjct: 1583 ERAAGGRGTVIRGWAPQVAALRHRAVGWFWTHCGWN 1476
5 Score = 30.8 bits (61), Expect = 4.0
Identities = 12/34 (35%), Positives = 19/34 (55%)
Frame = -3 / +1
Query: 340 TAYQFHPQ*LMNPPTDG*AKISSCGAQSLTIPL 239
++ +FHPQ + N PT ++CGA +PL
10 Sbjct: 1465 SSVEFHPQCVTNHPTARCRSAATCGAHPRITVPL 1566
>CL014445.211
Length = 1877

Score = 53.8 bits (111), Expect(2) = 8e-14
15 Identities = 21/45 (46%), Positives = 27/45 (59%)
Frame = +3 / +1
Query: 18 WXDKQGKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLR
152
W D Q SV+YVS GS ++ +Q TE +GL G F+WVLR
20 Sbjct: 1270
WLDGQADRSVVYVSLGSLTVISPEQFTEFLSGLVAAGHPFLWVLR 1404
Score = 42.8 bits (87), Expect(2) = 8e-14
Identities = 13/23 (56%), Positives = 18/23 (77%)
Frame = +3 / +1
25 Query: 261 WAPQLEILAHPSVGGFMSHCGWN 329
WAPQ ++L H +VG F++H GWN
Sbjct: 1495 WAPQRDVL RHRAVGCFLTHAGWN 1563
>CL018085.225.139
Length = 10165
30
Score = 51.0 bits (105), Expect(2) = 1e-13
Identities = 21/45 (46%), Positives = 28/45 (61%)
Frame = +3 / +1
Query: 18 WXDKQGKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLR
35 152
W DKQ +SV+YVSFGS S+ ++ E A GL F+WV+R
Sbjct: 2665
WLDKQEAESVLYVSFGSLASMDSQELLETAWGLVDSEIPFLWVIR 2799
Score = 45.0 bits (92), Expect(2) = 1e-13
40 Identities = 15/27 (55%), Positives = 20/27 (73%)
Frame = +3 / +1
Query: 249 IVRDWAPQLEILAHPSVGGFMSHCGWN 329
+V WAPQ ++L H +VGGF +H GWN
Sbjct: 2872 MVVSWAPQQDVLKHRAVGGFWTHNGWN 2952
45 Score = 30.8 bits (61), Expect = 4.0
Identities = 13/28 (46%), Positives = 15/28 (53%)

Frame = -3 / -3
 Query: 331 QFHPQ*LMNPPTDG*AKISSCGAQSLTI 248
 +FHP + PPT S CGAQ TI
 Sbjct: 2954 EFHPLCVQKPPTARCFSTSCCGAQETTI 2871
 5 >CL056271.83.103
 Length = 8892

 Score = 53.3 bits (110), Expect(2) = 1e-13
 Identities = 21/45 (46%), Positives = 27/45 (59%)
 10 Frame = +3 / +2
 Query: 18 WSDKQKGKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLR
 152
 W D Q SV+YVS GS ++ +Q TE +GL G F+WVLR
 Sbjct: 7757
 15 WLDGQADRSVVYVSLGSLTVISPEQFTEFLSGLVAAGXPFLWVLR 7891
 Score = 42.8 bits (87), Expect(2) = 1e-13
 Identities = 13/23 (56%), Positives = 18/23 (77%)
 Frame = +3 / +2
 Query: 261 WAPQLEILAHPSVGGFMSHCGWN 329
 20 WAPQ ++L H +VG F++H GWN
 Sbjct: 7985 WAPQRDVLRHRAVGCFLTHAGWN 8053
 >CL012295.141
 Length = 5808

 25 Score = 53.3 bits (110), Expect(2) = 1e-13
 Identities = 21/45 (46%), Positives = 27/45 (59%)
 Frame = +3 / -2
 Query: 18 WSDKQKGKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLR
 152
 30 W D Q SV+YVS GS ++ +Q TE +GL G F+WVLR
 Sbjct: 4619
 WLDCQADRSVVYVSLGSLTVISPEQFTEFLSGLVAAGNPFLWVLR 4485
 Score = 42.8 bits (87), Expect(2) = 1e-13
 Identities = 13/23 (56%), Positives = 18/23 (77%)
 35 Frame = +3 / -2
 Query: 261 WAPQLEILAHPSVGGFMSHCGWN 329
 WAPQ ++L H +VG F++H GWN
 Sbjct: 4394 WAPQRDVLRHRAVGCFLTHAGWN 4326
 >CL037891.52.70
 40 Length = 5094

 Score = 52.4 bits (108), Expect(2) = 1e-13
 Identities = 21/45 (46%), Positives = 27/45 (59%)
 Frame = +3 / -2
 45 Query: 18 WSDKQKGKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLR
 152

WD+ +V YVSFG+ S D++ ELA GLE G F+W LR
 Sbjct: 5018
 WLDRHAPRTVAYVSFGTVASPRPDELRELAAGLEASGAPFLWSLR 4884
 Score = 43.2 bits (88), Expect(2) = 1e-13
 5 Identities = 14/26 (53%), Positives = 19/26 (72%)
 Frame = +3 / -2
 Query: 249 IVRDWAPQLEILAHPSVGGFMSHCGW 326
 +V WAPQ+ +L H SVG F++H GW
 Sbjct: 4817 LVVPWAPQVGVLRRHASVGAFVTHAGW 4740
 10 >CL010173.141
 Length = 11045

 Score = 53.3 bits (110), Expect(2) = 2e-13
 Identities = 17/45 (37%), Positives = 31/45 (68%)
 15 Frame = +3 / +1
 Query: 18 WXD KQGKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLR
 152
 WD+ SV++V++GS ++++D++ E A GL CG F+W++R
 Sbjct: 7354
 20 WLDGREPRSVVFNYSITTMSNDELVEFAWGLANCGHGLWIVR 7488
 Score = 41.8 bits (85), Expect(2) = 2e-13
 Identities = 12/27 (44%), Positives = 18/27 (66%)
 Frame = +3 / +1
 Query: 249 IVRDWAPQLEILAHPSVGGFMSHCGWN 329
 25 ++ W Q +L H +VG F++HCGWN
 Sbjct: 7558 LLASWCEQEAVLRHGAVGAFLTHCGWN 7638
 >CL017801.43
 Length = 1489

 30 Score = 41.4 bits (84), Expect(2) = 3e-13
 Identities = 18/45 (40%), Positives = 23/45 (51%)
 Frame = +3 / +2
 Query: 9 LSNWXDKQGKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIW
 143
 35 L W ++ +V+YVSFGS L LA LER G F+W
 Sbjct: 575
 LCAWLNQFADGAVVYVSFGSMAVLQPPXAAALAAALERTGTAFVW 709
 Score = 53.3 bits (110), Expect(2) = 3e-13
 Identities = 16/30 (53%), Positives = 23/30 (76%)
 40 Frame = +3 / +2
 Query: 240 RGIIVRDWAPQLEILAHPSVGGFMSHCGWN 329
 RG ++R W PQ+ +L H +VG F++HCGWN
 Sbjct: 776 RGKVIKRWTPQVPVLRHRAVGRFVTHCGWN 865
 >CL006712.198
 45 Length = 741

Score = 55.1 bits (114), Expect(2) = 3e-13
Identities = 22/46 (47%), Positives = 30/46 (64%)
Frame = +3 / -3

Query: 18

5 WXDQKQKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLRR 155
W D Q SV+YV+ GS + L D++ ELA GLE G +F+W LR+

Sbjct: 598

WLDAQPAKSVVYVALGSEVPLRVDKVHELALGLEVAGTRFLWDLRK 461

Score = 39.6 bits (80), Expect(2) = 3e-13

10 Identities = 14/28 (50%), Positives = 19/28 (67%)
Frame = +3 / -3

Query: 207 LLADYEERVKDRGIIVRDWAPQLEILAH 290

L A +EER + RG++ W PQ+ ILAH

Sbjct: 433 LPAGFEERTRGRGVMATRWVPQMSILAH 350

15 >CL011675.53

Length = 4268

Score = 30.4 bits (60), Expect(2) = 5e-13
Identities = 11/21 (52%), Positives = 15/21 (71%)

20 Frame = +3 / +2

Query: 93 ITELANGLERCGEKFIWVLRR 155

+ ELA GLE G +F+W LR+

Sbjct: 3452 LQELALGLELAGVRFLWALRK 3514

Score = 63.4 bits (132), Expect(2) = 5e-13

25 Identities = 19/36 (52%), Positives = 28/36 (77%)
Frame = +3 / +2

Query: 219 YEERVKDRGIIVRDWAPQLEILAHPSVGGFMSHCGW 326

+EER + RG++ W PQ+E+LAH +VG F++HCGW

Sbjct: 3578 FEERTRGRGVVWTGWVPQVEVLAAHAAVGAFLTHCGW 3685

30 >CL005939.33

Length = 1042

Score = 49.6 bits (102), Expect(2) = 5e-13
Identities = 18/62 (29%), Positives = 37/62 (59%)

35 Frame = +3 / +3

Query: 15

NWXDKQKQKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLRRADPND
IFTEADKV 194

+W + SV+Y+SFGS+ ++ +Q+ E+A + + F+WV+R++ D + + +

40 Sbjct: 618

DWLGTKPARSVVYISFGSSSVMSKNQVAEIAAAMAESKKPFLWVIRKDNCK
DDDDDDNEAI 797

Query: 195 KK 200

KK

45 Sbjct: 798 KK 803

Score = 44.1 bits (90), Expect(2) = 5e-13

- Identities = 13/24 (54%), Positives = 18/24 (74%)
 Frame = +3 / +3
 Query: 258 DWAPQLEILAHPSVGGFMSHCGWN 329
 +W Q +L+H SVG F++HCGWN
- 5 Sbjct: 855 EWCDQARVLSHASVGCFTVTHCGWN 926
 >CL000663.406
 Length = 4867
- Score = 47.3 bits (97), Expect(2) = 7e-13
- 10 Identities = 20/46 (43%), Positives = 28/46 (60%)
 Frame = +3 / +3
 Query: 18
 WXDKQGKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLRR 155
 W D Q DSV+YV+ GS + L + + ELA LE G +F+ LR+
- 15 Sbjct: 1236
 WLDAQPPDSVVYVALGSEVPLRVELVHELALRLELAGTRFLLALRK 1373
 Score = 46.0 bits (94), Expect(2) = 7e-13
 Identities = 16/35 (45%), Positives = 21/35 (59%)
 Frame = +3 / +3
- 20 Query: 225 ERVKDRGIIVRDWAPQLEILAHPSVGGFMSHCGWN 329
 E+ G + W P Q ILAH +VG F++HCG N
 Sbjct: 1419 EQTHGHGHVAMGWVPQTILAHAAVGAFLTHCGRN 1523
 Score = 33.1 bits (66), Expect = 0.82
 Identities = 16/46 (34%), Positives = 25/46 (53%)
- 25 Frame = -2 / -3
 Query: 152 SKHPYKLLPASFPVSQLCDLIICQ*YCRPKRNIYH*IFPLFVXPI
 15
 S+ K P P SQL + Q + P+R+++H*I+ L V P+
 Sbjct: 1370
- 30 SQRQEKTCPGEL*PESQLVHQLHAQRHLAPQRDVHH*IWRLRVQPL 1233
 >CL033762.101
 Length = 3994
- Score = 41.4 bits (84), Expect(2) = 7e-13
- 35 Identities = 18/47 (38%), Positives = 22/47 (46%)
 Frame = +3 / +2
 Query: 9
 LSNWDXDKQKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVL 149
 L W D+ SV+YVSFGS L L LER F+W +
- 40 Sbjct: 3053
 LCAWLDQFADRSVVYVSFGSMSQLQPPHAAALTAALERTSAAFVWAV
 3193
 Score = 51.9 bits (107), Expect(2) = 7e-13
 Identities = 17/30 (56%), Positives = 22/30 (72%)
- 45 Frame = +3 / +2
 Query: 240 RGIIVRDWAPQLEILAHPSVGGFMSHCGWN 329

RG ++ WAPQL L H +VG F++HCGWN
 Sbjct: 3257 RGTVIIGWAPQLAALRHRAVGWFVTHCGWN 3346
 Score = 33.6 bits (67), Expect = 0.60
 Identities = 13/31 (41%), Positives = 18/31 (57%)
 5 Frame = -3 / -2
 Query: 331 QFHPQ*LMNPPTDG*AKISSCGAQSLTIPL 239
 +FHPQ + N PT +SCGA + +PL
 Sbjct: 3348 EFHPQWVTNHPTARCRSAASC GAHPMITVPL 3256
 >CL007660.29
 10 Length = 2087

 Score = 49.2 bits (101), Expect(2) = 7e-13
 Identities = 21/45 (46%), Positives = 28/45 (61%)
 Frame = +3 / +3
 15 Query: 18 WXD KQGKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLR
 152
 W D Q SV+YVS GS +S++ Q+ E+A GL F+WVLR
 Sbjct: 537 WLDAQPVGSLYVSLGSFLSVSRPQLDEIAAGLADSKVTFLWVLR
 671
 20 Score = 44.1 bits (90), Expect(2) = 7e-13
 Identities = 16/29 (55%), Positives = 20/29 (68%)
 Frame = +3 / +3
 Query: 243 GIIVRDWAPQLEILAHPSVGGFMSHCGWN 329
 G +V W QL++L HPSVGGF +H G N
 25 Sbjct: 708 GGMVVPWTDQLKVLCHPSVGGFFTHSGMN 794
 Score = 21.7 bits (41), Expect(2) = 5.6
 Identities = 9/33 (27%), Positives = 16/33 (48%)
 Frame = -3 / -2
 Query: 340 TAYQFHPQ*LMNPPTDG*AKISSCGAQSLTIIP 242
 30 ++ +F P++ PPT+G S T+ P
 Sbjct: 805 SSVEFMPEWVKKPTEGWHSTFSWSVHGTTMPP 707
 Score = 27.2 bits (53), Expect(2) = 5.6
 Identities = 14/46 (30%), Positives = 18/46 (38%)
 Frame = -3 / -2
 35 Query: 148
 STHINFSPHLSNPLANXXXXXXXXXXXXDPKET YITESFPCL SXQLL 11
 STH N + + P A P+ETY TE C S +
 Sbjct: 667 STHKNVTLLSARPAAISSSCGRDTERKLPRETYSTEPTGCASSHAM
 530
 40 >CL001522.659
 Length = 11602

 Score = 39.6 bits (80), Expect(2) = 9e-13
 Identities = 17/47 (36%), Positives = 25/47 (53%)
 45 Frame = +3 / -1

Sbjct: 4230 WCPQEKVLEHDAVGVFLTHSGWN 4298
>CL032230.57

Length = 3687

5 Score = 51.9 bits (107), Expect(2) = 2e-12
Identities = 21/48 (43%), Positives = 28/48 (57%)
Frame = +3 / -2
Query: 9
LSNWDXDKQGKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLR 152

10 L W D SV+YVS+GS +T+Q+ E A GL G F+WV+R

Sbjct: 2300

LLEWLDGHRPSSVYVSYSIAVMTSEQLLEFAWGLADSGYAFVWVVR
2157

Score = 40.0 bits (81), Expect(2) = 2e-12
15 Identities = 12/23 (52%), Positives = 17/23 (73%)
Frame = +3 / -2

Query: 261 WAPQLEILAHPSVGGFMSHCGWN 329
W PQ ++L H +VG F++H GWN

Sbjct: 2066 WCPQEKVLEHDAVGVFLTHSGWN 1998

20 >CL011181.132

Length = 10356

Score = 22.6 bits (43), Expect(3) = 2e-12
Identities = 7/17 (41%), Positives = 11/17 (64%)
25 Frame = +3 / -3

Query: 18 WDXDKQGKDSVIYVSFGS 68
W D Q S++++ FGS

Sbjct: 793 WLDGQPDRSIVFLCFGS 743

Score = 37.7 bits (76), Expect(3) = 2e-12
30 Identities = 12/25 (48%), Positives = 20/25 (80%)
Frame = +3 / -3

Query: 84 DDQITELANGLERCGEKFIWVLRRA 158
+ Q+ E+A GL++ G +F+WV+RRA

Sbjct: 724 EQQLREIAAGLDKSGHRFLWVVRRA 650

35 Score = 50.5 bits (104), Expect(3) = 2e-12
Identities = 15/34 (44%), Positives = 21/34 (61%)
Frame = +3 / -3

Query: 228 RVKDRGIIVRDWAPQLEILAHPSVGGFMSHCGWN 329
R RG++V W PQ +L H + F++HCGWN

40 Sbjct: 601 RTSGRGLVVNTWVPQPSVLRHRATAAFVTHCGWN 500
Score = 35.0 bits (70), Expect = 0.23

Identities = 11/29 (37%), Positives = 17/29 (57%)
Frame = +3 / -3

Query: 243 GIIVRDWAPQLEILAHPSVGGFMSHCGWN 329

45 G + PQL++L H + F++H GWN

Sbjct: 3421 GYFINTQVPQLDVLCHLTDTDFVTHYGWN 3335

>CL009819.69

Length = 1558

Score = 47.8 bits (98), Expect(2) = 3e-12

5 Identities = 19/48 (39%), Positives = 29/48 (59%)

Frame = +3 / -3

Query: 9

LSNWDXDKQGKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLR 152

L W D + SV+YV++GS +T++Q+ E A GL G F+W +R

10 Sbjct: 722

LLEWLDGRPPRSVVYVNYGSIAVMTNEQLLEFAWGLAHSGYPFLWNVR

579

Score = 43.7 bits (89), Expect(2) = 3e-12

Identities = 12/27 (44%), Positives = 20/27 (73%)

15 Frame = +3 / -3

Query: 249 IVRDWAPQLEILAHPSVGGFMSHCGWN 329

++ W PQ +++ HP+VG F++H GWN

Sbjct: 509 LLTTWCPQEQVIEHPAVGVFLTHSGWN 429

>CL003318.273

20 Length = 2506

Score = 53.8 bits (111), Expect(3) = 3e-12

Identities = 21/47 (44%), Positives = 29/47 (61%)

Frame = +3 / +1

25 Query: 9

LSNWDXDKQGKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVL 149

+ W D ++ SV+Y+SFGS SL DQ+ +LA LE G FIW +

Sbjct: 211

VKRWLDTREERSVLYISFGSXNSLRXDQMVDLAMALETGRPFIWAI 351

30 Score = 29.9 bits (59), Expect(3) = 3e-12

Identities = 11/23 (47%), Positives = 16/23 (68%)

Frame = +3 / +1

Query: 234 KDRGIIVRDWAPQLEILAHPSVG 302

K+ G+++ APQ+ ILAH S G

35 Sbjct: 445 KNIGLLIHGXAPQVSILAHASTG 513

Score = 26.7 bits (52), Expect(3) = 3e-12

Identities = 7/8 (87%), Positives = 8/8 (99%)

Frame = +3 / +2

Query: 306 FMSHCGWN 329

40 F+SHCGWN

Sbjct: 515 FLSHCGWN 538

>CL041904.109.89

Length = 6349

45 Score = 29.0 bits (57), Expect(2) = 3e-12

Identities = 11/31 (35%), Positives = 17/31 (54%)

Frame = +3 / +3
Query: 18 WXDQKQGKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLR
152

W D Q SV++VSFG+ ++ + E+A GL F+WV+R

5 Sbjct: 1629

WLDTQAPSSVLFVSFGTMATIDAQEFLEVAWGGLAGTKLPFLWVVR 1763

Score = 45.5 bits (93), Expect(2) = 2e-11

Identities = 15/23 (65%), Positives = 18/23 (78%)

Frame = +3 / +3

10 Query: 261 WAPQLEILAHPSVGGFMSHCGWN 329

WAPQ ++L HPSV FM+H GWN

Sbjct: 1854 WAPQEKVLGHPSVRAFMTHNGWN 1922

Score = 32.2 bits (64), Expect(2) = 0.38

Identities = 13/24 (54%), Positives = 16/24 (66%)

15 Frame = -3 / -2

Query: 331 QFHPQ*LMNPPTDG*AKISSCGAQ 260

+FHP +MN T+G* SCGAQ

Sbjct: 1924 EFHPLCVMNARTEG*PSTFSCGAQ 1853

Score = 20.8 bits (39), Expect(2) = 0.38

20 Identities = 14/45 (31%), Positives = 17/45 (37%)

Frame = -3 / -2

Query: 148 STHINFSPHLSNPLANXXXXXXXXXXXXDPKETYITESFPCLSXQL
14

+TH N S + P A PK T TE C+S L

25 Sbjct: 1759

TTHRNGSLVPAKPHATSRNS*ASMVAMVPKLTNNTLGLGACVSSHL 1625

>CL014413.56.69

Length = 5093

30 Score = 33.1 bits (66), Expect(2) = 5e-11

Identities = 11/22 (50%), Positives = 17/22 (77%)

Frame = +3 / -1

Query: 87 DQITELANGLERCGEKFIWVLR 152

+Q+ ELA GLE G +F+WV++

35 Sbjct: 5093 EQLRELAAGLETSGHRFLWVVK 5028

Score = 53.8 bits (111), Expect(2) = 5e-11

Identities = 18/35 (51%), Positives = 25/35 (71%)

Frame = +3 / -1

Query: 225 ERVKDRGIIVRDWAPQLEILAHPSVGGFMSHCGWN 329

40 +RV+ RG++ + W Q E+L H SV F+SHCGWN

Sbjct: 4964 KRVEKRGLVTKAWVDQEEVLKHESVALFVSHCGWN 4860

>CL036169.42

Length = 3796

45 Score = 65.7 bits (137), Expect = 1e-10

Identities = 22/47 (46%), Positives = 32/47 (67%)

- Frame = +3 / +3
Query: 189
KVKKPQLLADYEERVKDRGIIVRDWAPQLEILAHPSVGGFMSHCGWN 329
+V+K + R K RG++V WAPQ ++L H +VGGF++HCGWN
- 5 Sbjct: 1917
RVEKAPFPEGFLRRTKGRGLVVMSSWAPQRKVLEHSAVGGFVTHCGWN
2057
Score = 35.4 bits (71), Expect = 0.17
Identities = 14/34 (41%), Positives = 20/34 (58%)
- 10 Frame = -3 / -1
Query: 340 TAYQFHPQ*LMNPPTDG*AKISSCGAQSLTIHPL 239
++ +FHPQ + NPPT + CGA +T PL
Sbjct: 2068 SSIEFHPQCVTNPPTALCSSTLRCAHDMTTSP 1967
>CL022193.143
Length = 2779
- Score = 65.7 bits (137), Expect = 1e-10
Identities = 24/58 (41%), Positives = 36/58 (61%)
Frame = +3 / +1
- 20 Query: 156
ADPNDIFTEADKVKKPQLLADYEERVKDRGIIVRDWAPQLEILAHPSVGGFM
SHCGWN 329
A P T + + L A + ER K RG++V++WAPQ E++ H + G F++HCGWN
Sbjct: 103
APPEXQSTSPEPDLERLLPAGFLERTKHRGMVVKNWAPQAEVVRHEAAGAF
VTHCGWN 276
Score = 39.6 bits (80), Expect = 0.010
Identities = 21/62 (33%), Positives = 28/62 (44%)
Frame = -3 / -3
- 30 Query: 340
TAYQFHPQ*LMNPPTDG*AKISSCGAQSLTIHPLSFTLXXXXXXX*GFFTLAS
VKMSFG 161
++ +FHPQ + N P S+CGAQ LT +P F L + S V S G
Sbjct: 287
SSVEFHPQCVTNAPAAASCRTTSACGAQFLTTMPRCFVLSKNPAGSSRSRSGS
GDVLXSSG 108
Query: 160 SA 155
A
Sbjct: 107 GA 102
>CL019829.73
Length = 6143
- Score = 57.4 bits (119), Expect(2) = 1e-10
Identities = 24/62 (38%), Positives = 36/62 (57%)
- 45 Frame = +3 / -3

Query: 18
WXDKQGKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLRRADPNDF
TEADKVK 197

W D Q SV+++ FGS ++QI E+A GLE G++F+WV+R +D +DK

5 Sbjct: 321

WLDTQPNGSVVFLCFGSIGLFSAEQIKEVAAGLEASGQRFLWVVRSPPSDDP
AKKFDKPP 142

Query: 198 KP 203

P

10 Sbjct: 141 DP 136

Score = 28.1 bits (55), Expect(2) = 1e-10

Identities = 9/24 (37%), Positives = 14/24 (57%)

Frame = +3 / -3

Query: 240 RGIIVRDWAPQLEILAHPSVGGFM 311

15 RG++V+ W LAH+ GF+

Sbjct: 90 RGLVVKSWRRSATFLAHAAFXGFV 19

>CL008718.5

Length = 1125

20 Score = 43.2 bits (88), Expect(2) = 2e-10

Identities = 20/62 (32%), Positives = 30/62 (48%)

Frame = +3 / -1

Query: 18

WXDKQGKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLRRADPNDF

25 TEADKVK 197

W SV+YVS GS ++ E+A GL G F+WV+R I++A +

Sbjct: 741

WLHAHSPRSVLYVSLGVARIDREVFDALGLAGSGVPFLWVIRPGFVTGI
VSDALPLT 562

30 Query: 198 KP 203

+P

Sbjct: 561 EP 556

Score = 41.8 bits (85), Expect(2) = 2e-10

Identities = 12/16 (75%), Positives = 15/16 (93%)

35 Frame = +3 / -2

Query: 282 LAHPSVGGFMSHCGWN 329

LAHP++GGF +HCGWN

Sbjct: 485 LAHPAIGGFWTHCGWN 438

>CL002954.21

40 Length = 888

Score = 64.8 bits (135), Expect = 2e-10

Identities = 21/34 (61%), Positives = 27/34 (78%)

Frame = +3 / -3

45 Query: 228 RVKDRGIIVRDWAPQLEILAHPSVGGFMSHCGWN 329

R K RG++V WAPQ E+L H +VGGF++HCGWN

Sbjct: 724 RTKGRGLVMSWAPQREVLEHGAVGGFVTHCGWN 623

Score = 38.6 bits (78), Expect = 0.018

Identities = 15/31 (48%), Positives = 19/31 (60%)

Frame = -3 / +3

5 Query: 331 QFHPQ*LMNPPTDG*AKISSCGAQSLTIPL 239
+FHPQ + NPPT + S CGA +T PL

Sbjct: 621 EFHPQCVTNPPTAPCSSTSRCGAHDMTTSPL 713

>CL038203.17

Length = 876

10

Score = 24.9 bits (48), Expect(2) = 3e-10

Identities = 8/15 (53%), Positives = 12/15 (79%)

Frame = +3 / -1

Query: 105 ANGLERCGEKFIWVL 149

15

A GLE G++F+WV+

Sbjct: 852 AAGLEMXXGQRFLWVV 808

Score = 59.7 bits (124), Expect(2) = 3e-10

Identities = 19/35 (54%), Positives = 25/35 (71%)

Frame = +3 / -2

20

Query: 225 ERVKDRGIIVRDWAPQLEILAHPSVGGFMSHCGWN 329

ER + RG V WAPQ+ +L+HP+ F+SHCGWN

Sbjct: 722 ERTRGRGXAVAAWAPQVRVLSHPATAAFVSHCGWN 618

>CL035030.166.173

Length = 11257

25

Score = 47.3 bits (97), Expect(2) = 5e-10

Identities = 17/38 (44%), Positives = 27/38 (70%)

Frame = +3 / -3

Query: 42 SVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLRR 155

30

SV+Y++ GS + L D++ ELA GL+ G +F+W LR+

Sbjct: 9635 SVVYIALGSEVPLRVDPKVELALGLDVAGTRFLWALRK 9522

Score = 36.3 bits (73), Expect(2) = 5e-10

Identities = 14/28 (50%), Positives = 18/28 (64%)

Frame = +3 / -3

35

Query: 207 LLADYEERVVKDRGIIVRDWAPQLEILAH 290

L A +EER RG++ W PQ+ ILAH

Sbjct: 9494 LPAGFEERSCGRGVVETRWPQMSILAH 9411

>CL013048.66

Length = 567

40

Score = 47.3 bits (97), Expect(2) = 5e-10

Identities = 18/46 (39%), Positives = 28/46 (60%)

Frame = +3 / -2

Query: 18

45

WXDKQKGKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLRR 155

W D + SV+YV+FGS + Q+ EL +GLE G ++ V+R+

Sbjct: 353

Score = 36.3 bits (73), Expect(2) = 5e-10

Identities = 12/30 (40%), Positives = 18/30 (60%)

5 Frame = +3 / -2

Query: 240 RGIIVRDWAPQLEILAHPSVGGFMSHCGWN 329

R + V + O + L H + G F + HCGWN

Sbjct: 158 RRGVVVEXCDQVXLXHAAFGCFVXHCGWN 69

>CL008671.33

10 Length = 2946

Score = 54.2 bits (112), Expect(2) = 9e-10

Identities = 21/55 (38%), Positives = 30/55 (54%)

Frame = +3 / +1

15 Query: 18

W X D K O G K D S V I Y V S F G S T I S L T D D O I T E L A N G L E R C G E K F I W V L R R A D P N D I F

TE 182

W D Q SV+Y S+G+ L Q+ EL NG G+ F+WV+R D++ E

Sbjct: 283

20 WLDNQPPCSVVYASYGTVADLDPTOLDELGNGFCNSGKPFLWVVRSCDEH

KLSEE 447

Score = 28.6 bits (56), Expect(2) = 9e-10

Identities = 8/18 (44%), Positives = 13/18 (71%)

Frame = +3 / +1

25 Query: 249 IVRDWAPQLEILAHPSVG 302

++ W POLE+L+H + G

Sbjct: 475 LIVSWCPQLEVLCHKATG 528

Score = 32.7 bits (65), Expect = 1.1

Identities = 10/17 (58%), Positives = 13/17 (75%)

30 Frame = +3 / +3

Query: 279 ILAHPSVGGFMSHCGWN 329

I+ H S G F++HCGWN

Sbjct: 1287 IILH*STGCFLTHCGWN 1337

>CL037496.141

35 Length = 8755

Score = 29.9 bits (59), Expect(2) = 1e-09

Identities = 15/43 (34%), Positives = 22/43 (50%)

Frame = +3 / +2

40 Query: 42 SVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLRRADPND 170

SV+++ FGS L ++ E+A LER G + R P D

Sbjct: 4250 SVLFLCFGSKGLLPVKVPEIAAALERSGGHRFLWVLRGPPKD

4378

Score = 52.4 bits (108), Expect(2) = 1e-09

45 Identities = 19/35 (54%), Positives = 25/35 (71%)

Frame = +3 / +2

Query: 225 ERVKDRGIIVRDWAPQLEILAHPSVGGFMSHCGWN 329
 ER K +G++ APQ EIL +VGGF++HCGWN
 Sbjct: 4445 ERTKGKGLVWPTRAPQKEILGXAAVGGFVTHCGWN 4549
 Score = 35.0 bits (70), Expect = 0.23
 5 Identities = 13/24 (54%), Positives = 17/24 (70%)
 Frame = -3 / -2
 Query: 331 QFHPQ*LMNPPTDG*AKISSCGAQ 260
 +FHPQ + NPPT +IS CGA+
 Sbjct: 4551 EFHPQWVTNPPTAAXPRISFCGAR 4480
 10 >CL000509.218.7
 Length = 1142

 Score = 62.5 bits (130), Expect = 1e-09
 Identities = 20/37 (54%), Positives = 26/37 (70%)
 15 Frame = +3 / -3
 Query: 219 YEERVKDRGIIVRDWAPQLEILAHPSVGGFMSHCGWN 329
 + ER RG+ V WAPQ+ +LAHP+ F+SHCGWN
 Sbjct: 1071 FVERTXGRGLAVASWAPQVRVLAHPATAAFVSHCGWN 961
 >CL026417.121
 20 Length = 1010

 Score = 56.5 bits (117), Expect(2) = 1e-09
 Identities = 22/45 (48%), Positives = 29/45 (63%)
 Frame = +3 / -3
 25 Query: 18 WXDQKQGKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLR
 152
 W D Q SV+ VSFGS +T+ Q+ E+A GLE G F+WV+R
 Sbjct: 405
 WLDGQEPGSVVLVSFGSEYFMTEKQLAEMARGLELSGAAFVWVVR 271
 30 Score = 25.8 bits (50), Expect(2) = 1e-09
 Identities = 10/21 (47%), Positives = 13/21 (61%)
 Frame = +3 / -3
 Query: 240 RGIIVRDWAPQLEILAHPSVG 302
 RG++V APQ L+H S G
 35 Sbjct: 186 RGLVVXGCAPQRRFLSHRSCG 124
 >CL006249.99
 Length = 1774

 Score = 54.2 bits (112), Expect(2) = 2e-09
 40 Identities = 21/55 (38%), Positives = 33/55 (59%)
 Frame = +3 / -2
 Query: 18
 WXDQKQGKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLRRADPNDIF
 TE 182
 45 W D K Q SV+ S+G+ S L ++ EL NGL G+ F+WV+R + + + + E

Score = 26.3 bits (51), Expect(4) = 4e-09
 Identities = 10/18 (55%), Positives = 11/18 (60%)
 Frame = +3 / +1
 Query: 99 ELANGLERCGEKFIWVLR 152
 5 ELA LE G FIW +R
 Sbjct: 1627 ELAAALESSGRPFIWAIR 1680
 Score = 29.5 bits (58), Expect(4) = 4e-09
 Identities = 10/17 (58%), Positives = 13/17 (75%)
 Frame = +3 / +2
 10 Query: 240 RGIIVRDWAPQLEILAH 290
 RG +V WAP++ ILAH
 Sbjct: 1757 RGHVVHGWAPRVSILAH 1807
 Score = 31.3 bits (62), Expect(4) = 4e-09
 Identities = 9/12 (75%), Positives = 10/12 (83%)
 15 Frame = +3 / +3
 Query: 294 SVGGFMSHCGWN 329
 S G F+SHCGWN
 Sbjct: 1818 STGAFLSHCGWN 1853
 >CL026049.88
 20 Length = 4232

 Score = 51.9 bits (107), Expect(2) = 4e-09
 Identities = 20/55 (36%), Positives = 30/55 (54%)
 Frame = +3 / +1
 25 Query: 18
 WXDKQGKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLRADPN
 TE 182
 W D Q SV+Y S+G+ L Q+ EL NG G+ F+WV+R + + + E
 Sbjct: 1489
 30 WLDNQPPCSVVYASYGTVADLDPTQLDELGNGFCNSGKPFLWVVRSCNEH
 KLSEE 1653
 Score = 28.6 bits (56), Expect(2) = 4e-09
 Identities = 8/18 (44%), Positives = 13/18 (71%)
 Frame = +3 / +1
 35 Query: 249 IVRDWAPQLEILAHPSVG 302
 ++ W PQLE+L+H + G
 Sbjct: 1681 LIVSWCPQLEVLCHKATG 1734
 Score = 32.7 bits (65), Expect = 1.1
 Identities = 10/17 (58%), Positives = 13/17 (75%)
 40 Frame = +3 / +2
 Query: 279 ILAHPSVGGFMSHCGWN 329
 I+ H S G F++HCGWN
 Sbjct: 2423 IILH*STGCFLTHCGWN 2473
 >CL025248.34.28
 45 Length = 3765

Query: 18
WSDKQGKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLRRADPNDIF
TE 182

W DKQ SV++VS+G+ S ++ E+ NGL G+ F+WV+R + + + E

5 Sbjct: 684
WLDKQPPRSVVFVSYGTFSSYDAAKLEEVGNGLCNSGKPFLWVVRNNEEH
KLSRE 848

Score = 24.9 bits (48), Expect(2) = 2e-07
Identities = 8/18 (44%), Positives = 13/18 (71%)

10 Frame = +3 / +3

Query: 249 IVRDWAPQLEILAHPSVG 302

++ + PQLE+LAH + G

Sbjct: 876 LIVPFCPQLEVLAHKATG 929

>CL004311.41

15 Length = 3451

Score = 55.1 bits (114), Expect = 2e-07
Identities = 17/30 (56%), Positives = 24/30 (79%)
Frame = +3 / +3

20 Query: 240 RGIIVRDWAPQLEILAHPSVGGFMSHCGWN 329

+G++ WAPQ EILAH ++G F++HCGWN

Sbjct: 75 KGLVWPTWAPQKEILAHAAIGSFVTHCGWN 164

>CL006249.98

Length = 1158

25 Score = 49.2 bits (101), Expect(2) = 3e-07
Identities = 20/58 (34%), Positives = 33/58 (56%)
Frame = +3 / -1

Query: 18

30 WSDKQGKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLRRADPNDIF
TEADK 191

W DKQ SV+ VS+G+ + ++ EL NGL G+ F+WV+R + + + + K

Sbjct: 663

WLDKQPPRSVVLVSYGTVSTFDVAKLEELGNGLCNSGKPFLWVVRNNEEH

35 KLSVQLRK 490

Score = 24.9 bits (48), Expect(2) = 3e-07
Identities = 8/18 (44%), Positives = 13/18 (71%)
Frame = +3 / -1

Query: 249 IVRDWAPQLEILAHPSVG 302

40 ++ + PQLE+LAH + G

Sbjct: 471 LIVPFCPQLEVLAHKATG 418

>CL006250.59

Length = 2276

45 Score = 48.7 bits (100), Expect(3) = 3e-07
Identities = 20/58 (34%), Positives = 33/58 (56%)

Score = 47.8 bits (98), Expect = 3e-05
 Identities = 17/32 (53%), Positives = 21/32 (65%)
 Frame = +3 / +2
 Query: 234 KDRGIIVRDWAPQLEILAHPSVGGFMSHCGWN 329
 5 + RG W PQ+ ILAH S+G F+SH GWN
 Sbjct: 302 RTRGSSFTGWLPQVAILAHASIGTFLSHYGWN 397
 >CL047288.95.94
 Length = 5704

10 Score = 47.8 bits (98), Expect = 3e-05
 Identities = 20/48 (41%), Positives = 26/48 (53%)
 Frame = +3 / -1
 Query: 18
 WXDKQGKDSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLRRAD 161
 15 W D + V Y SFGS SL Q+ EL GL G+ F+WV+R +
 Sbjct: 4342
 WLDTKPLSFVAYFSFGSFASLGTAQMEELTRGLHAAGKPFLWVVRATE
 4199
 >CL001395.104
 20 Length = 837

Score = 46.0 bits (94), Expect = 1e-04
 Identities = 15/26 (57%), Positives = 18/26 (68%)
 Frame = +3 / -1
 25 Query: 252 VRDWAPQLEILAHPSVGGFMSHCGWN 329
 V WAPQ E+LA P+ F +HCGWN
 Sbjct: 759 VVSWAPQEEVLAXPATAAFWTHCGWN 682
 Score = 30.8 bits (61), Expect = 4.0
 Identities = 13/30 (43%), Positives = 18/30 (59%)
 30 Frame = -3 / +2
 Query: 340 TAYQFHPQ*LMNPPTDG*AKISSCGAQSLT 251
 ++ +F PQ+ N G A+ SSCGAQ T
 Sbjct: 671 SSVEFQPQCVCVQNAAVAGXARTSSCGAQLTT 760
 >CL046651.78.92
 35 Length = 8149

Score = 22.1 bits (42), Expect(2) = 1e-04
 Identities = 14/38 (36%), Positives = 16/38 (41%)
 Frame = +3 / -3
 40 Query: 96 TELANGLERCGEKFIWVLRRADPNDIFTEADKVKKPQL 209
 TEL GLE F+ VL D E K+ P L
 Sbjct: 7064 TELLGLEATALPFLAVLNFPKGTDAEAE LRKLTPPGL 6951
 Score = 42.8 bits (87), Expect(2) = 1e-04
 Identities = 18/34 (52%), Positives = 21/34 (60%)
 45 Frame = +3 / -3
 Query: 222 EERVKDRGIIVRDWAPQLEILAHPSVGGFMSHCG 323

ERVK RGI+ W Q IL H SVG F++H G
Sbjct: 6950 EXRVKGRGILHTGWVQQQHILRHRSVGC FVN HSG 6849
>CL012879.91

Length = 3774

5

Score = 44.1 bits (90), Expect = 4e-04
Identities = 17/48 (35%), Positives = 25/48 (51%)
Frame = +3 / +3

Query: 18

10 WXD KQ GK DSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLRRAD 161

W D + SV+Y SFGS + + + E+ GL G F+WV R +

Sbjct: 3549

WLDARPA GSVVYASFGSIAAPGPETMAEVPEGLYSSGSPFLWVFRATE 3692

>CL037422.184

15

Length = 5074

Score = 44.1 bits (90), Expect = 4e-04
Identities = 20/45 (44%), Positives = 23/45 (50%)
Frame = +3 / +2

20 Query: 9 LSNW XDKQ GK DSVIYVSFGSTISLTDDQITELANGLERCGEKFIW
143

L W D+ SV+YVSFGS L LA LER G F+W

Sbjct: 158

LCAWLDQFADRSVVYVSFGSMSQLQPLHAAALAAALERTGA AFVW 292

25

>CL024561.203

Length = 12861

Score = 40.9 bits (83), Expect = 0.004
Identities = 14/41 (34%), Positives = 28/41 (68%)
Frame = +3 / -2

30

Query: 39 DSVIYVSFGSTISLTDDQITELANGLERCGEKFIWVLRRAD 161

+SV+YV+F S T + + + +GLE G+ F+WV+++++

Sbjct: 3764 NSVVYVNFSSIACKTPKYLKVGHGLEDTGK PFLWVVKKSE
3642

35

>CL031911.221

Length = 1347

Score = 38.6 bits (78), Expect = 0.018
Identities = 17/37 (45%), Positives = 19/37 (50%)
Frame = +3 / +2

40

Query: 51 YVSFGSTISLTDDQITELANGLERCGEKFIWVLRRAD 161

YVSF S + Q EL GLE G FIWV+ D

Sbjct: 1169 YVSFXSIXXXEEXQAVELGLGLEASGHPFIWVVXSPD 1279

>CL009894.82

45

Length = 1090

Score = 38.6 bits (78), Expect = 0.018
 Identities = 16/52 (30%), Positives = 27/52 (51%)
 Frame = +3 / +2

Query: 18
 5 W X D K Q G K D S V I Y V S F G S T I S L T D D Q I T E L A N G L E R C G E K F I W V L R R A D P N D I
 173
 W SV++ SFGS L ++ E+A L G F+WV+R ++++
 Sbjct: 833
 W L G A H P P R S V V F A S F G S L S D L D P A E M R E V A L A L L D A G A P F L W V V R S S E S H K
 10 L 988
 >CL017435.41
 Length = 2310

Score = 34.5 bits (69), Expect = 0.32
 15 Identities = 12/29 (41%), Positives = 14/29 (47%)
 Frame = +3 / +1
 Query: 246 I I V R D W A P Q L E I L A H P S V G G F M S H C G W N W 332
 I V W A+PS G +SHC W W
 Sbjct: 1066 I S V E F W R T D W S E S A N P S F A G V V S H C S W E W 1152
 20 >CL025804.138
 Length = 1664

Score = 33.1 bits (66), Expect = 0.82
 Identities = 11/36 (30%), Positives = 22/36 (60%)
 25 Frame = -2 / -2
 Query: 203 R L F Y F I S F C K N V V W I C S S K H P Y K L L P A S F Q P V S Q L C 96
 +L Y I+F N+ WIC+S+ + +F+ +++C
 Sbjct: 745 K L V Y A I T F G N N L C W I C A S R K K D E S K D S D F K D A A E V C 638
 30 >CL016357.110
 Length = 5312

Score = 32.7 bits (65), Expect = 1.1
 Identities = 9/27 (33%), Positives = 17/27 (62%)
 Frame = -2 / +1
 35 Query: 215 C K K L R L F Y F I S F C K N V V W I C S S K H P Y K 135
 C +F ++ C +++IC ++HPYK
 Sbjct: 3340 C S N N H V F L Y V L H C W D N I Y I C V N R H P Y K 3420
 >CL016373.76
 Length = 1201

Score = 31.8 bits (63), Expect = 2.1
 Identities = 11/23 (47%), Positives = 13/23 (55%)
 Frame = +3 / -1
 40 Query: 264 A P Q L E I L A H P S V G G F M S H C G W N W 332
 +P E+ A H P S V C G W W
 45 Sbjct: 916 S P C A E L A A H P S V E L V A R G C G W G W 848

>CL006799.122

Length = 6571

Score = 31.8 bits (63), Expect = 2.1

5 Identities = 12/32 (37%), Positives = 18/32 (55%)

Frame = +3 / -3

Query: 9 LSNWXDKQGKDSVIYVSFGSTISLTDDQITEL 104

+ WDKQ SV+YV+ G+ +T +EL

Sbjct: 5771 MMRWLDKQLARSVVYVALGTEAPITSGTVREL 5676

10 >CL021508.93

Length = 796

Score = 30.8 bits (61), Expect = 4.0

Identities = 7/21 (33%), Positives = 14/21 (66%)

15 Frame = -2 / +1

Query: 215 CKKLRLFYFISFCKNVVWICS 153

C++L+ FC+++W+CS

Sbjct: 373 CRSMALLFHCPFCRSMTWLCS 435

>CL021508.96

20 Length = 7429

Score = 30.8 bits (61), Expect = 4.0

Identities = 7/21 (33%), Positives = 14/21 (66%)

Frame = -2 / -3

25 Query: 215 CKKLRLFYFISFCKNVVWICS 153

C++L+ FC+++W+CS

Sbjct: 1565 CRSMALLFHCPFCRSMTWLCS 1503

>CL040417.30.45

Length = 8520

30

Score = 30.4 bits (60), Expect = 5.5

Identities = 15/35 (42%), Positives = 18/35 (50%)

Frame = +3 / +1

Query: 51 YVSFGSTISLTDDQITELANGLERCGEKFIWVLRR 155

35 +VSF+ISLT LA G RC F W +R

Sbjct: 1297 FVSFLTILSLTGSWT*NLAEGFVRCSFVFSWSKQR 1401

>CL003447.129

Length = 5246

40 Score = 30.4 bits (60), Expect = 5.5

Identities = 16/42 (38%), Positives = 22/42 (52%)

Frame = -3 / +1

Query: 241 LSFTLXXXXXXXX*GFFTLASVKMSFGSALLSTHINFSPHLS 116

L+T F+LS S S +L+STH++FSP LS

45 Sbjct: 1666 LKWTACENGLNTRSLFSLSISSIFSPPHSLISTHLSFSPLLS 1791

>CL018287.77.89

Length = 7016

Score = 30.4 bits (60), Expect = 5.5

Identities = 12/42 (28%), Positives = 19/42 (44%)

5 Frame = -2 / -2

Query: 209 KLRLFYFISFCKNVVWICSSKHPYKLLPASFQPVSQLCDLII 84

+ R Y + WICSS H L++ Q S C+++

Sbjct: 1660 RCRSIYLCVYGSTFAWICSSNHSITLIQSVCSHSLTCVVLV 1535

>CL004077.196

10 Length = 1818

Score = 30.4 bits (60), Expect = 5.5

Identities = 11/27 (40%), Positives = 17/27 (62%)

Frame = -2 / +2

15 Query: 188 ISFCKNVVWICSSKHPYKLLPASFQPV 108

IS C N++ CSSK P+++L P+

Sbjct: 68 ISVCVNILQTCSSKFPFQVLHVFLVPL 148

>CL002787.44

Length = 2698

20

Score = 30.4 bits (60), Expect = 5.5

Identities = 10/32 (31%), Positives = 17/32 (52%)

Frame = -2 / +1

Query: 176 KNVVWICSSKHPYKLLPASFQPVSQLCDLIIC 81

25 +++++CS +PY P S P C L+ C

Sbjct: 1018 QKILYLCSHCYPYLSNPISASPTIYFCTLISC 1113

>HTC170138-B01.1.56

Length = 4728

30 Score = 29.9 bits (59), Expect = 7.6

Identities = 9/24 (37%), Positives = 14/24 (57%)

Frame = -2 / +1

Query: 215 CKKLRLFYFISFCKNVVWICSSKH 144

C K ++F S +N++WIC H

35 Sbjct: 184 CTKCAFYHFCSKHQNILWICQCVH 255

>CL000396.374

Length = 1360

Score = 29.9 bits (59), Expect = 7.6

40 Identities = 13/30 (43%), Positives = 16/30 (53%)

Frame = -2 / -1

Query: 215 CKKLRLFYFISFCKNVVWICSSKHPYKLLP 126

C + L FI+CKN W+ PY LLP

Sbjct: 139 CIRDSLILFIVWCKNCSWMGQ*VVPYGLLP 50

45 >CL032065.41

Length = 2449

- Score = 29.9 bits (59), Expect = 7.6
 Identities = 12/33 (36%), Positives = 18/33 (54%)
 Frame = +1 / -1
- 5 Query: 115 WKDAGRSLYGCLEEQITTFLOKLIK*KSLNFL 213
 WDAGRSL+ C+ + T +L+ K F+
 Sbjct: 1420 WIDAGRSLFACIGAFMYNTVRARLLGAKQRRFM 1322
 >CL003934.253
 Length = 7101
- 10 Score = 29.9 bits (59), Expect = 7.6
 Identities = 9/22 (40%), Positives = 13/22 (58%)
 Frame = -2 / +2
 Query: 197 FYFISFCKNVVWICSSKHPYKL 132
 FY+ +F +VW C S H Y +
 Sbjct: 4640 FYWCNLFYIVWFCDSNHIYSI 4705
 >CL036158.8
 Length = 980
- 20 Score = 29.9 bits (59), Expect = 7.6
 Identities = 11/23 (47%), Positives = 15/23 (64%)
 Frame = -2 / +1
 Query: 212 KKLRLFYFISFCKNVVWICSSKH 144
 KK+R YFIS CK + S++H
 Sbjct: 781 KKVRFQYFISICKQTLQTTSTQH 849
 >CL044924.114.138
 Length = 9672
- 30 Score = 29.9 bits (59), Expect = 7.6
 Identities = 10/28 (35%), Positives = 17/28 (60%)
 Frame = +2 / -2
 Query: 257 RLGTTARNLGSSISWRVHESLWMELVRS 340
 RL + LGS + + HES W++++ S
 Sbjct: 5807 RLPLAIKTLGSMLRYETHESRWIDILES 5724
- 35 Database:
 Posted date:
 Number of letters in database: 359,911,985
 Number of sequences in database: 154,797
- 40 Lambda K H
 0.318 0.135 0.401
 Matrix: BLOSUM62
 Number of Hits to DB: 260575520
 Number of Sequences: 154797
- 45 Number of extensions: 2943256
 Number of successful extensions: 86298

DESCA8 Blast result against nonredundant proteins

DeCypher Results for: NCBI BLASTX Translated Search

Results by Query

Click on a query below to view its search results.

5 Your_Query starting with: GATGAGTCCTGAGTAACAAA

Search Details

Results for: Your_Query starting with:

10 **GATGAGTCCTGAGTAACAAA; (Length=239)**

Return to query summary

	RANK	Sequences producing significant alignments:	(bits)	Value
15	<u>1</u>	dbj BAB11300.1 AB026651 disease resistance protein [Arabidop...	36	0.058
	<u>2</u>	gb AAF82158.1 AC034256_22 AC034256 Contains similarity to NBS...	36	0.058
	<u>3</u>	pir T06049 hypothetical protein T24A18.140 - Arabidopsis thali...	36	0.077
	<u>4</u>	pir T02236 NBS-LRR type resistance protein - rice (fragment) >...	35	0.13
20	<u>5</u>	dbj BAB11301.1 AB026651 disease resistance protein [Arabidop...	35	0.17
	<u>6</u>	dbj BAA97160.1 AB018117 NBS/LRR disease resistance protein [...	34	0.39
25	<u>7</u>	dbj BAA37123.1 AB022318 inducible nitric oxide synthase [Hom...	33	0.51
	<u>8</u>	dbj BAB09983.1 AB010692 NBS/LRR disease resistance protein [...	33	0.51
	<u>9</u>	gb AAC19133.1 AF068236 inducible nitric oxide synthase [Homo...	33	0.51
30	<u>10</u>	pir JX0345 nitric-oxide synthase (EC 1.14.13.39) - human >gi 9...	33	0.51
	<u>11</u>	pir I38933 nitric-oxide synthase (EC 1.14.13.39), airway epith...	33	0.51
	<u>12</u>	ref XP_008631.1 nitric oxide synthase 2A (inducible, hepatocyt...	33	0.51
	<u>13</u>	gb AAF34847.1 AC022355 hypothetical protein; 11196-13892 [Ar...	33	0.66
35	<u>14</u>	gb AAF19702.1 AC008047_9 AC008047 F2K11.27 [Arabidopsis thali...	33	0.66
	<u>15</u>	sp Q94637 VIT6_OSCBR VITELLOGENIN 6 PRECURSOR		
		>gi 7522166 pir ... 33	0.66	
40	<u>16</u>	dbj BAB00756.1 AB017071 contains similarity to RPS-2 disease...	33	0.66
	<u>17</u>	sp P22467 MYSA_DICDI MYOSIN IA HEAVY CHAIN (MYOSIN-LIKE		
		PROTEIN... 32	0.87	

18 pir|[A82497](#) ribose ABC transporter, ATP-binding protein VCA0128... 32
0.87
19 gb|[AAC69557.2](#)| [AF076529](#) ATP binding protein BviA [Butyrivibri... 32
0.87
5 20 pir|[A47475](#) nitric-oxide synthase (EC 1.14.13.39), inducible - ... 32 0.87
21 pir|[S38572](#) myosin IA - *Caenorhabditis elegans* >gi|[7511498](#)|pir|... 32 1.1
22 gb|[AAC26125.1](#)| [AF074916](#) NBS/LRR disease resistance protein [A... 32
1.1
23 gb|[AAC13911.1](#)|[AAC13911](#) [AC004255](#) T1F9.21 [*Arabidopsis thaliana*]
10 32 1.1
24 gb|[AAB69192.1](#)| [AF005744](#) YsaN [*Yersinia enterocolitica*] 32 1.1
25 pir|[T49593](#) hypothetical protein B3E4.60 [imported] - *Neurospor...* 32 1.1
26 gb|[AAG12764.1](#)|[AC024261_12](#) [AC024261](#) hypothetical protein; 4644... 31
2.0
15 27 dbj|[BAB09158.1](#)| [AB017065](#) disease resistance protein-like [Ara... 31 2.0
28 ref|NP_000616.1| nitric oxide synthase 2A (inducible, hepatocyt... 31 2.0
29 gb|[AAC15102.1](#)| [AF057353](#) translation elongation factor 3 [Ther... 31 2.0
30 dbj|[BAB10817.1](#)| [AB019223](#) disease resistance protein-like [Ara... 31 2.0

20 RANK 1 ITERATION 0>dbj|[BAB11300.1](#)| [AB026651](#) disease resistance protein
[*Arabidopsis*
thaliana]
Length = 848

25 Score = 36.4 bits (82), Expect = 0.058
Identities = 19/55 (34%), Positives = 33/55 (59%), Gaps = 2/55 (3%)
Frame = +1Query: 49 LPMVEDQYIGTT--
LSGIRDSAYQAMTGGRAQCIGIYGHRGAGKTNLMKHLHNKAFE 213
+P E ++I TT L + A++++ ++G+YG G GKT L++ L+NK E
30 Sbjct: 142
IPKAEKKHIQTTVGLDTMVGIAWESLIDDEIRTLGLYGMGGIGKTTLLESLNN
KFVE 198

RANK 2 ITERATION 0>gb|[AAF82158.1](#)|[AC034256_22](#) [AC034256](#) Contains
35 similarity to NBS/LRR
disease resistance protein gi|3309619 from *Arabidopsis*
thaliana gb|[AF074916](#) and contains a NB-ARC PF|00931
domain and multiple Leucine Rich PF|00560 Repeats
Length = 921
40
Score = 36.4 bits (82), Expect = 0.058
Identities = 19/54 (35%), Positives = 31/54 (57%), Gaps = 2/54 (3%)
Frame = +1Query: 52 PMVEDQYIGTT--
LSGIRDSAYQAMTGGRAQCIGIYGHRGAGKTNLMKHLHNKAFE 213
45 P VE ++I TT L + A++ ++G+YG G GKT L+ ++NK E

Sbjct: 215
PKVEKKHIQTTVGLDAMVGRAWNSLMKDERRTLGLYGMGGVGKTTLLASI
NNKFLE 270

5 RANK 3 ITERATION 0>pir|[T06049] hypothetical protein T24A18.140 -
Arabidopsis thaliana
 >gi|4490715|emb|CAB38849.1| (AL035680) putative protein
 [Arabidopsis thaliana] >gi|7269572|emb|CAB79574.1|
 (AL161566) putative protein [Arabidopsis thaliana]
10 Length = 985

Score = 36.0 bits (81), Expect = 0.077

Identities = 23/61 (37%), Positives = 35/61 (56%), Gaps = 3/61 (4%)

Frame = +1Query: 34 KRGEKLP---

15 MVEDQYIGTTLSGIRDSAYQAMTGGRAQCIGIYGHRGAGKTNLMKHLHNK
204

 +R E +P +V L+ IRD +T +AQ IG++G G GKT L++ L+NK

Sbjct: 132 ERVEHVPGVSVVHQTMASNMLAKIRDG----

LTSEKAQKIGVWGMGGVGKTTLVRTLNNK 187Query: 205 AFED 216

20 E+

Sbjct: 188 LREE 191

RANK 4 ITERATION 0>pir|[T02236] NBS-LRR type resistance protein - rice
(fragment)

25 >gi|2792248|gb|AAB96999.1| (AF032702) NBS-LRR type
 resistance protein [Oryza sativa]
 Length = 321

Score = 35.2 bits (79), Expect = 0.13

30 Identities = 21/57 (36%), Positives = 32/57 (55%), Gaps = 3/57 (5%)

Frame = +1Query: 58 VEDQYIGTTLSGIR---

DSAYQAMTGGRAQCIGIYGHRGAGKTNLMKHLHNKAFEDVQEL 228

 VE ++IGT++ G+ D A + +GI+G G GKT L+K +HN+ V L

Sbjct: 40

35 VERRHIGTSVVGMECYLDKALGYLRKRDIPVLGIWGMGGVGKTTLLKLIHN
EFLGTV DGL 99

RANK 5 ITERATION 0>dbj|[BAB11301.1| AB026651] disease resistance protein
[Arabidopsis

40 thaliana]
 Length = 862

Score = 34.8 bits (78), Expect = 0.17

Identities = 20/57 (35%), Positives = 32/57 (56%), Gaps = 2/57 (3%)

45 Frame = +1Query: 43 EKLP MVEDQYIGTT--

LSGIRDSAYQAMTGGRAQCIGIYGHRGAGKTNLMKHLHNKAFE 213

E + VE + I T T L + + A + + + + G + Y G G G K T L + + L + N K E
 Sbjct: 139
 EIIHKVEKKLIQTTVGLDKLVEMAWSSLMNDEIGTLGLYGMGGVGKTTLLE
 SLNNKFVE 197

5

RANK 6 ITERATION 0>dbj|BAA97160.1| AB018117 NBS/LRR disease
 resistance protein
 [Arabidopsis thaliana]
 Length = 885

10

Score = 33.6 bits (75), Expect = 0.39
 Identities = 19/62 (30%), Positives = 31/62 (49%)
 Frame = +1Query: 46

KLPMVEDQYIGTTLSGIRDSAYQAMTGGRAQCIGIYGHRGAGKTNLMKHLH
 15 NKA FEDVQE 225

K + P + + + + + D + A + + + G I Y G G G K T L + L N K D
 Sbjct: 143 KMPPIQ---
 LTVSQAKLLDTAWARLMDINVGT L G I Y G R G G V G K T T L L T K L R N K L L V D A F G
 199Query: 226 LV 231
 20 LV
 Sbjct: 200 LV 201

25

RANK 7 ITERATION 0>dbj|BAA37123.1| AB022318 inducible nitric oxide
 synthase [Homo
 sapiens]
 Length = 1114

Score = 33.2 bits (74), Expect = 0.51
 Identities = 19/60 (31%), Positives = 30/60 (49%), Gaps = 5/60 (8%)
 30 Frame = +2Query: 17 QTTXLESVERSYPPWWRISTLARRC-----
 LG*GIQLIKP*QEVVLNALVSMATEEPERPI 181

Q T L E + + + S + W C L + + P + + + L L + A T E E P E R
 Sbjct: 760
 QTVRLEALDESGSYWVSDKRLPPCSLSQALTYFLDITTPPTQLLLQKLAQVA
 35 TEEPERQR 819Query: 182 S*STC 196
 + C
 Sbjct: 820 LEALC 824

40

RANK 8 ITERATION 0>dbj|BAB09983.1| AB010692 NBS/LRR disease
 resistance protein
 [Arabidopsis thaliana]
 Length = 874

Score = 33.2 bits (74), Expect = 0.51
 45 Identities = 18/52 (34%), Positives = 29/52 (55%), Gaps = 3/52 (5%)

Frame = +1Query: 49 LPMVEDQYIGTTLSG---

IRDSAYQAMTGGRAQCIGIYGHRGAGKTNLMKHLHNK 204

+P VE++ +G I+S++M +GIYG G GKT L+ ++NK

Sbjct: 144

5 IPKVEERLFHQEIVGQEAIVESTWNSMMEVGVGLLGIYGMGGVGKTTLLSQI
NNK 198

RANK 9 ITERATION 0>gb|AAC19133.1| AF068236 inducible nitric oxide
synthase [Homo

10 sapiens]

Length = 1153

Score = 33.2 bits (74), Expect = 0.51

Identities = 19/60 (31%), Positives = 30/60 (49%), Gaps = 5/60 (8%)

15 Frame = +2Query: 17 QTTXLESVERSYPPWRISTLARRC-----

LG*GIQLIKP*QEVVLNALVSMATEEPERPI 181

QT LE+++ S +W C L ++ P +++L L +ATEEPER

Sbjct: 799

QTVRLEALDESGSYWVSDKRLPPCSLSQALTYFLDITTPPTQLLLQKLAQVA

20 TEEPERQR 858Query: 182 S*STC 196

+ C

Sbjct: 859 LEALC 863

RANK 10 ITERATION 0>pir|JX0345 nitric-oxide synthase (EC 1.14.13.39) -
25 human

>gi|951321|gb|AAB49041.1| (U31511) nitric oxide synthase

[Homo sapiens] >gi|1228940|dbj|BAA05531.1| (D26525)

inducible type of nitric oxide synthase [Homo sapiens]

Length = 1153

30

Score = 33.2 bits (74), Expect = 0.51

Identities = 19/60 (31%), Positives = 30/60 (49%), Gaps = 5/60 (8%)

Frame = +2Query: 17 QTTXLESVERSYPPWRISTLARRC-----

LG*GIQLIKP*QEVVLNALVSMATEEPERPI 181

35 QT LE+++ S +W C L ++ P +++L L +ATEEPER

Sbjct: 799

QTVRLEALDESGSYWVSDKRLPPCSLSQALTYFLDITTPPTQLLLQKLAQVA

TEEPERQR 858Query: 182 S*STC 196

+ C

40 Sbjct: 859 LEALC 863

RANK 11 ITERATION 0>pir|J38933 nitric-oxide synthase (EC 1.14.13.39), airway
epithelium

- human >gi|687681|gb|AAB60366.1| (U20141) nitric oxide

45 synthase [Homo sapiens]

Length = 1153

Sbjct: 144
VEEQQLQPTIVGQETMLDNAWNHLMEDGVGIMGLYGMGGVGKTTLLTQIN
NK 195

5 RANK 14 ITERATION 0>gb|AAAF19702.1|AC008047_9 AC008047 F2K11.27
[Arabidopsis thaliana]
Length = 556

Score = 32.8 bits (73), Expect = 0.66
10 Identities = 17/49 (34%), Positives = 29/49 (58%), Gaps = 3/49 (6%)
Frame = +1Query: 58 VEDQYIGTTLSG---
IRDSAYQAMTGGRAQCIGIYGHRGAGKTNLMKHLHNK 204
VE+Q + T+ G + D+A+ + +G+YG G GKT L+ ++NK

Sbjct: 144
15 VEEQQLQPTIVGQETMLDNAWNHLMEDGVGIMGLYGMGGVGKTTLLTQIN
NK 195

RANK 15 ITERATION 0>sp|Q94637|VIT6_OSCBR VITELLOGENIN 6
PRECURSOR >gi|7522166|pir|T18561
20 vitellogenin CEW1-vit-6 - Oscheius sp. (PS1131)
>gi|1515337|gb|AAB49749.1| (U35449) vitellogenin [Oscheius
sp. CEW1]
Length = 1660

25 Score = 32.8 bits (73), Expect = 0.66
Identities = 18/70 (25%), Positives = 32/70 (45%)
Frame = +1Query: 28
IRKRGEKLP MVEDQYIGTTLSGIRDSAYQAMTGGRAQCIGIYGHRGAGKTNL
MKHLHNKA 207

30 I +RGE+ + + + + G + + QC G+ GH KTN + N+
Sbjct: 1449 ISQRGEEKFFIDAEEKVTVEFDGFQAKIQMSSLYKNKQC-
GLCGHYDGEKTNEFRRADNEE 1507Query: 208 FEDVQELVRS 237
+D++E RS
Sbjct: 1508 TDDIEEFSRS 1517

35 RANK 16 ITERATION 0>dbj|BAB00756.1| AB017071 contains similarity to
RPS-2 disease
resistance protein~gene_id:MSJ11.10 [Arabidopsis
thaliana]
40 Length = 375

Score = 32.8 bits (73), Expect = 0.66
Identities = 15/51 (29%), Positives = 27/51 (52%)
Frame = +1Query: 61
45 EDQYIGTTLSGIRDSAYQAMTGGRAQCIGIYGHRGAGKTNLMKHLHNKA
213

+DQ+G L + ++ MT IG+YG G GKT ++ ++N+ +
 Sbjct: 138 DDQTVG--
 LEAVSGLVWRCMTVDNTGIIIGLYGVEGVGKTTVLTQVNNRLLQ 186

5 RANK 17 ITERATION 0>sp|P22467|MYSA_DICDI MYOSIN IA HEAVY
 CHAIN (MYOSIN-LIKE PROTEIN ABMA)

>gi|84153|pir|JQ0151 myosin heavy chain IA - slime mold
 (Dictyostelium sp.) >gi|241268|gb|AAB20711.1| (S73909)
 actin-based motor [Dictyostelium, Peptide, 994 aa]

10 Length = 994

Score = 32.5 bits (72), Expect = 0.87

Identities = 17/34 (50%), Positives = 21/34 (61%), Gaps = 1/34 (2%)

Frame = +1Query: 94 IRDSAYQAMTG-GRAQCIGIYGHRGAGKTNLMKHL

15 195

IDAY+A+ G QCIIG GAGKT K++

Sbjct: 84 IADKAYRALRSEGENQCIISGESGAGKTEASKYI 118

20 RANK 18 ITERATION 0>pir|A82497 ribose ABC transporter, ATP-binding
 protein VCA0128

[imported] - Vibrio cholerae (group O1 strain N16961)
 >gi|9657516|gb|AAF96042.1| (AE004354) ribose ABC
 transporter, ATP-binding protein [Vibrio cholerae]
 Length = 500

25

Score = 32.5 bits (72), Expect = 0.87

Identities = 21/56 (37%), Positives = 32/56 (56%), Gaps = 7/56 (12%)

Frame = +1Query: 31 RKRGEKLPMVEDQY-----

IGTTLSGIRDSAYQAMTGGRAQCIGIYGHRGAGKTNLMK 189

30 RK E+P+Q IG TSG+D++ G ++G+G GAG+T LMK

Sbjct: 241 RKLEEQYPRIAAQQGDISLEVIGLTGSGVHDVSFTLKKG---

EILGVSGLMGAGRTELMK 297Query: 190 HLH 198

++

Sbjct: 298 VIY 300

35

RANK 19 ITERATION 0>gb|AAC69557.2| AF076529 ATP binding protein BviA
 [Butyrivibrio

fibrisolvens]

Length = 280

40

Score = 32.5 bits (72), Expect = 0.87

Identities = 14/35 (40%), Positives = 22/35 (62%)

Frame = +1Query: 127 GRAQCIGIYGHRGAGKTNLMKHLHNKAFEDVQELV

231

45 G+ QCIG+ G GAGK+ L+K + +D E++

Sbjct: 28 GKGQCIGLIGENGAGKSTLIKILQLIGKDSGEIL 62

RANK 20 ITERATION 0>pir|A47475 nitric-oxide synthase (EC 1.14.13.39),
inducible - human

5 >gi|292242|gb|AAA59171.1| (L09210) inducible nitric oxide
synthase [Homo sapiens]
Length = 1153

Score = 32.5 bits (72), Expect = 0.87

Identities = 19/60 (31%), Positives = 29/60 (47%), Gaps = 5/60 (8%)

10 Frame = +2Query: 17 QTTXLESVERSYPPWWRISTLARRC-LG*GI----
QLIKP*QEVVLNALVSMATEEPERPI 181

QT LE ++ S +W C L + + P +++L L +ATEEPER

Sbjct: 799

QTVRLEDLDESGSYWVSDKRLPPCSLSQALTYSPDITTPPTQLLLQKLAQVA

15 TEEPERQR 858Query: 182 S*STC 196
+ C

Sbjct: 859 LEALC 863

[END

ALIGNMENTS]

20

Job DetailsReturn to top

[BEGIN JOB STATUS][BEGIN SEARCH TIME]

[END SEARCH TIME]

25 [VERSION]

[SEARCH ID]

[EOL] CRLF

[COMMENT] /Comment=NCBI BLASTX Translated Search

[COMMENT]

30 [ALGORITHM] BLASTX

[MATRIX] D:\DECYPHER\MATRIX\BLOSUM62.MAA

[QUERY FORMAT] FASTA/PEARSON

[QUERY TYPE] NT

[QUERY FILTER] T

35 [QUERY SEARCH] -1 -2 -3 1 2 3

[QUERY PATH] d:\decypher\query

[QUERY SET]

[TARGET TYPE] AA

[TARGET FRAMES] 1

40 [TARGET PATH] d:\decypher\target\blast

[TARGET SET] nr

[MAX SCORES] 30

[MAX ALIGNMENTS] 20

[THRESHOLD] 1

45 [RESULT PATH] d:\decypher\output

[OUTPUT FORMAT] TEXT EXTRACTALIGNED[SHOW GI] F

[EXPECTATION] 10

[GAPPED ALIGNMENT] TBLASTX
BLASTX

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),

- 5 "Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs", Nucleic Acids Res. 25:3389-3402. Query= Your_Query starting with:
GATGAGTCCTGAGTAACAAA /QuerySize=239

(239 letters) Database: Nonredundant Proteins

598,029 sequences; 189,012,571 total letters Database: Nonredundant

- 10 Proteins

Posted date:

Number of letters in database: 189,012,571

Number of sequences in database: 598,029

- 15 Lambda K H

0.318 0.135 0.401 Gapped

Lambda K H

0.270 0.0470 0.230

Matrix: BLOSUM62.MAA

- 20 Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 92994311

Number of Sequences: 598029

Number of extensions: 1804307

Number of successful extensions: 10056

- 25 Number of sequences better than 10.0: 125

Number of HSP's better than 10.0 without gapping: 56

Number of HSP's successfully gapped in prelim test: 39

Number of HSP's that attempted gapping in prelim test: 9989

Number of HSP's gapped (non-prelim): 106

- 30 length of query: 79

length of database: 189,012,571

effective HSP length: 50

effective length of query: 29

effective length of database: 159,111,121

- 35 effective search space: 4614222509

effective search space used: 4614222509

frameshift window, decay const: 50, 0.1

T: 12

A: 40

- 40 X1: 16 (7.3 bits)

X2: 38 (14.8 bits)

X3: 64 (24.9 bits)

S1: 41 (21.7 bits)

S2: 63 (29.0 bits)[JOB MESSAGES] [END JOB STATUS]

DeCypher Results for: NCBI TBLASTX Similarity Search

Results by Query

Click on a query below to view its search results.

5 Your_Query starting with: GATGAGTCCTGAGTAACAAA

Search Details

Results for: Your_Query starting with:

10 **GATGAGTCCTGAGTAACAAA; (Length=239)**

[Return to query summary](#)

	RANK	Sequences producing significant alignments:	(bits)	Value
	<u>1</u>	CL060908.67.73	36	0.043
15	<u>2</u>	CL032760.119.138	36	0.059
	<u>3</u>	CL024028.95	35	0.15
	<u>4</u>	CL021513.204.73	35	0.15
	<u>5</u>	CL015419.270	34	0.21
	<u>6</u>	CL036494.267	33	0.40
20	<u>7</u>	CL025661.91	33	0.40
	<u>8</u>	CL019516.125.76	33	0.40
	<u>9</u>	CL015886.192.138	33	0.55
	<u>10</u>	CL013394.84.64	32	0.75
	<u>11</u>	CL030496.91	32	0.75
25	<u>12</u>	CL013342.49	32	1.0
	<u>13</u>	CL009892.38	32	1.0
	<u>14</u>	CL000247.130	32	1.0
	<u>15</u>	CL023282.125	32	1.0
	<u>16</u>	HTC151029-A01.F.23.52	31	1.4
30	<u>17</u>	HTC042332-A01.36.37	31	1.4
	<u>18</u>	CL025188.174	31	1.4
	<u>19</u>	CL032303.110	31	1.4
	<u>20</u>	CL025461.108	31	1.9
	<u>21</u>	CL011546.147	31	1.9
35	<u>22</u>	CL039064.163	31	1.9
	<u>23</u>	CL031245.96.70	31	1.9
	<u>24</u>	CL007686.97	31	1.9
	<u>25</u>	CL008320.138	31	1.9
	<u>26</u>	CL014810.281	31	1.9
40	<u>27</u>	CL010697.204	31	1.9
	<u>28</u>	CL002646.146	30	2.7
	<u>29</u>	CL009859.50	30	2.7
	<u>30</u>	CL004039.66	30	2.7

RANK 1 ITERATION 0>CL060908.67.73

Length = 4997

- 5 Score = 36.3 bits (73), Expect = 0.043
Identities = 16/41 (39%), Positives = 24/41 (58%)
Frame = +1 / +2
Query: 94 IRDSAYQAMTGGRAQCIGIYGHRGAGKTNLMKHLHNKAFED
216
- 10 I + A ++T G + IGI G G GKT+L+K ++N D
Sbjct: 2207 ILEEALRCITEGPSAIIIGICPGGVGKTHLLKRINNNFVGD 2329
Score = 29.9 bits (59), Expect = 3.7
Identities = 12/40 (30%), Positives = 21/40 (52%)
Frame = +1 / +3
- 15 Query: 94 IRDSAYQAMTGGRAQCIGIYGHRGAGKTNLMKHLHNKAFE 213
+ A ++ + IGI G G GKT+++K ++N E
Sbjct: 4440 VLQDALRYIADDSVEMIGIRGAAGVGKTHILKKINNSFHE 4559

RANK 2 ITERATION 0>CL032760.119.138

20 Length = 8857

- Score = 35.9 bits (72), Expect = 0.059
Identities = 10/29 (34%), Positives = 17/29 (58%)
Frame = -1 / +3
- 25 Query: 173 FPAPLWP*IPMH*ARPPVMA**AESLIPD 87
+P+PLWP + +H + PP + +PD
Sbjct: 7830 YPSPLWPPVALHRSGPPHASPSLSPRVPD 7916

RANK 3 ITERATION 0>CL024028.95

30 Length = 5268

- Score = 34.5 bits (69), Expect = 0.15
Identities = 14/29 (48%), Positives = 16/29 (54%)
Frame = +1 / -1
- 35 Query: 115 AMTGGRAQCIGIYGHRGAGKTNLMKHLHN 201
A G IGIYG G GKT L+ H +N
Sbjct: 3837 AFQEGGTSVIGIYGAPGVGKTTLLHHFNN 3751

RANK 4 ITERATION 0>CL021513.204.73

40 Length = 4958

- Score = 34.5 bits (69), Expect = 0.15
Identities = 16/45 (35%), Positives = 20/45 (43%)
Frame = -2 / +3
- 45 Query: 199
CAGAS*DWSFRLLCGHRYQCIEHDLLSWLDKLNPLSQTTSCQCTD 65

C S DWS L CG R EH + + + S TS C+D
Sbjct: 1812 CRVQSEDWSISLSCGDRVTHAEHPVQIFYCLDHLSSETS YGCSD
1946

5 RANK 5 ITERATION 0>CL015419.270
Length = 3703

Score = 34.1 bits (68), Expect = 0.21
Identities = 12/30 (40%), Positives = 19/30 (63%)

10 Frame = +3 / +3

Query: 30 *KAWREVTTHGGG SVHWH DVVWDKGFSLSSH 119

KA+ +V GG + W+D++ KGFS+ H

Sbjct: 1998 QKAFGQVLGGGNKLCWNDILSLKGFSVDRH 2087

15 RANK 6 ITERATION 0>CL036494.267
Length = 2725

Score = 33.1 bits (66), Expect = 0.40
Identities = 16/41 (39%), Positives = 22/41 (53%)

20 Frame = -2 / -1

Query: 166 LLCGHRYQCIEHDLLSWLDKLNPLSQTTSCQCTDPPP W VTS 44

L G + + EH LL LD+L LS + C PPP V++

Sbjct: 853 LSSGRQLEAREHSLHRLDRLPLLSIVATFHCHYPPPRVSA 731

25 RANK 7 ITERATION 0>CL025661.91
Length = 4094

Score = 33.1 bits (66), Expect = 0.40
Identities = 11/35 (31%), Positives = 21/35 (59%)

30 Frame = +1 / +1

Query: 91 GIRDSAYQAMTGGRAQCIGIYGHRGAGKTNLMKHL 195

G++ S++Q T G ++ + HR A T+ ++HL

Sbjct: 1636 GVQKSSFQVETTGLSELSAHRPASSTHFLRHL 1740

35 RANK 8 ITERATION 0>CL019516.125.76
Length = 6278

Score = 33.1 bits (66), Expect = 0.40
Identities = 14/28 (50%), Positives = 16/28 (57%)

40 Frame = -2 / +3

Query: 154 HRYQCIEHDLLSWLDKLNPLSQTTSCQC 71

H+Y C DLL + L PLSQT S C

Sbjct: 1461 HKYHCYFSDLLEIICNLAPLSQTLSSFC 1544

45 RANK 9 ITERATION 0>CL015886.192.138
Length = 10067

Score = 32.7 bits (65), Expect = 0.55

Identities = 14/38 (36%), Positives = 19/38 (49%)

Frame = -2 / -2

5 Query: 214 LQRLCCAGAS*DWSFRLLCGHRYQCIEHDLLSWLDKLN 101

L CC+GAS +SF+ Y C + + WL LN

Sbjct: 7834 LTSCCCSGASETYSFCISHLKTYTCNLYIKMQWLVLN 7721

RANK 10 ITERATION 0>CL013394.84.64

10 Length = 3918

Score = 32.2 bits (64), Expect = 0.75

Identities = 13/21 (61%), Positives = 13/21 (61%)

Frame = -2 / -3

15 Query: 76 QCTDPPPWVTS LHAF*XRCLL 14

QCTD P W SLHA R LL

Sbjct: 616 QCTDAPRWGRSLHAAYTRLLL 554

RANK 11 ITERATION 0>CL030496.91

20 Length = 8212

Score = 32.2 bits (64), Expect = 0.75

Identities = 11/28 (39%), Positives = 16/28 (56%)

Frame = -1 / +3

25 Query: 212 SKALLCRCFMRLVFPAPLWP*IPMH*AR 129

++ CRC++RL+ P P P P H R

Sbjct: 3204 ARVTACRCWLRL LAPPPAPPPPAHAGR 3287

RANK 12 ITERATION 0>CL013342.49

30 Length = 1993

Score = 31.8 bits (63), Expect = 1.0

Identities = 18/63 (28%), Positives = 23/63 (35%)

Frame = -1 / -3

35 Query: 227

NSCTSSKALLCRCFMRLVFPAPLWP*IPMH*ARPPVMA**AESLIPDNV VPM

Y*SSTMGN 48

N C + L R P +WP + +PP A P SST G+

Sbjct: 227

40 NRCVTPCLSLTGLCRRRNHPLSIWPWVEGGKSVPTTPAAASXPTCAASXPT

LRSSTAGS 48

Query: 47 FSP 39

FSP

Sbjct: 47 FSP 39

45

RANK 13 ITERATION 0>CL009892.38

Length = 3569

Score = 31.8 bits (63), Expect = 1.0

Identities = 10/26 (38%), Positives = 14/26 (53%)

5 Frame = +3 / -1

Query: 9 LSNKQRY*KAWREVTHGGGSVHWHDV 86

L +RY W TH G+VH H++

Sbjct: 3308 LQKSERYSFHWATATHNSGAVHLHEL 3231

10 RANK 14 ITERATION 0>CL000247.130

Length = 5737

Score = 31.8 bits (63), Expect = 1.0

Identities = 11/27 (40%), Positives = 15/27 (54%)

15 Frame = -2 / +3

Query: 121 SWLDKLNPLSQTTSCQCTDPPPWVTSL 41

SWL+ +P Q T+ T PPW T +

Sbjct: 3867 SWLEMADPALQITNDSATAAPPWSTDI 3947

20 RANK 15 ITERATION 0>CL023282.125

Length = 1145

Score = 31.8 bits (63), Expect = 1.0

Identities = 11/42 (26%), Positives = 22/42 (52%)

25 Frame = -1 / +3

Query: 161 LWP*IPMH*ARPPVMA**AESLIPDNVVP MY*SSTMGNFSPR 36

L+P P A P+ A ++P V+ Y++++ ++PR

Sbjct: 630 LYPQFPKLPAPSPALPTQARAPLPAGVLQPYTTASLASTAPR 755

30 RANK 16 ITERATION 0>HTC151029-A01.F.23.52

Length = 4714

Score = 31.3 bits (62), Expect = 1.4

Identities = 11/19 (57%), Positives = 13/19 (67%)

35 Frame = +3 / -1

Query: 21 QRY*KAWREVTHGGGSVHW 77

+R AWREV GGS+HW

Sbjct: 4504 RRRRCNAWREVVA*GGSIIHW 4448

40 RANK 17 ITERATION 0>HTC042332-A01.36.37

Length = 3273

Score = 31.3 bits (62), Expect = 1.4

Identities = 15/49 (30%), Positives = 23/49 (46%)

45 Frame = -2 / -3

Query: 148

YQCIHDLKLSWLDKLNPLSQTTSCQCTDPPPWVTS LHAF*XRCLLLRTH 2

Y CI S++ P+S +T+C P W+ SL F L ++ H

Sbjct: 1546

5 YICIYFLFRSYMLVHTPMSTSTTCSLASLPRWLKSLSGFW*AWLNIKIH 1400

RANK 18 ITERATION 0>CL025188.174

Length = 5425

10 Score = 31.3 bits (62), Expect = 1.4

Identities = 11/19 (57%), Positives = 13/19 (67%)

Frame = +1 / +2

Query: 130 RAQCIGIYGHRGAGKTNLM 186

R QC G+ G GAGKT L+

15 Sbjct: 5189 RGQCFGVLGPNGAGKTTLI 5245

Score = 29.9 bits (59), Expect = 3.7

Identities = 11/25 (44%), Positives = 14/25 (56%)

Frame = -1 / -2

Query: 203 LLCRCFMRLVFPAPLWP*IPMH*AR 129

20 ++ MR+VFPAP P P H R

Sbjct: 5262 IILTMLMRVVFPAPFGPRTPKHCPR 5188

RANK 19 ITERATION 0>CL032303.110

Length = 4898

25

Score = 31.3 bits (62), Expect = 1.4

Identities = 11/19 (57%), Positives = 13/19 (67%)

Frame = +1 / +1

Query: 130 RAQCIGIYGHRGAGKTNLM 186

30 R QC G+ G GAGKT L+

Sbjct: 988 RGQCFGVLGPNGAGKTTLI 1044

RANK 20 ITERATION 0>CL025461.108

Length = 4552

35

Score = 30.8 bits (61), Expect = 1.9

Identities = 14/38 (36%), Positives = 19/38 (49%)

Frame = -3 / +2

Query: 168 GSSVAIDTNALSTTSCHGLIS*IPYPRQRRANVLILHH 55

40 GSS+A+D+N +GLIS I + I HH

Sbjct: 1025 GSSLALDSN*RGNIRLNGLISEIQTVPINLTATYHH 1138

[END

ALIGNMENTS]

45 Job Details[Return to top](#)

[BEGIN JOB STATUS][BEGIN SEARCH TIME]

```

[END SEARCH TIME]
[VERSION]
[SEARCH ID]
[EOL] CRLF
5 [COMMENT] /Comment=NCBI TBLASTX Similarity Search
[COMMENT] /CGI
[ALGORITHM] TBLASTX
[MATRIX] D:\DECYPHER\MATRIX\BLOSUM62.MAA
[QUERY FORMAT] FASTA/PEARSON
10 [QUERY TYPE] NT
[QUERY FILTER] T
[QUERY SEARCH] -1 -2 -3 1 2 3
[QUERY PATH] d:\decypher\query
[QUERY SET]
15 [TARGET TYPE] NT
[TARGET FRAMES] -1 -2 -3 1 2 3
[TARGET PATH] d:\decypher\target\blast
[TARGET SET]
[MAX SCORES] 30
20 [MAX ALIGNMENTS] 20
[THRESHOLD] 1
[RESULT PATH] d:\decypher\output
[OUTPUT FORMAT] TEXT EXTRACTALIGNED[SHOW GI] F
[EXPECTATION] 10
25 [GAPPED ALIGNMENT] TTBLASTX
TBLASTX
Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
30 programs", Nucleic Acids Res. 25:3389-3402.Query= Your_Query starting with:
GATGAGTCCTGAGTAACAAA /QuerySize=239
(239 letters)Database:
154,797 sequences; 359,911,975 total letters Database:
Posted date:
35 Number of letters in database: 359,911,975
Number of sequences in database: 154,797

Lambda K H
0.318 0.135 0.401
40 Matrix: BLOSUM62.MAA
Number of Hits to DB: 241533722
Number of Sequences: 154797
Number of extensions: 3568717
Number of successful extensions: 187206
45 Number of sequences better than 10.0: 439
length of query: 79

```


DESCA9 Blast result against nonredundant proteins

DeCypher Results for: NCBI BLASTX Translated Search

Results by Query

Click on a query below to view its search results.

5 Your Query starting with: GACTGCGTACCAATTCAAGA

Search Details

Results for: Your Query starting with:

10 **GACTGCGTACCAATTCAAGA; (Length=283)**

[Return to query summary](#)

RANK	Sequences producing significant alignments:	(bits)	Value
15	<u>1</u> pir [T03634 cytochrome P450 - common tobacco >gi 1237250 emb CA...	131	2e-030
	<u>2</u> pir [T03275 probable cytochrome P450, hypersensitivity-related ...	125	1e-028
	<u>3</u> sp [P48418 C751_PETHY FLAVONOID 3',5'-HYDROXYLASE 1 (F3'5'H) (CY...	66	1e-010
20	<u>4</u> pir [S32110 cytochrome P450 PET-1 - garden petunia (fragment) >...	66	1e-010
	<u>5</u> gb [AAD56282.1 AF155332_1 AF155332 flavonoid 3'-hydroxylase [P...	64	5e-010
	<u>6</u> pir [T45624 flavonoid 3'-hydroxylase-like protein [imported] - ...	62	1e-009
25	<u>7</u> sp [O04773 C756_CAMME FLAVONOID 3',5'-HYDROXYLASE (F3'5'H) (CYTO...	61	5e-009
	<u>8</u> sp [P48419 C753_PETHY FLAVONOID 3',5'-HYDROXYLASE 2 (F3'5'H) (CY...	59	1e-008
30	<u>9</u> dbj [BAB09016.1 AB007645 cytochrome P450 [Arabidopsis thaliana]	57	4e-008
	<u>10</u> dbj [BAA74465.1 AB022732 cytochrome P450 [Glycyrrhiza echinata]	57	4e-008
	<u>11</u> sp [P93147 C81E_GLYEC CYTOCHROME P450 81E1 (ISOFLAVONE 2'-HYDROX...	57	7e-008
35	<u>12</u> emb [CAA09850.1 AJ011862 flavonoid 3',5'-hydroxylase [Cathara...	56	1e-007
	<u>13</u> emb [CAA04117.1 AJ000478 cytochrome P450 [Helianthus tuberosus]	55	2e-007
40	<u>14</u> pir [T10896 cytochrome P450 (EC 1.14.-.-) 81B1c - Jerusalem art...	55	2e-007
	<u>15</u> gb [AAF97323.1 AC023628_4 AC023628 Putative cytochrome P450 [A...	55	2e-007
	<u>16</u> emb [CAB65335.1 AJ010324 ferulate-5-hydroxylase [Populus bals...	55	3e-007

17 sp|P37119|C713_SOLME CYTOCHROME P450 71A3 (CYPLXXIA3) (P-450EG3... 54 3e-007

18 pir|JC7172 cytochrome P450 CYP703A1 - garden petunia >gi|73396... 54 3e-007

5 19 sp|O04790|C757_EUSGR FLAVONOID 3',5'-HYDROXYLASE (F3'5'H) (CYTO... 53 6e-007

20 sp|Q96418|C755_EUSGR FLAVONOID 3',5'-HYDROXYLASE (F3'5'H) (CYTO... 53 8e-007

21 sp|P37120|C752_SOLME FLAVONOID 3',5'-HYDROXYLASE (F3'5'H) (CYTO... 53 8e-007

10 22 sp|Q96581|C754_GENTR FLAVONOID 3',5'-HYDROXYLASE (F3'5'H) (CYTO... 53 8e-007

23 gb|AAC49188.2|U29333 cytochrome P450 monooxygenase [Pisum sa... 53 8e-007

15 24 sp|O49859|C824_SOYBN CYTOCHROME P450 82A4 (P450 CP9) >gi|743068... 53 1e-006

25 sp|Q42799|C932_SOYBN CYTOCHROME P450 93A2 >gi|7430614|pir|T071... 53 1e-006

26 sp|Q42798|C931_SOYBN CYTOCHROME P450 93A1 >gi|2129824|pir|S628... 52 1e-006

20 27 gb|AAG09208.1|AF175278_1 AF175278 wound-inducible P450 hydrox... 52 2e-006

28 sp|Q43068|C821_PEA CYTOCHROME P450 82A1 (CYPLXXXII) >gi|7430689... 52 2e-006

25 29 sp|P24465|CP71_PERAE CYTOCHROME P450 71A1 (CYPLXXIA1) (ARP-2) >... 52 2e-006

30 gb|AAA32913.1|M32885 cytochrome P-450LXXIA1 (cyp71A1) [Perse... 52 2e-006

30 RANK 1 ITERATION 0>pir|T03634 cytochrome P450 - common tobacco >gi|1237250|emb|CAA65580.1| (X96784) cytochrome P450 [Nicotiana tabacum] Length = 498

35 Score = 131 bits (327), Expect = 2e-030
Identities = 64/89 (71%), Positives = 76/89 (84%)
Frame = +2Query: 2
TAYQFKMMLDELFLNGVKNLGDWIPCLKYIDVQGYVKRMKVLGKKFDM
FMEHVLDEHNA 181

40 T +FK MLDELFLNGV N+GD+IP + ++D+QGYVKRMKVL KFD
F+E+VLDEHNA
Sbjct: 201
TPEEFKKMLDELFLNGVLNIGDYIPWIDFMDLQGYVKRMKVL SNKFDRFL
EYVLDEHNA 260Query: 182 KRENDKENWVPKDMVDVLLQLADDPTLEV

45 268
+R N +EN+V KDMVDVLLQ ADDPTLEV

Sbjct: 261 RR-NAEENYVAKDMVDVLLQFADDP TLEV 288

RANK 2 ITERATION 0>pir|[T03275] probable cytochrome P450, hypersensitivity-related -

5 common tobacco >gi|1171579|emb|CAA64635.1| (X95342)
cytochrome P450 [Nicotiana tabacum]
Length = 509

Score = 125 bits (311), Expect = 1e-028

10 Identities = 61/86 (70%), Positives = 72/86 (82%)

Frame = +2Query: 11

QFKMMLDELFLNGVKNLGDWIPCLKYIDVQGYVKRMKVLGKKFDMFME
HVLDEHNAKRE 190

+FK MLDELFLNGV N+GD IP + ++D+QGYVKRMKV+ KKFD

15 F+EHV+DEHN +R

Sbjct: 204

EFKKMLDELFLNGVLNIGDSIPWIDFMDLQGYVKRMKVVSKKFDKFLEHV
IDEHNIRR- 262Query: 191 NDKENWVPKDMVDVLLQLADDP TLEV 268

N EN+V KDM DVLLQLADDP LEV

20 Sbjct: 263 NGVENYVAKDMEDVLLQLADDPKLEV 288

RANK 3 ITERATION 0>sp|[P48418]C751_PETHY FLAVONOID 3',5'-
HYDROXYLASE 1 (F3'5'H)

(CYTOCHROME P450 75A1) (CYPLXXVA1) >gi|629710|pir|[S38985]
25 flavonoid 3',5'-hydroxylase Hfl - garden petunia
>gi|311656|emb|CAA80266.1| (Z22545) flavonoid
3',5'-hydroxylase [Petunia x hybrida]
>gi|1853972|dbj|BAA03438.1| (D14588)
flavonoid-3',5'-hydroxylase [Petunia x hybrida]
30 >gi|3426337|gb|AAC32274.1| (AF081575) flavonoid
3',5'-hydroxylase [Petunia x hybrida]
>gi|738772|prf|[2001426B flavonoid 3',5'-hydroxylase
[Petunia x hybrida]
Length = 506

35 Score = 65.6 bits (157), Expect = 1e-010
Identities = 34/81 (41%), Positives = 49/81 (59%)

Frame = +2Query: 11

QFKMMLDELFLNGVKNLGDWIPCLKYIDVQGYVKRMKVLGKKFDMFME
40 HVLDEHNAKRE 190

+FK M+ EL + G N+GD+IPCL ++D+QG KRMK L KKFD + + DEH A

Sbjct: 203

EFKDMVVELMTIAGYFNIGDFIPCLAWMDLQGIEKRMKRLHKKFDALLTKM
FDEHKATTY 262Query: 191 NDKENWVPKDMVDVLLQLADD 253

45 K D +DV+++ D+

Sbjct: 263 ERKGK---PDFLDVVMENGDN 280

RANK 4 ITERATION 0>pir|S32110 cytochrome P450 PET-1 - garden petunia (fragment)

5 >gi|287909|emb|CAA50442.1| (X71130) P450 hydroxylase
[Petunia x hybrida]
Length = 425

Score = 65.6 bits (157), Expect = 1e-010
Identities = 34/81 (41%), Positives = 49/81 (59%)

10 Frame = +2Query: 11
QFKMMLDELFLNGVKNLGDWIPCLKYIDVQGYVKRMKVLGKKFDMFME
HVLDEHNAKRE 190
+FK M+ EL + G N+GD+IPCL ++D+QG KRMK L KKFD + + DEH A
Sbjct: 203
15 EFKDMVVELMTIAGYFNIGDFIPCLAWMDLQGIEKRMKRLHKKFDALLTKM
FDEHKATTY 262Query: 191 NDKENWVPKDMVDVLLQLADD 253
K D +DV+++ D+
Sbjct: 263 ERKGK---PDFLDVVMENGDN 280

20 RANK 5 ITERATION 0>gb|AAD56282.1|AF155332_1 AF155332 flavonoid 3'-
hydroxylase [Petunia
x hybrida]
Length = 512

25 Score = 63.6 bits (152), Expect = 5e-010
Identities = 31/83 (37%), Positives = 51/83 (61%)
Frame = +2Query: 5

AYQFKMMLDELFLNGVKNLGDWIPCLKYIDVQGYVKRMKVLGKKFDMF
MEHVLDEHNAK 184
30 A +FK M+ E+ ++ GV N+GD+IP L ++D+QG +MK L +FD F+ +L+EH K
Sbjct: 203
AAEFKSMVEMMVVAGVFNIGDFIPQLNWLDIQGVA AKMKKLHARFDAFL
TDILEEHKGK 262Query: 185 RENDKENWVPKDMVDVLLQLADD 253
+ KD++ L+ L +D
35 Sbjct: 263 IFGEM-----KDLLSTLISLKN D 280

RANK 6 ITERATION 0>pir|T45624 flavonoid 3'-hydroxylase-like protein
[imported] -

40 Arabidopsis thaliana >gi|6562313|emb|CAB62611.1|
(AL133421) flavonoid 3'-hydroxylase-like protein
[Arabidopsis thaliana] >gi|7330287|gb|AAF60189.1|
(AF241646) flavonoid 3'-hydroxylase [Arabidopsis thaliana]
>gi|8132328|gb|AAF73253.1|AF155171_1 (AF155171) flavonoid
3'-hydroxylase [Arabidopsis thaliana]
45 >gi|10334806|gb|AAG16745.1|AF271650_1 (AF271650)
flavonoid 3'-hydroxylase [Arabidopsis thaliana]

>gi|10334808|gb|AAG16746.1|AF271651_1 (AF271651)
 flavonoid 3'-hydroxylase [Arabidopsis thaliana]
 Length = 513

5 Score = 62.5 bits (149), Expect = 1e-009
 Identities = 30/80 (37%), Positives = 48/80 (59%)
 Frame = +2Query: 5
 AYQFKMMLDELFLNGVKNLGDWIPCLKYIDVQGYVKRMKVLGKKFDMF
 MEHVLDEHNAK 184

10 A +F+ M+ E+ L GV N+GD++P L ++D+QG +MK L K+FD F+ +L EH
 Sbjct: 200
 ADEFMSVMTEMMALAGVFNIGDFVPSLDWLDLQGVAGKMKRLHKKRFDFAF
 LSSILKEHEMN 259Query: 185 RENDKENWVPKDMVDVLLQL 244
 ++ K DM+ L+ L

15 Sbjct: 260 GQDQKHT----DMLSTLISL 275

RANK 7 ITERATION 0>sp|O04773|C756_CAMME FLAVONOID 3',5'-
HYDROXYLASE (F3'5'H) (CYTOCHROME
P450 75A6) >gi|1785488|dbj|BAA03440.1| (D14590) flavonoid
 20 3',5'-hydroxylase [Campanula medium]
 Length = 523

Score = 60.5 bits (144), Expect = 5e-009
 Identities = 28/83 (33%), Positives = 51/83 (60%)
 25 Frame = +2Query: 11
 QFKMMLDELFLNGVKNLGDWIPCLKYIDVQGYVKRMKVLGKKFDMFME
 HVLDEHNAKRE 190

+F+ M+ EL + G+ N+GD+IP + ++D+QG + MKV+ KKFD+ + ++ EH
 Sbjct: 219
 30 EFQYVMELMRMAGLFNIGDFIPYIAWMDLQGIQRDMKVIQKKFDVLLNK
 MIKEHTESAH 278Query: 191 NDKENWVPKDMVDVLLQLADDPT 259
 + K+N D +D+L+ + T
 Sbjct: 279 DRKDN---PDFLDILMAATQENT 298

35 RANK 8 ITERATION 0>sp|P48419|C753_PETHY FLAVONOID 3',5'-
HYDROXYLASE 2 (F3'5'H)
(CYTOCHROME P450 75A3) (CYPLXXVA3) >gi|629709|pir||S38984
flavonoid 3',5'-hydroxylase Hf2 - garden petunia
 40 >gi|311654|emb|CAA80265.1| (Z22544) flavonoid
 3',5'-hydroxylase [Petunia x hybrida]
 >gi|738771|prf||2001426A flavonoid 3',5'-hydroxylase
 [Petunia x hybrida]
 Length = 508

45 Score = 59.3 bits (141), Expect = 1e-008
 Identities = 32/81 (39%), Positives = 46/81 (56%)

Frame = +2Query: 11
QFKMMLDELFLNGVKNLGDWIPCLKYIDVQGYVKRMKVLGKKFDMFME
HVLDEHNAKRE 190

+FK M+ EL G N+GD+IPCL ++D+QG K MK L KKFD + + DEH A

5 Sbjct: 203

EFKDMVVELMTTAGYFNIGDFIPCLAWMDLQGIEKGMKRLHKKFDALLTK
MFDEHKATSY 262Query: 191 NDKENWVPKDMVDVLLQLADD 253

K D +D +++ D+

Sbjct: 263 ERKGK---PDFLDCVMENRDN 280

10

RANK 9 ITERATION 0>dbj|BAB09016.1| AB007645 cytochrome P450

[Arabidopsis thaliana]

Length = 496

15

Score = 57.4 bits (136), Expect = 4e-008

Identities = 32/89 (35%), Positives = 49/89 (54%)

Frame = +2Query: 11

QFKMMLDELFLNGVKNLGDWIPCLKYIDVQGYVKRMKVLGKKFDMFME
HVLDEHNAKRE 190

20

+ + + + E+F GV +GD++P LK D+ GY KR K L K D FM+ ++DEH R+

Sbjct: 203

EVRKLIREVDFAGVNYVGDFLPTLKLFDLDGYRKRAKKLASKLDKFMQKL
VDEH---RK 259Query: 191 NDKENWVPKDMVDVLLQLADDPTEVTQD 277

N + + K M+ LL L + T D

25

Sbjct: 260 NRGKAELEKTMITRLLSLQESEPECYTDD 288

RANK 10 ITERATION 0>dbj|BAA74465.1| AB022732 cytochrome P450

[Glycyrrhiza echinata]

Length = 499

30

Score = 57.4 bits (136), Expect = 4e-008

Identities = 30/82 (36%), Positives = 46/82 (55%)

Frame = +2Query: 5

AYQFKMMLDELFLNGVKNLGDWIPCLKYIDVQGYVKRMKVLGKKFDMF
MEHVLDEHNAK 184

35

A QF+ M+ EL L+G N D++P L+++D + KR+K + K D F+ ++ EH AK

Sbjct: 206

ASQFRDMVSELLQLSGANNKTDFMPLLRFLDFENLEKRLKDISGKTDAFLRG
LIQEHRAK 265Query: 185 RENDKENWVPKDMVDVLLQLAD 250

40

+E M+D LL L D

Sbjct: 266 KER-----ANTMIDHLLNLQD 281

RANK 11 ITERATION 0>sp|P93147|C81E_GLYEC CYTOCHROME P450 81E1
(ISOFLAVONE 2'-HYDROXYLASE)

45

(P450 91A4) (CYP GE-3) >gi|2443348|dbj|BAA22422.1|

(AB001379) cytochrome P450 [Glycyrrhiza echinata]

Length = 499

Score = 56.6 bits (134), Expect = 7e-008
Identities = 29/82 (35%), Positives = 46/82 (55%)

5 Frame = +2Query: 5

AYQFKMMLDELFLNGVKNLGDWIPCLKYIDVQGYVKRMKVLGKKFDMF
MEHVLDEHNAK 184

A QF+ M+ EL L+G N D++P L+++D + KR+K + K D F+ +++EH K

Sbjct: 206

10 ASQFRDMVSELLQLSGANNKTD FMP LLRFLDFENLEKRLKDISGKTDAFLRG
LIEHRTK 265Query: 185 RENDKENWVPKDMVDVLLQLAD 250

+E M+D LL L D

Sbjct: 266 KER-----ANTMIDHLLNLQD 281

15 RANK 12 ITERATION 0>emb|CAA09850.1| AJ011862 flavonoid 3',5'-
hydroxylase [Catharanthus

roseus]

Length = 512

20 Score = 55.8 bits (132), Expect = 1e-007
Identities = 30/81 (37%), Positives = 46/81 (56%)

Frame = +2Query: 11

QFKMMLDELFLNGVKNLGDWIPCLKYIDVQGYVKRMKVLGKKFDMFME
HVLDEHNAKRE 190

25 +FK M+ EL G N+GD+HP + ++D+QG + MK L KKFD + +L+EH +

Sbjct: 208

EFKDMVVELMTTAGYFNIGDFIPSIWMDLQGIERGGMKRLHKKFDALLTKM
LEEKSSSH 267Query: 191 NDKENWVPKDMVDVLLQLADD 253

KE D +D +L D+

30 Sbjct: 268 KRKEK---PDFLDYVLANRDN 285

RANK 13 ITERATION 0>emb|CAA04117.1| AJ000478 cytochrome P450
[Helianthus tuberosus]

Length = 520

35 Score = 55.4 bits (131), Expect = 2e-007
Identities = 27/80 (33%), Positives = 50/80 (61%)

Frame = +2Query: 11

40 QFKMMLDELFLNGVKNLGDWIPCLKYIDVQGYVKRMKVLGKKFDMFME
HVLDEHNAKRE 190

+F+ MLDE F+L G N+GD++P L ++ V+G K++ L +K D+F + ++D+ +

Sbjct: 220

RFRDMLDETFLVLAGASNVGDYLPVLSWLGVKGLEKKLIKLQEKRDVFFQGL
IDQLRKSKG 279Query: 191 NDKENWVPKDMVDVLLQLAD 250

45 + N K M+++LL L +

Sbjct: 280 TEDVN-KKKTMIELLLSLQE 298

RANK 14 ITERATION 0>pir|T10896 cytochrome P450 (EC 1.14.-.-) 81B1c -
Jerusalem artichoke

5 >gi|3059129|emb|CAA04116.1| (AJ000477) cytochrome P450
[Helianthus tuberosus]
Length = 505

Score = 55.4 bits (131), Expect = 2e-007
Identities = 27/80 (33%), Positives = 50/80 (61%)

10 Frame = +2Query: 11
QFKMMLDELFLNGVKNLGDWIPCLKYIDVQGYVKRMKVLGKKFDMFME
HVLDEHNAKRE 190
+F+ MLDE F+L G N+GD++P L ++ V+G K++ L +K D+F + ++D+ +
Sbjct: 205
15 RFRDMLDETFLVLAGASNVGDYLPVLSWLGVGKLEKKLIKLEKRDVFFQGL
IDQLRKSKG 264Query: 191 NDKENWVPKDMVDVLLQLAD 250
+ N K M+++LL L +
Sbjct: 265 TEDVN-KKKTMIELLLSLQE 283

20 RANK 15 ITERATION 0>gb|AAF97323.1|AC023628_4 AC023628 Putative
cytochrome P450
[Arabidopsis thaliana]
Length = 510

25 Score = 55.0 bits (130), Expect = 2e-007
Identities = 29/80 (36%), Positives = 45/80 (56%)
Frame = +2Query: 5
AYQFKMMLDELFLNGVKNLGDWIPCLKYIDVQGYVKRMKVLGKKFDMF
MEHVLDEHNAK 184
30 A +F + +LF L GV LGD++P +++D G K M+ +K+ D F ++DEH
Sbjct: 204
AQEFLHITHKLFWLLGVIYLG DYLPFWRWVDPSGCEKEMRDVEKRVDEFHT
KIIDEHRRRA 263Query: 185 RENDKENWVPKDMVDVLLQL 244
+ D++ D VDVLL L
35 Sbjct: 264 KLEDEKNGDMDFVDVLLSL 283

RANK 16 ITERATION 0>emb|CAB65335.1| AJ010324 ferulate-5-hydroxylase
[Populus
balsamifera subsp. trichocarpa]
40 Length = 513

Score = 54.7 bits (129), Expect = 3e-007
Identities = 30/83 (36%), Positives = 45/83 (54%), Gaps = 1/83 (1%)
Frame = +2Query: 11
45 QFKMMLDELFLNGVKNLGDWIPCLKYIDVQGYVKRMKVLGKKFDMFME
HVLDEHNAKR- 187

+F +L E L G N+ D+IP L +ID QG R+ K D F++H++D+H KR

Sbjct: 200

EFIKILQEFSKLF GAFNISDFIPWLGWIDPQGLTARLVKARKALDKFIDHIIDD
HIQKRK 259Query: 188 ENDKENWVPKDMVDVLLQLADDPT 259

5 +N+ DMVD +L +T

Sbjct: 260 QNNYSEEAETDMVDDMLTFYSEET 283

RANK 17 ITERATION 0>sp|P37119|C713_SOLME CYTOCHROME P450 71A3
(CYPLXXIA3) (P-450EG3)

10 >gi|480397|pir|S36807 cytochrome P450 71A3 - eggplant
(fragment) >gi|408142|emb|CAA50313.1| (X70982) P450
hydroxylase [Solanum melongena]
Length = 365

15 Score = 54.3 bits (128), Expect = 3e-007
Identities = 27/76 (35%), Positives = 48/76 (62%), Gaps = 2/76 (2%)
Frame = +2Query: 17 KMMLDELFLNGVKNLGDWIPCLKYID-
VQGYVKRMKVLGKKFDMFMHVLDEHNAKREN 193

K LD+ L G N+GD+IPCL++++ + G+ ++ + K D F+E V++ H + E

20 Sbjct: 193
KATLDKFVELLGTFNVGDYIPCLEWVNKITGFDSKVDKVAKDLDTFLEFVIE
AHMIRNEK 252Query: 194 DKEN-WVPKDMVDVLLQL 244

++ KD+VDVLL++

Sbjct: 253 EENRAGESKDLVDVLLEI 270

25 RANK 18 ITERATION 0>pir|J|C7172 cytochrome P450 CYP703A1 - garden
petunia

30 >gi|7339658|dbj|BAA92894.1| (AB006790) cytochrome P450
[Petunia x hybrida]
Length = 539

Score = 54.3 bits (128), Expect = 3e-007
Identities = 31/80 (38%), Positives = 45/80 (55%)
Frame = +2Query: 5

35 AYQFKMMLDELFLNGVKNLGDWIPCLKYIDVQGYVKRMKVLGKKFDMF
MEHVLDEHNAK 184

A +F + ELF L GV LGD++P ++ID G K+M++ K+ D F +++EH

Sbjct: 222

40 AMEFMHITHELFWLLGVIYLG DYLP LWRWIDPHGCEKKMREVEKRVDDFH
MRIIEEHRKN 281Query: 185 RENDKENWVPKDMVDVLLQL 244

+N E D VDVLL L

Sbjct: 282 GKNVDEG--EMDFVDVLLSL 299

45 RANK 19 ITERATION 0>sp|O04790|C757_EUSGR FLAVONOID 3',5'-
HYDROXYLASE (F3'5'H) (CYTOCHROME
P450 75A7) >gi|1785486|dbj|BAA03439.1| (D14589) flavonoid

3',5'-hydroxylase [Eustoma russellianum]
Length = 510

Score = 53.5 bits (126), Expect = 6e-007
5 Identities = 29/81 (35%), Positives = 46/81 (55%)
Frame = +2Query: 11
QFKMMLDELFLNGVKNLGDWIPCLKYIDVQGYVKRMKVLGKKFDMFME
HVLDEHNAKRE 190
+FK M+ EL + G N+GD+IP + ++D+QG MK L KKFD + +L+EH A
10 Sbjct: 207
EFKDMVVELMTVAGYFNIGDFIPSIWMDLQGIQGGMKRLHKKFDALLTRL
LEEHTASAH 266Query: 191 NDKENWVPKDMVDVLLQLADD 253
K + D +D ++ D+
Sbjct: 267 ERKGS---PDFLDFVVANGDN 284
15 RANK 20 ITERATION 0>sp|Q96418|C755_EUSGR FLAVONOID 3',5'-
HYDROXYLASE (F3'5'H) (CYTOCHROME
P450 75A5) >gi|1644388|gb|AAB17562.1| (U72654) flavonoid
3'5'-hydroxylase [Eustoma grandiflorum]
20 Length = 510

Score = 53.1 bits (125), Expect = 8e-007
Identities = 26/63 (41%), Positives = 38/63 (60%)
Frame = +2Query: 11
25 QFKMMLDELFLNGVKNLGDWIPCLKYIDVQGYVKRMKVLGKKFDMFME
HVLDEHNAKRE 190
+FK M+ EL + G N+GD+IP + ++D+QG MK L KKFD + +L+EH A
Sbjct: 207
EFKDMVVELMTVAGYFNIGDFIPSIWMDLQGIQGGMKRLHKKFDALLTRL
30 LEEHTASAH 266Query: 191 NDK 199
K
Sbjct: 267 ERK 269
[END
ALIGNMENTS]

35 Job DetailsReturn to top
[BEGIN JOB STATUS][BEGIN SEARCH TIME]
[END SEARCH TIME]
40 [VERSION]
[SEARCH ID]
[EOL] CRLF
[COMMENT] /Comment=NCBI BLASTX Translated Search
[COMMENT]
45 [ALGORITHM] BLASTX
[MATRIX] D:\DECYPHER\MATRIX\BLOSUM62.MAA
[QUERY FORMAT] FASTA/PEARSON

```

[QUERY TYPE] NT
[QUERY FILTER] T
[QUERY SEARCH] -1 -2 -3 1 2 3
[QUERY PATH] d:\decypher\query
5 [QUERY SET]
  [TARGET TYPE] AA
  [TARGET FRAMES] 1
  [TARGET PATH] d:\decypher\target\blast
  [TARGET SET] nr
10 [MAX SCORES] 30
  [MAX ALIGNMENTS] 20
  [THRESHOLD] 1
  [RESULT PATH] d:\decypher\output
  [OUTPUT FORMAT] TEXT EXTRACTALIGNED[SHOW GI] F
15 [EXPECTATION] 10
  [GAPPED ALIGNMENT] TBLASTX
  BLASTX
  Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
  Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
20 "Gapped BLAST and PSI-BLAST: a new generation of protein database search
  programs", Nucleic Acids Res. 25:3389-3402.Query= Your_Query starting with:
  GACTGCGTACCAATTCAAGA /QuerySize=283
    (283 letters)Database: Nonredundant Proteins
    598,029 sequences; 189,012,571 total letters Database: Nonredundant
25 Proteins
    Posted date:
    Number of letters in database: 189,012,571
    Number of sequences in database: 598,029

30 Lambda K H
    0.318 0.135 0.401 Gapped
    Lambda K H
    0.270 0.0470 0.230
    Matrix: BLOSUM62.MAA
35 Gap Penalties: Existence: 11, Extension: 1
    Number of Hits to DB: 94654798
    Number of Sequences: 598029
    Number of extensions: 1716287
    Number of successful extensions: 7679
40 Number of sequences better than 10.0: 218
    Number of HSP's better than 10.0 without gapping: 87
    Number of HSP's successfully gapped in prelim test: 107
    Number of HSP's that attempted gapping in prelim test: 7567
    Number of HSP's gapped (non-prelim): 196
45 length of query: 94
    length of database: 189,012,571

```


effective HSP length: 51
 effective length of query: 42
 effective length of database: 158,513,092
 effective search space: 6657549864
 5 effective search space used: 6657549864
 frameshift window, decay const: 50, 0.1
 T: 12
 A: 40
 X1: 16 (7.3 bits)
 10 X2: 38 (14.8 bits)
 X3: 64 (24.9 bits)
 S1: 41 (21.7 bits)
 S2: 64 (29.3 bits)[JOB MESSAGES][END JOB STATUS]

DeCypher Results for: NCBI TBLASTX Similarity Search

15 **Results by Query**

Click on a query below to view its search results.

Your Query starting with: GACTGCGTACCAATTCAAGA

Search Details

20 **Results for: Your_Query starting with:**

GACTGCGTACCAATTCAAGA; (Length=283)

[Return to query summary](#)

25	RANK	Sequences producing significant alignments:	(bits)	Value
	<u>1</u>	CL007624.91	144	1e-034
	<u>2</u>	CL015361.151	140	2e-033
	<u>3</u>	CL019611.148.126	138	8e-033
	<u>4</u>	CL007624.92	125	1e-028
30	<u>5</u>	CL025323.80	121	1e-027
	<u>6</u>	CL021721.82	119	7e-027
	<u>7</u>	CL009531.134	106	4e-023
	<u>8</u>	CL032856.12	59	8e-009
	<u>9</u>	CL015900.50	58	1e-008
35	<u>10</u>	CL025286.98.125	58	1e-008
	<u>11</u>	CL008331.186	56	7e-008
	<u>12</u>	CL036748.180	54	4e-007
	<u>13</u>	CL001913.295.181	53	5e-007
	<u>14</u>	CL026838.72	51	2e-006
40	<u>15</u>	CL011445.65	47	3e-005
	<u>16</u>	CL001029.99	46	6e-005
	<u>17</u>	CL008592.114.91	39	0.013
	<u>18</u>	CL019029.208.198	38	0.017
	<u>19</u>	CL019209.61	37	0.045

	20	CL013696.51	36	0.061
	21	CL002920.69	35	0.16
	22	CL032036.76.88	34	0.30
	23	CL002093.239.141	34	0.41
5	24	CL030746.151	33	0.57
	25	HTC040782-A01.43.49	33	0.57
	26	CL025232.91.106	33	0.57
	27	CL020770.308	33	0.78
	28	CL020786.235.37	33	0.78
10	29	CL019912.177.147	32	1.1
	30	CL004083.122	32	1.1

RANK 1 ITERATION 0>CL007624.91

Length = 4186

15

Score = 144 bits (310), Expect = 1e-034
Identities = 59/88 (67%), Positives = 72/88 (81%)
Frame = +2 / +3

Query: 5

20 AYQFKMMLDELFLNGVKNLGDWIPCLKYIDVQGYVKRMKVLGKKFDMF
MEHVLDEHNAK 184

A +FK MLDELFLNGV N+GD IP L ++D+QGY+KRMK LGK FD

F+EHV+DEHN +

Sbjct: 1443

25 AGEFKWMLDELFLNGVLNIGDSIPWLDWLDLQGYIKRMKKLGKMFDRFL
EHVVDEHNER 1622

Query: 185 RENDKENWVPKDMVDVLLQLADDPTLEV 268

R + E++V KDMVDVLLQ AD+P LEV

Sbjct: 1623 RRREGESFVAKDMVDVLLQFADNP NLEV 1706

30 Score = 34.1 bits (68), Expect(2) = 6e-010
Identities = 13/22 (59%), Positives = 19/22 (86%)
Frame = -2 / -1

Query: 270 VTSRVGSSASCNKTSTISLGTQ 205

+TSR+G SA+C+ TST+SL T+

35 Sbjct: 1708 LTSRLGLSANCSSTSTMSLTK 1643

Score = 48.7 bits (100), Expect(2) = 6e-010
Identities = 21/41 (51%), Positives = 25/41 (60%)
Frame = -2 / -1

Query: 135 LPKTFILFT*PCTSMYFKQGIQSPRFFTPFSKNNSSSIILN 13

40 LP FIL PC S G++SP TP S+N+SSSI LN

Sbjct: 1573 LPSFFILLMYPCRSSQSSHGMESPMLSTPLSRNSSSSIHLN 1451

RANK 2 ITERATION 0>CL015361.151

Length = 1168

45

Score = 140 bits (301), Expect = 2e-033

Identities = 55/89 (61%), Positives = 71/89 (78%)

Frame = +2 / -1

Query: 2

TAYQFKMMLDELFLNGVKNLGDWIPCLKYIDVQGYVKRMKVLGKKFDM

5 FMEHVLDEHNA 181

T +FK MLDEL L NGV N+GDWIP + ++D+QGYV+RMK +GK FD

FMEHVLDEH+

Sbjct: 892

TLSEFKWMLDELLXNGVLNVGDWIPWVDWMDLQGYVRRMKKVGKMFD

10 AFMEHVLDEHSE 713

Query: 182 KRENDKENWVPKDMVDVLLQLADDP TLEV 268

+R + E +V +DMVDVL+ LADDP+LE+

Sbjct: 712 RRRREGEAFVARDMVDVLM DLADDP SLEI 626

Score = 60.6 bits (126), Expect = 3e-009

15 Identities = 34/84 (40%), Positives = 38/84 (44%)

Frame = -2 / +3

Query: 264

SRVGSSASCNK TSTISLGTQXXXXXXXXXXXXXXXXXXXXXXXXXN FLPKTFILF

T*PCTSMYF 85

20 SR GSSA TST+SL T N LP FI T PC S+

Sbjct: 630

SREGSSARSMSTSTMSLATNASPSRRRRSLCSSRTC SMNASNILPTFFIRRTYP

CRSIQS 809

Query: 84 KQGIQSPRFFTPFSKNNSSSIILN 13

25 GIQSP TP ++SSSI LN

Sbjct: 810 THGIQSPTLRTPLXRRSSSSIHLN 881

RANK 3 ITERATION 0>CL019611.148.126

Length = 7888

30

Score = 138 bits (297), Expect = 8e-033

Identities = 55/89 (61%), Positives = 71/89 (78%)

Frame = +2 / -2

Query: 2

35 TAYQFKMMLDELFLNGVKNLGDWIPCLKYIDVQGYVKRMKVLGKKFDM

FMEHVLDEHNA 181

T +FKMM+DELFLL+GV N+GD+IP L ++D+QGY++RMK +GKK D

FMEHVLDEH+

Sbjct: 4995

40 TPEEFKMMMDELFLLSGVLNIGDFIPWLDWLDLQGYIRRMKRVGKKLDRF

MEHVLDEHDK 4816

Query: 182 KRENDKENWVPKDMVDVLLQLADDP TLEV 268

R ++ +D+VDVLLQLADDP LEV

Sbjct: 4815 VRRQQGDRFAARDLVDVLLQLADDP NLEV 4729

45 Score = 32.7 bits (65), Expect(2) = 2e-010

Identities = 14/18 (77%), Positives = 15/18 (82%)

Sbjct: 2298 FILRMYPGRSSQPNHGIESPMSSTPLSRKSSSIHLN 2188

RANK 5 ITERATION 0>CL025323.80

Length = 5241

5

Score = 121 bits (259), Expect = 1e-027
Identities = 47/89 (52%), Positives = 68/89 (75%)
Frame = +2 / +3

Query: 2

10 TAYQFKMMLDELFLNGVKNLGDWIPCLKYIDVQGYVKRMKVLGKKFDM
FMEHVLDEHNA 181

T +FK ML+ELFL+NGV N+GD+IP L ++D+QGY++RMK ++ F++

VLDEH+

Sbjct: 192

15 TPEEFKWMLEELFLMNGVLNIGDFIPWLDWLDLQGYIRRMKNVNRLIHRFL
DRVLDEHDE 371

Query: 182 KRENDKENWVPKDMVDVLLQLADDP TLEV 268

+R ++V +DMVD+LLQLADDP L+V

Sbjct: 372 RRRLQGDGFVARDMVDILLQLADDPNLDV 458

20 Score = 35.4 bits (71), Expect(2) = 5e-009
Identities = 14/21 (66%), Positives = 18/21 (85%)
Frame = -2 / -3

Query: 267 TSRVGSSASCNKTSTISLGTQ 205

TSR+GSSASC + ST+SL T+

25 Sbjct: 457 TSRLGSSASCKRMSTMSLATK 395

Score = 44.1 bits (90), Expect(2) = 5e-009
Identities = 19/37 (51%), Positives = 23/37 (61%)
Frame = -2 / -3

Query: 123 FILFT*PCTSMYFKQGIQSPRFFTPFSKNNSSSIHLN 13

30 FIL PC S G++SP TPF +N+SSSI LN

Sbjct: 313 FILLMYPGRSSQSSHGMKSPMLSTPFIRNSSSIHLN 203

RANK 6 ITERATION 0>CL021721.82

Length = 1880

35

Score = 119 bits (254), Expect = 7e-027
Identities = 45/85 (52%), Positives = 64/85 (74%)
Frame = +2 / -2

Query: 14

40 FKMMMLDELFLNGVKNLGDWIPCLKYIDVQGYVKRMKVLGKKFDMFMEH
VLDEHNAKREN 193

F+ M++E+F LNGV N+GD +P L ++D QGY+ RMK LG FD F+EH+LDEH

+R

Sbjct: 1501

45 FRWMIEEIFFLNGVFNIGDMVPWLGLDLPQGYIGRMKRLGGMFDRFLEHIL
DEHVERRRR 1322

RANK 8 ITERATION 0>CL032856.12

Length = 588

Score = 59.3 bits (123), Expect = 8e-009

5 Identities = 24/59 (40%), Positives = 39/59 (65%)

Frame = +2 / -3

Query: 5

AYQFKMMLDELFLNGVKNLGDWIPCLKYIDVQGYVKRMKVLGKKFDMF
MEHVLDEHNA 181

10 A +FK ++ E+ + GV N+GD++P L+++D QG V RMK L ++FD M ++ E A

Sbjct: 400

AREFKEIVLEVMEVGGVLNVGDFVPALRWLDPQGVVARMKKLHRRFDDM
MNAIIAERRA 224

Score = 38.6 bits (78), Expect = 0.013

15 Identities = 18/37 (48%), Positives = 22/37 (58%)

Frame = -2 / +3

Query: 123 FILFT*PCTSMYFKQGIQSPRFFTPFSKNNSSSIILN 13

FIL T PC S + G +SP F TP + SS+I LN

Sbjct: 282 FILATTPCGSSSHRSAGTKSPTFSTPPTSITSSTISLN 392

20

RANK 9 ITERATION 0>CL015900.50

Length = 4403

Score = 58.3 bits (121), Expect = 1e-008

25 Identities = 25/65 (38%), Positives = 39/65 (59%)

Frame = +2 / -3

Query: 5

AYQFKMMLDELFLNGVKNLGDWIPCLKYIDVQGYVKRMKVLGKKFDMF
MEHVLDEHNAK 184

30 A +F + ELF L G+ LGD++P +++D G K+M+ + KK D F + ++DEH

Sbjct: 1239

AMEFMHITHELFWLLGLIYLG DYLP AWRWLD PYGCEKKMREVEKKVDDFH
QKIIDEHRKA 1060

Query: 185 RENDK 199

35 RE K

Sbjct: 1059 REAKK 1045

Score = 36.8 bits (74), Expect = 0.045

Identities = 16/32 (50%), Positives = 19/32 (59%)

Frame = -3 / +3

40 Query: 125 PSFSSHNLVHQCTSNKVSNPQDSSLHLVRTIH 30

PS SSH + Q TS S+PQD S RT+H

Sbjct: 1119 PSSSSH THMDQATSRLASSPQDRSGPAARTVH 1214

45

RANK 10 ITERATION 0>CL025286.98.125

Length = 9900

R+
Sbjct: 675 RK 670

RANK 13 ITERATION 0>CL001913.295.181

5 Length = 3006

Score = 53.3 bits (110), Expect = 5e-007
Identities = 22/63 (34%), Positives = 36/63 (56%)
Frame = +2 / -1

10 Query: 5
AYQFKMMLDELFLNGVKNLGDWIPCLKYIDVQGYVKRMKVLGKKFDMF
MEHVLDEHNAK 184

A +FK +LDEL L G NL D++P L+ DV G +++ L + D F+ ++D +

Sbjct: 2823

15 AQEFKNVLDELNPLLGAANLWDYLPALRVFDVLGVKRKIATLANRRDAFV
RRLIDAERQR 2644

Query: 185 REN 193

+N

Sbjct: 2643 MDN 2635

20

RANK 14 ITERATION 0>CL026838.72

Length = 1254

Score = 51.5 bits (106), Expect = 2e-006
25 Identities = 23/81 (28%), Positives = 43/81 (52%)
Frame = +2 / -2

Query: 17
KMMLDELFLNGVKNLGDWIPCLKYIDVQGYVKRMKVLGKKFDMFMEHV
LDEHNAKREND 196

30 +++L E L G N+GD+IP L ++D G +R++ D ++ ++DEH + D

Sbjct: 860

EVLLQEFSKLFGAFNVGDFIPWLAWLDPHGINRRLRAARAALDSVIDRIIDEH
VSNPAGD 681

Query: 197 KENWVPKDMVDVLLQLADDPT 259

35 ++ + DM+ L + D T

Sbjct: 680 EDADMVDDMLAFLDEAGRDT 618

RANK 15 ITERATION 0>CL011445.65

Length = 1851

40

Score = 47.3 bits (97), Expect = 3e-005
Identities = 20/61 (32%), Positives = 32/61 (51%)
Frame = +2 / +3

Query: 11
45 QFKMMLDELFLNGVKNLGDWIPCLKYIDVQGYVKRMKVLGKKFDMFME
HVLDEHNAKRE 190

Sbjct: 11041
EFRELVADITELLGAPNVSDFFPALAPLDIQGIRNKSDLLKDRFDDIFARIQKR
TESDH 11220

Query: 191 NDKENWVPKDMVDVLLQL 244

5 D ++ +L+L

Sbjct: 11221 AAAAGETASDFLEYMLKL 11274

Score = 29.9 bits (59), Expect = 5.2

Identities = 8/23 (34%), Positives = 12/23 (51%)

Frame = +1 / -2

10 Query: 181 *KRK*QGKLGS*RYGGCFVTTC* 249

+R+ QG R+GGC + C

Sbjct: 10486 QRRREQGGXEQHRWGGCHLHDCQ 10418

RANK 19 ITERATION 0>CL019209.61

15 Length = 2040

Score = 36.8 bits (74), Expect = 0.045

Identities = 14/39 (35%), Positives = 25/39 (63%)

Frame = +2 / -1

20 Query: 5 AYQFKMMLDELFLNGVKNLGDWIPCLKYIDVQGYVKRM 121

A +FK ++DE+ G NL D++P L++ DV G +++

Sbjct: 324 AQEFKQVVDEIIPHIGAANLWDYLPALRWFDVFGVRRKI 208

RANK 20 ITERATION 0>CL013696.51

25 Length = 3522

Score = 36.3 bits (73), Expect = 0.061

Identities = 15/45 (33%), Positives = 25/45 (55%)

Frame = -1 / -2

30 Query: 220 IFRNPIFLVIFSFSIMFI*YMLHKHIKFLTQNLHSLHITLYINVL 86

+F +F +I FS +LH HIKF LH L++ +++ +L

Sbjct: 2147 VFYMIVFYIILKFSCPLFLVLLHTHIKFSMVLLHILNVPVFLFLL
2013

[END

35 ALIGNMENTS]

Job Details[Return to top](#)

[BEGIN JOB STATUS][BEGIN SEARCH TIME]

40 [END SEARCH TIME]

[VERSION]

[SEARCH ID]

[EOL] CRLF

[COMMENT] /Comment=NCBI TBLASTX Similarity Search

45 [COMMENT]

[ALGORITHM] TBLASTX

[MATRIX] D:\DECYPHER\MATRIX\BLOSUM62.MAA

[END JOB STATUS]

DeCypher Results for: NCBI BLASTX Translated Search

Results by Query

Click on a query below to view its search results.

Your Query starting with: TGACTGCGTACCAATTCGAT

5

Search Details

Results for: Your Query starting with:

TGACTGCGTACCAATTCGAT; (Length=285)

10 [Return to query summary](#)

RANK		Sequences producing significant alignments:		(bits)	Value
	<u>1</u>	emb CAA05625.1	AJ002584	AtMRP4 [Arabidopsis thaliana]	>gi 37... 52 2e-006
15	<u>2</u>	gb AAC49797.1	U96399	MRP-like ABC transporter [Arabidopsis t...	52 2e-006
	<u>3</u>	pir T48059	ABC transporter-like protein - Arabidopsis thaliana... 46 1e-004		
	<u>4</u>	pir T00961	hypothetical protein F20D22.11 - Arabidopsis thalia... 36 0.086		
	<u>F5</u>	emb CAA72120.1	Y11250	multi resistance protein [Arabidopsis ...	36 0.086
20	<u>6</u>	sp P07653 PSTC	ECOLI PHOSPHATE TRANSPORT SYSTEM PERMEASE PROTEI... 33 0.75		
	<u>7</u>	dbj BAA22862.1	D89963	peripheral membrane protein C [Enterob...	33 0.98
25	<u>8</u>	sp Q10064 YAMB	SCHPO HYPOTHETICAL 420.8 KD PROTEIN C1F5.11C IN ... 33 0.98		
	<u>9</u>	gb AAF49311.1	AE003523	CG13735 gene product [Drosophila mela...	32 1.3
	<u>10</u>	pir T47840	multi resistance protein homolog - Arabidopsis thal... 32 2.2		
30	<u>11</u>	pir T50518	ABC transporter-like protein - Arabidopsis thaliana... 32 2.2		
	<u>12</u>	dbj BAB01399.1	AP000375	multidrug resistance-associated prot...	31 3.8
	<u>13</u>	gb AAC49791.1	U92650	MRP-like ABC transporter [Arabidopsis t...	31 3.8
	<u>14</u>	gb AAB54099.1	U67264	AcMNPV ORF5/Ep23 homolog [Helicoverpa z...	31 5.0
35	<u>15</u>	gb AAA52815.1	M12870	immunoglobulin heavy chain [Homo sapiens]	30 6.5
	<u>16</u>	dbj BAA11312.1	D78208	light-independent protochlorophyllide ...	30 8.5
	<u>17</u>	ref NP_050154.1	hypothetical protein [Lactobacillus bacterioph... 30 8.5		
40	<u>18</u>	pir T32795	hypothetical protein F14D2.3 - Caenorhabditis eleg... 30 8.5		

RANK 1 ITERATION 0>emb|CAA05625.1| AJ002584 AtMRP4 [Arabidopsis thaliana]

>gi|3738292|gb|AAC63634.1| (AC005309)

glutathione-conjugate transporter AtMRP4 [Arabidopsis
thaliana] >gi|7716583|gb|AAF68441.1|AF243509_1 (AF243509)
MRP4 [Arabidopsis thaliana]
Length = 1516

5

Score = 51.9 bits (122), Expect = 2e-006
Identities = 24/31 (77%), Positives = 29/31 (93%)
Frame = +3Query: 6 AYQFDSPARLLDRPSIFAALVQEYANRSSGL 98
A +FDSPARLL+RPS+FAALVQEYA RS+G+

10 Sbjct: 1486 AKEFDSPARLLERPSLFAALVQEYALRSAGI 1516

RANK 2 ITERATION 0>gb|AAC49797.1| U96399 MRP-like ABC transporter
[Arabidopsis
thaliana]
15 Length = 245

Score = 51.9 bits (122), Expect = 2e-006
Identities = 24/31 (77%), Positives = 29/31 (93%)
Frame = +3Query: 6 AYQFDSPARLLDRPSIFAALVQEYANRSSGL 98
20 A +FDSPARLL+RPS+FAALVQEYA RS+G+

Sbjct: 215 AKEFDSPARLLERPSLFAALVQEYALRSAGI 245

RANK 3 ITERATION 0>pir|T48059 ABC transporter-like protein - Arabidopsis
thaliana

25 >gi|7362750|emb|CAB83120.1| (AL162651) ABC
transporter-like protein [Arabidopsis thaliana]
Length = 1539

Score = 46.1 bits (107), Expect = 1e-004
30 Identities = 21/31 (67%), Positives = 27/31 (86%)
Frame = +3Query: 6 AYQFDSPARLLDRPSIFAALVQEYANRSSGL 98
A ++DSP RLL+R S+FAALVQEYA RS+G+
Sbjct: 1509 AKEYDSPVRLLERQSLFAALVQEYALRSAGI 1539

35 RANK 4 ITERATION 0>pir|T00961 hypothetical protein F20D22.11 - Arabidopsis
thaliana

>gi|3142303|gb|AAC16754.1| (AC002411) Strong similarity to
MRP-like ABC transporter gb|U92650 from A. thaliana and
canalicular multi-drug resistance protein gb|L49379 from
40 Rattus norvegicus. [Arabidopsis thaliana]
Length = 1355

Score = 36.4 bits (82), Expect = 0.086
Identities = 17/29 (58%), Positives = 25/29 (85%), Gaps = 1/29 (3%)
45 Frame = +3Query: 12 QFDSPARLL-DRPSIFAALVQEYANRSSGL 98
+FD+PARLL D+ S+F LV EY++RS+G+

Sbjct: 1323 EFDTPARLLEDKSSMFLKLVTEYSSRSTGI 1352

RANK 5 ITERATION 0>emb|CAA72120.1| Y11250 multi resistance protein
[Arabidopsis

5 thaliana] >gi|10197658|gb|AAG14965.1|AF225908_1 (AF225908)
sulfonylurea receptor-like protein [Arabidopsis thaliana]
Length = 1514

Score = 36.4 bits (82), Expect = 0.086

10 Identities = 17/29 (58%), Positives = 25/29 (85%), Gaps = 1/29 (3%)
Frame = +3Query: 12 QFDSPARLL-DRPSIFAALVQEYANRSSGL 98
+FD+PARLL D+ S+F LV EY++RS+G+

Sbjct: 1482 EFDTPARLLEDKSSMFLKLVTEYSSRSTGI 1511

15 RANK 6 ITERATION 0>sp|P07653|PSTC_ECOLI PHOSPHATE TRANSPORT
SYSTEM PERMEASE PROTEIN PSTC

>gi|7429019|pir|BVECPW phosphate transport system
permease protein pstC - Escherichia coli
20 >gi|42396|emb|CAA26507.1| (X02723) phoW gene product (aa
1-319) [Escherichia coli] >gi|147257|gb|AAA24379.1|
(K01992) peripheral membrane protein C [Escherichia coli]
>gi|290575|gb|AAA62078.1| (L10328) peripheral membrane
protein C [Escherichia coli] >gi|1790164|gb|AAC76750.1|
25 (AE000449) high-affinity phosphate-specific transport
system, cytoplasmic membrane component [Escherichia coli
K12]
Length = 319

Score = 33.2 bits (74), Expect = 0.75

30 Identities = 23/69 (33%), Positives = 34/69 (48%)
Frame = +3Query: 9
YQFDSPARLLDRPSIFAALVQEYANRSSGL*SSV*NLYNSHALMKLPLKMNA
LSFRVYVA 188

YQ DS + + SI +AL E+A SGL + ALM+L L + ++F V A
35 Sbjct: 253 YQLDSASLYMPGNSITSALANEFAEAESGLHVA-----
ALMELGLILFVITFIVLAA 304Query: 189 CPLMFLSLS 215
M + L+

Sbjct: 305 SKFMIMRLA 313

40 RANK 7 ITERATION 0>dbj|BAA22862.1| D89963 peripheral membrane protein
C [Enterobacter
cloacae]
Length = 319

45 Score = 32.8 bits (73), Expect = 0.98
Identities = 23/69 (33%), Positives = 34/69 (48%)

Frame = +3Query: 9
YQFDSPARLLDRPSIFAALVQEYANRSSGL*SSV*NLYNSHALMKLPLKMNA
LSFRVYVA 188

YQ DS + + SI+AL E+A SGL + ALM+L L + ++F V
5 Sbjct: 253 YQLDSASLYMPGNSITSALANEFAEAEESGLHVA-----
ALMELGLILFVITFIVLAI 304Query: 189 CPLMFLSLS 215
LM + L+
Sbjct: 305 SKLMIMRLA 313

10 RANK 8 ITERATION 0>sp|Q10064|YAMB_SCHPO HYPOTHETICAL 420.8 KD
PROTEIN C1F5.11C IN

CHROMOSOME I >gi|7493522|pir|T38084 TRAP-like protein -
fission yeast (Schizosaccharomyces pombe)
15 >gi|1103738|emb|CAA92239.1| (Z68136) TRAP-like protein
[Schizosaccharomyces pombe]
Length = 3655

Score = 32.8 bits (73), Expect = 0.98
Identities = 14/35 (40%), Positives = 22/35 (62%)

20 Frame = +3Query: 102 SSV*NLYNSHALMKLPLKMNALSFVRVYVACPLMFL
206

S + NS A+ PL+++ SFRVYV CP++ +
Sbjct: 184 SIIQQRVNSLAISTQPLELASQSFRVYVECPVIIV 218

25 RANK 9 ITERATION 0>gb|AAF49311.1| AE003523 CG13735 gene product
[Drosophila
melanogaster]
Length = 179

30 Score = 32.5 bits (72), Expect = 1.3
Identities = 13/59 (22%), Positives = 25/59 (42%)
Frame = -2Query: 239
SY*SKHRHAQAQEHQRTCNVNSER*SIHFQRKFHQCMVVEISD*RLQTR*A
ICVFLYQ 63

35 ++ K A + HQR + H RK H+C ++ + R++ + LY+
Sbjct: 75
THKRKQHRAHSHSHQRYHHHKEHEEPAHRIRKGHECRSIQRLGPARIRLGE
CVSRKLYR 133

40 RANK 10 ITERATION 0>pir|T47840 multi resistance protein homolog -
Arabidopsis thaliana
>gi|7076769|emb|CAB75931.1| (AL138658) multi resistance
protein homolog [Arabidopsis thaliana]
45 Length = 1490

Score = 31.7 bits (70), Expect = 2.2

Identities = 16/32 (50%), Positives = 23/32 (71%), Gaps = 1/32 (3%)
 Frame = +3Query: 12 QFDSPARLLDR-PSIFAALVQEYANRSSGL*SS 107
 +FDSPA+LL R S F+ L++EY+ RS+ S
 Sbjct: 1453 EFDSPAKLLQREDSFFSKLIKEYSLRSNHFAGS 1485

5

RANK 11 ITERATION 0>pir|T50518 ABC transporter-like protein - Arabidopsis thaliana

>gi|8388613|emb|CAB94133.1| (AL358732) ABC transporter-like protein [Arabidopsis thaliana]

10

Length = 1037

Score = 31.7 bits (70), Expect = 2.2

Identities = 16/32 (50%), Positives = 23/32 (71%), Gaps = 1/32 (3%)

Frame = +3Query: 12 QFDSPARLLDR-PSIFAALVQEYANRSSGL*SS 107

15

+FDSPA+LL R S F+ L++EY+ RS+ S

Sbjct: 1000 EFDSPAKLLQREDSFFSKLIKEYSLRSNHFAGS 1032

RANK 12 ITERATION 0>dbj|BAB01399.1| AP000375 multidrug resistance-associated protein

20

(MRP); ABC-transporter [Arabidopsis thaliana]

Length = 1514

Score = 30.9 bits (68), Expect = 3.8

Identities = 15/27 (55%), Positives = 21/27 (77%), Gaps = 1/27 (3%)

25

Frame = +3Query: 12 QFDSPARLL-DRPSIFAALVQEYANRSS 92

++D+P RLL D+ S F+ LV EY +RSS

Sbjct: 1483 EYDTPVRLLEDKSSSFSLVAEYTSRSS 1510

RANK 13 ITERATION 0>gb|AAC49791.1| U92650 MRP-like ABC transporter [Arabidopsis thaliana]

30

Length = 1515

Score = 30.9 bits (68), Expect = 3.8

Identities = 15/27 (55%), Positives = 21/27 (77%), Gaps = 1/27 (3%)

35

Frame = +3Query: 12 QFDSPARLL-DRPSIFAALVQEYANRSS 92

++D+P RLL D+ S F+ LV EY +RSS

Sbjct: 1484 EYDTPVRLLEDKSSSFSLVAEYTSRSS 1511

RANK 14 ITERATION 0>gb|AAB54099.1| U67264 AcMNPV ORF5/Ep23 homolog [Helicoverpa zea

40

nuclear polyhedrosis virus]

Length = 183

Score = 30.5 bits (67), Expect = 5.0

45

Identities = 18/68 (26%), Positives = 32/68 (46%), Gaps = 6/68 (8%)

Frame = +1Query: 73 NTQIAHLVCSLQS-----
 EISTTAMH**NFL*K*MLYRSEFTLHVL*CS*A*A*RCFDQ 234
 NT I LV +S +STT N + + + F L + S +CF +

Sbjct: 46

- 5 NTVITKLVS GHESGRNVSMNMSTTESWGENIIRDDVFIITMFRLPFVARSLIE
 DEKCFSR 105Query: 235 *LLMMNVSHGHFTQ 276
 +L++ V ++ T+

Sbjct: 106 PVLLLAVDYNNSTE 119

- 10 RANK 15 ITERATION 0>gb|AAA52815.1| M12870 immunoglobulin heavy chain
 [Homo sapiens]
 Length = 136

Score = 30.1 bits (66), Expect = 6.5

- 15 Identities = 17/53 (32%), Positives = 24/53 (45%), Gaps = 8/53 (15%)
 Frame = -3Query: 193 GHAT*TLNDKAFIFRGSFINAWLL*R-----
 FQTEDYRPDERFAYSCTSAANIDGLS 38
 GH A IFR S +++ R Q + RPD+ Y CT ++ L

Sbjct: 68

- 20 GHIEEKSKKYATIFRASVKGRFIISRDDSKNTAFLQMDSLRLPDDTALYYCTPP
 PEVESLR 127Query: 37 S 35
 S

Sbjct: 128 S 128

- 25 RANK 16 ITERATION 0>dbj|BAA11312.1| D78208 light-independent
 protochlorophyllide
 reductase subunit [Plectonema boryanum]
 Length = 508

- 30 Score = 29.7 bits (65), Expect = 8.5
 Identities = 12/38 (31%), Positives = 20/38 (52%), Gaps = 1/38 (2%)
 Frame = -1Query: 285 **VLSKMAV*DVH-H**LLIKTPSCSSRTSEDMQRKL*
 172

V+ + D H L++ TP+C+SS ED+Q +

- 35 Sbjct: 71 EKVVDNITRKDAEEHPDLIVLTPTCTSSILQEDLQNFVE 109

RANK 17 ITERATION 0>ref|NP_050154.1| hypothetical protein [Lactobacillus
 bacteriophage

- 40 phi adh] >gi|5730303|emb|CAB52524.1| (AJ131519)
 hypothetical protein [Lactobacillus bacteriophage phi
 adh]
 Length = 159

Score = 29.7 bits (65), Expect = 8.5

- 45 Identities = 14/41 (34%), Positives = 24/41 (58%)

Frame = +1Query: 7
RTNSIHQQGYSGHYSQHWYKNTQIAHLVCSLQSEISTTA 129
R+N I+++G S GH ++H +N + HL S+ + TA
Sbjct: 48 RSNEIYRRGRSAGHANAKHHNRNRKTKHLQDSITYKPGYTA 88

5
RANK 18 ITERATION 0>pir|[T32795 hypothetical protein F14D2.3 -
Caenorhabditis elegans
>gi|2746792|gb|AAB94957.1| (AF040643) F14D2.3 gene
product [Caenorhabditis elegans]
10 Length = 138

Score = 29.7 bits (65), Expect = 8.5
Identities = 18/55 (32%), Positives = 33/55 (59%)
Frame = +2Query: 53
15 IRSTGTRIRKSLIWSVVFSLKSLQQPCIDETSSNECFIVQSLRCMSSDVLELEH
217
I++TG RK L ++ F+L++L+Q CI S F ++S+ + SD+ ++H
Sbjct: 74 IQTTGKTYRKKLQMAIKFNLENLKQFCISMIKSP---FDLRSM--
IPSDISSIDH 123
20 [END
ALIGNMENTS]

Job DetailsReturn to top

25 [BEGIN JOB STATUS][BEGIN SEARCH TIME]
[END SEARCH TIME]
[VERSION]
[SEARCH ID]
[EOL] CRLF
30 [COMMENT] /Comment=NCBI BLASTX Translated Search
[COMMENT]
[ALGORITHM] BLASTX
[MATRIX] D:\DECYPHER\MATRIX\BLOSUM62.MAA
[QUERY FORMAT] FASTA/PEARSON
35 [QUERY TYPE] NT
[QUERY FILTER] T
[QUERY SEARCH] -1 -2 -3 1 2 3
[QUERY PATH] d:\decypher\query
[QUERY SET]
40 [TARGET TYPE] AA
[TARGET FRAMES] 1
[TARGET PATH] d:\decypher\target\blast
[TARGET SET] nr
[MAX SCORES] 30
45 [MAX ALIGNMENTS] 20
[THRESHOLD] 1
[RESULT PATH] d:\decypher\output

[OUTPUT FORMAT] TEXT EXTRACTION[SHOW GI] F
[EXPECTATION] 10
[GAPPED ALIGNMENT] TBLASTX
BLASTX

5 Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs", Nucleic Acids Res. 25:3389-3402. Query= Your_Query starting with:
TGACTGCGTACCAATTCGAT /QuerySize=285
10 (285 letters) Database: Nonredundant Proteins
598,029 sequences; 189,012,571 total letters Database: Nonredundant
Proteins
Posted date:
Number of letters in database: 189,012,571
15 Number of sequences in database: 598,029

Lambda K H
0.318 0.135 0.401 Gapped
Lambda K H
20 0.270 0.0470 0.230
Matrix: BLOSUM62.MAA
Gap Penalties: Existence: 11, Extension: 1
Number of Hits to DB: 86556766
Number of Sequences: 598029
25 Number of extensions: 1357127
Number of successful extensions: 6247
Number of sequences better than 10.0: 36
Number of HSP's better than 10.0 without gapping: 6
Number of HSP's successfully gapped in prelim test: 12
30 Number of HSP's that attempted gapping in prelim test: 6239
Number of HSP's gapped (non-prelim): 20
length of query: 95
length of database: 189,012,571
effective HSP length: 51
35 effective length of query: 43
effective length of database: 158,513,092
effective search space: 6816062956
effective search space used: 6816062956
frameshift window, decay const: 50, 0.1
40 T: 12
A: 40
X1: 16 (7.3 bits)
X2: 38 (14.8 bits)
X3: 64 (24.9 bits)
45 S1: 41 (21.7 bits)
S2: 65 (29.7 bits)[JOB MESSAGES][END JOB STATUS]

(285 letters)
 154,797 sequences; 359,911,985 total
 lettersSearching.....done
 Score E

5	Sequences producing significant alignments:	(bits)
	ValueCL005514.235.73	54 4e-07
	CL017067.119.107	54 4e-07
	CL021124.142.90	48 2e-05
	CL005241.277	34 0.42
10	CL022869.215	33 0.80
	CL022777.26	32 1.1
	CL015161.192	31 2.1
	CL027994.236	31 2.1
	CL001686.94	31 2.8
15	CL025797.154	31 2.8
	CL000509.194.78	31 2.8
	CL005712.59	30 3.9
	CL002590.139	30 5.4
	CL035905.67.57	30 5.4
20	HTC140261-A01.F.2.2	30 5.4
	CL018884.101	30 5.4
	HTC165966-B01.1.5	30 5.4
	CL018884.120	30 5.4
	CL000457.166	30 5.4
25	CL001598.125	29 7.4
	CL035968.22	29 7.4
	CL034646.55	29 7.4
	HTC141515-B01.1.1	29 7.4
	CL032445.130	29 7.4
30	CL030763.69	29 7.4
	CL005468.514.236	29 7.4
	CL035638.67.72	29 7.4
	CL008852.230	29 7.4>CL005514.235.73

Length = 4387

35

Score = 53.8 bits (111), Expect = 4e-07
 Identities = 22/32 (68%), Positives = 27/32 (83%)
 Frame = +3 / +2
 Query: 6 AYQFDSPARLLDRPSIFAALVQEYANRSSGL* 101
 A +FDSPA L++RPS+F ALVQEYA RSS +*

40

Sbjct: 1727 AKEFDSPANLIERPSLFGALVQEYATRSSDI* 1822
 Score = 38.6 bits (78), Expect = 0.013
 Identities = 18/32 (56%), Positives = 21/32 (65%)
 Frame = -3 / -2

45

Query: 100 YRPDERFAYSCTSAANIDGLSSNLAGESNWWYA 5
 Y D+R AYS T+A N DGLS AG SN +A

Sbjct: 1821 YISDDRVAYS*TNAPNSDGLSIRFAGLSNSFA 1726
>CL017067.119.107
Length = 7172

5 Score = 53.8 bits (111), Expect = 4e-07
Identities = 20/30 (66%), Positives = 28/30 (92%)
Frame = +3 / -1

Query: 12 QFDSPARLLDRPSIFAALVQEYANRSSGL* 101
+FDSP+RL+++PS+F A+V+EYANRSS L*

10 Sbjct: 413 EFDSPSRLIEQPSLFGAMVEEYANRSSNL* 324
Score = 45.5 bits (93), Expect = 1e-04
Identities = 20/34 (58%), Positives = 21/34 (60%)
Frame = -3 / +1

Query: 115 FQTEDYRPDERFAYSCTSAANIDGLSSNLAGESN 14

15 + YR DER AYS T A N DG S NL GESN

Sbjct: 310 YNRRSYRLDERLAYSSSTIAPNRDGCINLEGESN 411
>CL021124.142.90
Length = 5069

20 Score = 47.8 bits (98), Expect = 2e-05
Identities = 17/26 (65%), Positives = 23/26 (88%)
Frame = +3 / +1

Query: 12 QFDSPARLLDRPSIFAALVQEYANRS 89
+FD P++L+ RPS+F A+VQEYANRS

25 Sbjct: 3328 EFDEPSKLMGRPSLFRAMVQEYANRS 3405
Score = 34.1 bits (68), Expect = 0.31
Identities = 16/25 (64%), Positives = 16/25 (64%)
Frame = -3 / -1

Query: 88 ERFAYSCTSAANIDGLSSNLAGESN 14

30 ERFAYS T A DGL NL G SN

Sbjct: 3404 ERFAYS*TIARKSDGLPINLDGSSN 3330
>CL005241.277
Length = 12632

35 Score = 33.6 bits (67), Expect = 0.42
Identities = 11/28 (39%), Positives = 19/28 (67%)
Frame = +3 / +1

Query: 129 HALMKLPLKMNALSFRVYVACPLMFLSL 212
HA+ LP++ N ++ R++VA PL F +

40 Sbjct: 10003 HAIKNLPIQKNVITIRLFVAVPLEFYKI 10086
>CL022869.215
Length = 6750

Score = 32.7 bits (65), Expect = 0.80
45 Identities = 15/50 (30%), Positives = 24/50 (48%)
Frame = +2 / +2

Query: 77
RKSLIWSVVFSLSLQQPCIDETSSSENECFIVQSLRCMSSDVLELEHHDGV 226
R + W++ L L+ C S+E++C +V S S L LEH +

Sbjct: 4664

5 RNPVSWTLKSLLPDLKPCCQYHISTESDCLVVHSCCLRGSGQLLLEHQSI
4813

>CL022777.26

Length = 1950

10 Score = 32.2 bits (64), Expect = 1.1
Identities = 13/19 (68%), Positives = 15/19 (78%)
Frame = -1 / +1

Query: 171 TIKHSFSEEVSSMHGCCRD 115

TI +S S+EVSSMH C RD

15 Sbjct: 1132 TILNSQSDEVSSMHACSRD 1188

>CL015161.192

Length = 3663

Score = 31.3 bits (62), Expect = 2.1
20 Identities = 13/29 (44%), Positives = 19/29 (64%)
Frame = -1 / +3

Query: 87 SDLRILVPVLRILMAYRVTLNVRIGTQS 1

S L+ L+P+LR+ ++ VTL N I T S

Sbjct: 1974 SPLQALIPILRLRLSTMVTLTTNMISTTS 2060

25 >CL027994.236

Length = 2149

Score = 31.3 bits (62), Expect = 2.1
Identities = 12/29 (41%), Positives = 18/29 (61%)
30 Frame = +3 / -3

Query: 126 SHALMKLPLKMNALSFRVYVACPLMFLSL 212

SHA+ LP+ N ++ R+YVA L F +

Sbjct: 1562 SHAITNLP I*KNITIRLYVAVTLKIFYKI 1476

>CL001686.94

35 Length = 1661

Score = 30.8 bits (61), Expect = 2.8
Identities = 9/28 (32%), Positives = 18/28 (64%)
Frame = +3 / +3

40 Query: 129 HALMKLPLKMNALSFRVYVACPLMFLSL 212

HA+ LP++ ++ R+++A PL F +

Sbjct: 1326 HAIANLP IQKKTITIRLFIAVPLKIFYKI 1409

>CL025797.154

Length = 4730

45 Score = 30.8 bits (61), Expect = 2.8

DESCA11 Blast result against nonredundant proteins

DeCypher Results for: NCBI BLASTX Translated Search

Results by Query

Click on a query below to view its search results.

5 Your Query starting with: CACTGCANCACATGATCTTG

Search Details

Results for: Your_Query starting with:

10 **CACTGCANCACATGATCTTG; (Length=297)**

[Return to query summary](#)

	RANK	Sequences producing significant alignments:	(bits)	Value
15	<u>1</u>	pir <u>T04209</u> hypothetical protein T5C23.50 - Arabidopsis thalian...	123	7e-028
	<u>2</u>	pir <u>T00958</u> hypothetical protein F20D22.8 - Arabidopsis thalian...	95	2e-019
	<u>3</u>	gb <u>AAF18518.1</u> <u>AC006551_4</u> <u>AC006551</u> Highly similar to phosphori...	86	9e-017
20	<u>4</u>	pir <u>T47922</u> anthranilate phosphoribosyltransferase-like protein...	83	8e-016
	<u>5</u>	gb <u>AAF15942.1</u> <u>AC011765_38</u> <u>AC011765</u> putative phosphoribosylant...	82	1e-015
	<u>6</u>	gb <u>AAD55273.1</u> <u>AC008263_4</u> <u>AC008263</u> Similar to gb D86180 phosph...	82	1e-015
25	<u>7</u>	gb <u>AAF03465.1</u> <u>AC009327_4</u> <u>AC009327</u> putative phosphoribosylanth...	70	8e-012
	<u>8</u>	dbj <u>BAB08397.1</u> <u>AB015473</u> phosphoribosylanthranilate transfera...	62	1e-009
30	<u>9</u>	dbj <u>BAB11070.1</u> <u>AB017064</u> phosphoribosylanthranilate transfera...	62	1e-009
	<u>10</u>	pir <u>T01234</u> probable anthranilate phosphoribosyltransferase (EC...	59	1e-008
	<u>11</u>	dbj <u>BAB15311.1</u> <u>AK025997</u> unnamed protein product [Homo sapiens]	50	6e-006
35	<u>12</u>	pir <u>T00634</u> hypothetical protein H_DJ0897G10.1 - human >gi 2822...	50	7e-006
	<u>13</u>	emb <u>CAA73554.1</u> <u>Y13100</u> Serine/Threonine protein kinase [Sycon...	49	1e-005
	<u>14</u>	ref <u>NP_035232.1</u> protein kinase C, gamma [Mus musculus] >gi 698...	48	2e-005
40	<u>15</u>	ref <u>NP_060819.1</u> hypothetical protein FLJ11175 [Homo sapiens] >...	48	3e-005
	<u>16</u>	sp <u>P05128</u> <u>KPCG_BOVIN</u> PROTEIN KINASE C, GAMMA TYPE (PKC-GAMMA) >...	48	3e-005

17	gb AAA60102.1 M13977	protein kinase C-gamma [Homo sapiens]	48
	3e-005		
18	emb CAA78820.1 Z15114	protein kinase C gamma [Homo sapiens]	48
	3e-005		
5	19	sp P05129 KPCG_HUMAN PROTEIN KINASE C, GAMMA TYPE (PKC-GAMMA) >...	48 3e-005
	20	sp P10829 KPCG_RABIT PROTEIN KINASE C, GAMMA TYPE (PKC-GAMMA) (...)	48 3e-005
21	gb AAD10190.1 AF098634	GLUT4 vesicle protein [Mus musculus]	48
10		3e-005	
	22	ref NP_035231.1 protein kinase C, alpha [Mus musculus] >gi 200...	48 4e-005
	23	sp P20444 KPCA_MOUSE PROTEIN KINASE C, ALPHA TYPE (PKC-ALPHA)	48 4e-005
15	24	emb CAA06507.1 AJ005377	eye-specific protein kinase C [Calli... 48 4e-005
	25	emb CAA73363.1 Y12858	protein kinase C [Hydra vulgaris] 47 5e-005
	26	emb CAA73362.1 Y12857	protein kinase C [Hydra vulgaris] 47 5e-005
20	27	gb AAA27770.1 M94883	protein kinase C [Aplysia californica] 47 6e-005
	28	sp P05696 KPCA_RAT PROTEIN KINASE C, ALPHA TYPE (PKC-ALPHA) >gi...	47 6e-005
25	29	pir KIMSCA protein kinase C (EC 2.7.1.-) alpha - mouse >gi 499...	47 6e-005
30	ref NP_002728.1 protein kinase C, alpha; Protein kinase C, alp...	47 6e-005	

```

30  RANK 1 ITERATION 0>pir|T04209 hypothetical protein T5C23.50 - Arabidopsis
    thaliana
        >gi|4539453|emb|CAB39933.1| (AL049500) putative protein
        [Arabidopsis thaliana] >gi|7267862|emb|CAB78205.1|
        (AL161532) putative protein [Arabidopsis thaliana]
        Length = 169

35  Score = 123 bits (305), Expect = 7e-028
    Identities = 55/90 (61%), Positives = 74/90 (82%)
    Frame = +2Query: 11
    HDLVPKDGEGSSSAYVELKFDDQRYRTSTKEKDLNPVWNEVFYFNISNPNN
40  LPNLTLEAV 190
        H+L PKDG+G+S+AYVEL FD Q++RT+ K++DLNPVWNE F+FNIS+P+ L
        L LEA
        Sbjct: 16
        HNLFPKDGQGTSNAYVELYFDGQKHRTTIKDRDLNPVWNESFFFNISDPSRL
45  HYLNLEAQ 75Query: 191 VYSYNQSTNAKDFLGKVCISGSSFVTYPEA 280
        YS+N+STN + FLGKV +SG+SFV ++A

```

Sbjct: 76 AYSHNRSTNGRSFLGKVSLSGTSFVPHSDA 105

RANK 2 ITERATION 0>pir|T00958 hypothetical protein F20D22.8 - Arabidopsis thaliana

- 5 >gi|3142295|gb|AAC16746.1| (AC002411) Strong similarity
to phosphoribosylanthranilate transferase gb|D86180 from
Pisum sativum. [Arabidopsis thaliana]
Length = 1012
- 10 Score = 94.8 bits (232), Expect = 2e-019
Identities = 43/83 (51%), Positives = 63/83 (75%)
Frame = +2Query: 11
HDLVPKDGEGSSSAYVELKFDDQRYRTSTKEKDLNPVWNEVFYFNISNPNN
LPNLTLEAV 190
- 15 H+L+PKDGE SSS +VE++F++QR RT K KDLNP+WNE F++ + N+L +
LE
Sbjct: 21
HNLMPKDGEDSSSPFVEVQFENQRLRTKVKPKDLNPIWNEKLVFHVNDVND
LRHKALEIN 80Query: 191 VYSYNQSTNAKDFLGKVCISGSS 259
- 20 VY+ +S+N+++FLGKV + GSS
Sbjct: 81 VYNEKRSSNSRNFLGKVRVLGSS 103

RANK 3 ITERATION 0>gb|AAF18518.1|AC006551_4 AC006551 Highly similar
to

- 25 phosphoribosylanthranilate transferase [Arabidopsis
thaliana]
Length = 1029
- 30 Score = 86.2 bits (210), Expect = 9e-017
Identities = 39/81 (48%), Positives = 55/81 (67%)
Frame = +2Query: 14
DLVPKDGEGSSSAYVELKFDDQRYRTSTKEKDLNPVWNEVFYFNISNPNNL
PNLTLEAVV 193
- 35 DL+PKDG+GS+S +VE++FD+QR RT T+ KDLNP WNE FN+ + L N T++
V
Sbjct: 13
DLMPKDGQGSASPFVEVEFDEQRQRTQTRFKDLNPQWNEKLVFNVGDLKR
LNNKTVDTV 72Query: 194 YSYNQSTNAKDFLGKVCISGS 256
- 40 Y + FLG+V I+G+
Sbjct: 73 YDDRRDNQPGKFLGRVKIAGA 93
Score = 41.4 bits (95), Expect = 0.003
Identities = 27/78 (34%), Positives = 39/78 (49%)
Frame = +2Query: 14
DLVPKDGEGSSSAYVELKFDDQRYRTSTKEKDLNPVWNEVFYFNISNPNNL
- 45 PNLTLLEAVV 193
DL D GS YVE+K ++ T EK+NP+W ++F F + L + LE V

Sbjct: 305 DLPVMDVSGSLDPYVEVKLGNYKGLTKHLEKNSNPIWKQIFAF---
SKERLQSNLLEVTV 361Query: 194 YSYNQSTNAKDFLGKVC I 247
+ T DF+G+V I

Sbjct: 362 KDKDLLTK-DDFVGRVHI 378

5 Score = 32.1 bits (71), Expect = 1.8
Identities = 17/48 (35%), Positives = 26/48 (53%), Gaps = 1/48 (2%)
Frame = +2Query: 14 DLVPKDGE GSSSAYVELKFDDQRYRTSTKE-
KDLNPVWNEVFYFNISNP 157

DLVP D A V+++ +Q T T + + +NP W+E F +S P

10 Sbjct: 468
DLVPSDKGRVPDAIVKIQAGNQMRAT RTPQMRTMNPQWHEELMFVVSEP
516

15 RANK 4 ITERATION 0>pir|[T47922 anthranilate phosphoribosyltransferase-like
protein -

Arabidopsis thaliana >gi|6850897|emb|CAB71060.1|
(AL137898) anthranilate phosphoribosyltransferase-like
protein [Arabidopsis thaliana]
Length = 972

20 Score = 83.1 bits (202), Expect = 8e-016
Identities = 43/88 (48%), Positives = 59/88 (66%)
Frame = +2Query: 17
LVPKDGE GSSSAYVELKFDDQRYRTSTKEKDLNPVWNEVFYFNISNPNNLP
25 NLTL EAVVY 196

L P++ G +AYVEL+FDDQ+ T TK D +PVWNE F+FNIS+ +L N L+A
VY

Sbjct: 16
LKPRE DYGGVNAYVELRFDDQKVITMTKIDDSSPVWNEKFFFNISDTE DLSN
30 QFLDAYVY 75Query: 197 SYNQSTNAKDFLGKVCISGSSFVTYPEA 280
+ S+ K LGK+ I G++F+ Y EA

Sbjct: 76 N-KTSSITK SCLGKIRILGTAFLPYSEA 102
Score = 43.0 bits (99), Expect = 0.001
Identities = 27/76 (35%), Positives = 40/76 (52%)
35 Frame = +2Query: 14

DLVPKDGE GSSSAYVELKFDDQRYRTSTKEKDLNPVWNEVFYFNISNPNNL
PNLTLEAVV 193

+L D GS Y+E+K + +T EK+ NPVWNEVF F+ SN + LE +V

Sbjct: 260
40 NLPSMDLTGSLDPYIEVKLGNYTGKTKHFEKNQNPVWNEVF AFSSKNQQ---
SNVLEVIV 316Query: 194 YSYNQSTNAKDFLGKV 241
+ + DF+G +

Sbjct: 317 MDKDMVKD--DFVGLI 330

45 RANK 5 ITERATION 0>gb|AAF15942.1|AC011765_38 AC011765 putative
phosphoribosylanthranilate transferase, 3' partial;

131493-134402 [Arabidopsis thaliana]

Length = 970

Score = 82.3 bits (200), Expect = 1e-015

5 Identities = 42/83 (50%), Positives = 58/83 (69%), Gaps = 4/83 (4%)

Frame = +2Query: 14

DLVPKDGEGSSSAYVELKFDDQRYRTSTKEKDLNPVWNEVFYFNISNPNNL
PNLTLEAVV 193

+++PKDG+GSSSAYV + FD Q+ RTSTK +DLNP+WNE+ F +S+P N+ L+

10 V

Sbjct: 28

NILPKDGGQSSSAYVVVDFDAQKKRTSTKFRDLNPIWNEMLDFAVSDPKNM
DYDELDIEV 87Query: 194 YSYNQSTNA----KDFLGKVCISGSSF 262

Y+ + N FLG+V I G S F

15 Sbjct: 88 YNDKRFGNGGGRKNHFLGRVKIYGSQF 114

Score = 30.9 bits (68), Expect = 4.1

Identities = 13/42 (30%), Positives = 23/42 (53%)

Frame = +2Query: 32

GEGSSSAYVELKFDDQRYRTSTKEKDLNPVWNEVFYFNISNP 157

20 G+GS+ AY K+ + RT T +P W+E + + + +P

Sbjct: 690 GKGSTDAYCVAKYGKKWVRTRTITDSFDPRWHEQYTWQVYDP
731

RANK 6 ITERATION 0>gb|AAD55273.1|AC008263_4 AC008263 Similar to
25 gb|D86180

phosphoribosylanthranilate transferase from Pisum sativum
and contains 2 PF|00168 C2 (phospholipid binding)
domains. ESTs gb|H76726, gb|T45544 and gb|N96377 come
from this gene. [Arabidopsis thaliana]

30 Length = 1276

Score = 82.3 bits (200), Expect = 1e-015

Identities = 42/83 (50%), Positives = 58/83 (69%), Gaps = 4/83 (4%)

Frame = +2Query: 14

35 DLVPKDGEGSSSAYVELKFDDQRYRTSTKEKDLNPVWNEVFYFNISNPNNL
PNLTLEAVV 193

+++PKDG+GSSSAYV + FD Q+ RTSTK +DLNP+WNE+ F +S+P N+ L+

V

Sbjct: 28

40 NILPKDGGQSSSAYVVVDFDAQKKRTSTKFRDLNPIWNEMLDFAVSDPKNM
DYDELDIEV 87Query: 194 YSYNQSTNA----KDFLGKVCISGSSF 262

Y+ + N FLG+V I G S F

Sbjct: 88 YNDKRFGNGGGRKNHFLGRVKIYGSQF 114

Score = 30.9 bits (68), Expect = 4.1

45 Identities = 13/42 (30%), Positives = 23/42 (53%)

Frame = +2Query: 32
 GEGSSSAYVELKFDDQRYRTSTKEKDLNPVWNEVFYFNISNP 157
 G+GS+ AY K+ + RT T +P W+E + + + +P
 Sbjct: 690 GKGSTDAYCVAKYGKKWVRTRTITDSFDPRWHEQYTWQVYDP
 5 731

RANK 7 ITERATION 0>gb|AAAF03465.1|AC009327_4 AC009327 putative
 phosphoribosylanthranilate transferase [Arabidopsis
 thaliana]
 10 Length = 1017

Score = 69.9 bits (168), Expect = 8e-012
 Identities = 35/88 (39%), Positives = 54/88 (60%)
 Frame = +2Query: 5
 15 AXHDLVPKDGEGSSSAYVELKFDDQRYRTSTKEKDLNPVWNEVFYFNISNP
 NNLPNLTLE 184
 + +L+PKDG+G++SAY + FD QR RT TK +DLNP W+E F + + + LE
 Sbjct: 15
 SARNLMPKDGQGTASAYAIVDFDGQRRRTKTKFRDLNPQWDEKLEFFVHD
 20 VATMGEEILE 74Query: 185 AVVYSYNQSTNAKDFLGKVCISGSSFVT 268
 + + ++ FLGKV I+GS+F +
 Sbjct: 75 INLCNDKKTGKRSTFLGKVKIAGSAFAS 102
 Score = 32.5 bits (72), Expect = 1.4
 Identities = 16/44 (36%), Positives = 26/44 (58%), Gaps = 1/44 (2%)
 25 Frame = +2Query: 26 KDG-
 EGSSSAYVELKFDDQRYRTSTKEKDLNPVWNEVFYFNISNP 157
 +DG G++ AYV K+ + RT T NP WNE + + + +P
 Sbjct: 622
 RDGTRGTTDAYVVAKYGPKWIRTRTILDRFNPRWNEQYTWDVYDP 666

30 RANK 8 ITERATION 0>dbj|BAB08397.1| AB015473 phosphoribosylanthranilate
 transferase-like protein [Arabidopsis thaliana]
 Length = 1049

35 Score = 62.5 bits (149), Expect = 1e-009
 Identities = 36/84 (42%), Positives = 48/84 (56%), Gaps = 4/84 (4%)
 Frame = +2Query: 14
 DLVPKDGEGSSSAYVELKFDDQRYRTSTKEKDLNPVWNEVFYFNISN--
 PNNLPNLTLEA 187
 40 DL PKDG G+SS YV L + QR RT T +DLNPVWNE F+++ + L LE
 Sbjct: 16
 DLTPKDGHGTTSSPYVVLDDYYGQRRRTRTIVRDLNPVWNETLEFSLAKRPSH
 QLFTDVLEL 75Query: 188 VVYSYNQ--STNAKDFLGKVCISGSSFV 265
 +Y T +FLG++ + FV
 45 Sbjct: 76 DMYHDKNFGQTRRNFLGRIRLGSDQFV 103
 Score = 36.7 bits (83), Expect = 0.072

Identities = 15/43 (34%), Positives = 25/43 (57%)

Frame = +2Query: 29

DGEGSSSAYVELKFDDQRYRTSTKEKDLNPVWNEVFYFNISNP 157

+G+GS+AY K+ + RT T L+P WNE + + + +P

5 Sbjct: 653

NGKGSTDAYTVAKYGSKWVRTRTVSDSLDPKWNEQYTWKVYDP 695

RANK 9 ITERATION 0>dbj|BAB11070.1| AB017064 phosphoribosylanthranilate

transferase-like protein [Arabidopsis thaliana]

10 Length = 1036

Score = 62.5 bits (149), Expect = 1e-009

Identities = 33/78 (42%), Positives = 48/78 (61%), Gaps = 1/78 (1%)

Frame = +2Query: 17

15 LVPKDGEGSSSAYVELKFDDQRYRTSTKEKDLNPVWNEVFYFNI-

SNPNNLPNLTLEAVV 193

L+P+DG+GS+S +VE+ F +Q +T T K LNPVWN+ YF+ + N N +E V

Sbjct: 17

LMPRDGQGSASPFVEVDFLNQLSKTRTPKSLNPVWNQKLYFDYDQSVINQ

20 HNQHIEVSV 76Query: 194 YSYNQSTNAKDFLGKVCIS 250

Y + + FLG+V IS

Sbjct: 77 YHERRPIPGRSFLGRVKIS 95

Score = 38.3 bits (87), Expect = 0.024

Identities = 20/47 (42%), Positives = 29/47 (61%), Gaps = 3/47 (6%)

25 Frame = +2Query: 17 LVP---

KDGEGSSSAYVELKFDDQRYRTSTKEKDLNPVWNEVFYFNISNP 157

LVP KDG GS++AY K+ + RT T L+P WNE + + + +P

Sbjct: 636

LVPMKLKDGRGSTNAYCVAKYGQKWVRTRTILDTLSPRWNEQYTWEVYD

30 P 685

RANK 10 ITERATION 0>pir|T01234 probable anthranilate

phosphoribosyltransferase (EC

2.4.2.18) F6N23.8 - Arabidopsis thaliana

35 >gi|30471119|gb|AAC13630.1| (AF058919) F6N23.8 gene

product [Arabidopsis thaliana]

>gi|7267409|emb|CAB80879.1| (AL161472) putative

phosphoribosylanthranilate transferase [Arabidopsis

thaliana]

40 Length = 675

Score = 58.9 bits (140), Expect = 1e-008

Identities = 26/50 (52%), Positives = 36/50 (72%)

Frame = +2Query: 17

45 LVPKDGEGSSSAYVELKFDDQRYRTSTKEKDLNPVWNEVFYFNISNPNNL

166

Score = 50.0 bits (117), Expect = 7e-006

Identities = 29/82 (35%), Positives = 47/82 (56%), Gaps = 5/82 (6%)

Frame = +2Query: 14 DLVPKDGEGSSSAYVEL-----

5 KFDDQRYRTSTKEKDLNPVWNEVFYFNISNPNNLPNLT 178

+LVP+D G S +V++ + + + RT +K LNP WN+ + + L T

Sbjct: 149

NLVPRDNNNGYSDFVKVYLLPGRGAEYKRRTKHKVQKSLNPEWNQTVIYKSI

SMEQLKKKT 208Query: 179 LEAVVYSYNQSTNAKDFLGKVCISGSS 259

10 LE V+ Y++ ++ DFLG+V I SS

Sbjct: 209 LEVTVWDYDR-FSSNDFLGEVLIDLSS 234

RANK 13 ITERATION 0>emb|CAA73554.1| Y13100 Serine/Threonine protein
kinase [Sycon

15 raphanus]

Length = 756

Score = 49.2 bits (115), Expect = 1e-005

Identities = 29/76 (38%), Positives = 46/76 (60%), Gaps = 5/76 (6%)

20 Frame = +2Query: 14 DLVPKDGEGSSSAYVELKFDDQ-----

RYRTSTKEKDLNPVWNEVFYFNISNPNNLPNLT 178

+L P D G + YV+L D + + T TK K LNPVW E F FN++ + + L

Sbjct: 192

NLPPMDANGLADPYVKLWLSDDPQKATKKKTETKMKTLNPVWGEKFSFNL

25 TQGDLKRS LI 251Query: 179 LEAVVYSYNQSTNAKDFLGKV 241

+E V+ ++++T DF+GK+

Sbjct: 252 IE--VWDWDRTR-NDFIGKM 269

RANK 14 ITERATION 0>ref|NP_035232.1| protein kinase C, gamma [Mus
30 musculus]

>gi|6981400|ref|NP_036760.1| protein kinase C, type I

(gamma type) [Rattus norvegicus]

>gi|125561|sp|P05697|KPCG_MOUSE PROTEIN KINASE C, GAMMA

TYPE (PKC-GAMMA) >gi|66727|pir||KIRTGC protein kinase C

35 (EC 2.7.1.-) gamma - rat >gi|423544|pir||JN0548 protein

kinase C (EC 2.7.1.-) gamma - mouse

>gi|53697|emb|CAA47608.1| (X67129) protein kinase C gamma

[Mus musculus] >gi|56918|emb|CAA30267.1| (X07287) protein

kinase C gamma (AA 1 - 697) [Rattus rattus]

40 >gi|206187|gb|AAA41874.1| (M13707) protein kinase C type

II [Rattus norvegicus] >gi|451186|gb|AAA39939.1| (L28035)

protein kinase C gamma [Mus musculus]

Length = 697

45 Score = 48.4 bits (113), Expect = 2e-005

Identities = 30/87 (34%), Positives = 48/87 (54%), Gaps = 5/87 (5%)

Frame = +2Query: 14 DLVPKDGEGSSSAYVELKFDDQ-----
RYRTSTKEKDLNPVWNEVFYFNISNPNNLPNLT 178

+L+P D G S YV+LK ++T T + LNPVWNE F FN+ + L+

Sbjct: 182

5 NLIPMDPNGLSDPYVKLKLIPDPRNLTKQKTKTVKATLNPVWNETFVFNLKP
GDVERRLS 241Query: 179 LEAVVYSYNQSTNAKDFLGKVCISGSSFVTYP
274

+E V+ +++ T+ DF+G + S + P

Sbjct: 242 VE--VWDWDR-TSRNDFMGAMSFGVSELLKAP 270

10

RANK 15 ITERATION 0>ref|NP_060819.1| hypothetical protein FLJ11175 [Homo sapiens]

>gi|11432771|ref|XP_007675.1| hypothetical protein

FLJ11175 [Homo sapiens] >gi|7023676|dbj|BAA92048.1|

15

(AK002037) unnamed protein product [Homo sapiens]

Length = 466

Score = 48.0 bits (112), Expect = 3e-005

Identities = 29/78 (37%), Positives = 41/78 (52%)

20

Frame = +2Query: 14

DLVPKDGEGSSSAYVELKFDDQRYRTSTKEKDLNPVWNEVFYFNISNPNNL
PNLTLEAVV 193

DL+ D G S + L+ + R +T T K+LNP WN+VF F I + +++ LE V

Sbjct: 108

25

DLAADFSGKSDPFCLLELGNDRLQHTTVYKNLNPWKNKVFTFPIKDIHDV--
--LEVTV 163Query: 194 YSYNQSTNAKDFLGKVC I 247

+ DFLGKV I

Sbjct: 164 FD-EDGDKPPDFLGKVAI 180

30

RANK 16 ITERATION 0>sp|P05128|KPCG_BOVIN PROTEIN KINASE C,
GAMMA TYPE (PKC-GAMMA)

>gi|66729|pir|KIBOGC protein kinase C (EC 2.7.1.-) gamma

- bovine (fragment) >gi|163526|gb|AAA30704.1| (M13976)

gamma type protein kinase C [Bos taurus]

35

Length = 682

Score = 48.0 bits (112), Expect = 3e-005

Identities = 30/87 (34%), Positives = 48/87 (54%), Gaps = 5/87 (5%)

Frame = +2Query: 14 DLVPKDGEGSSSAYVELKFDDQ-----

40

RYRTSTKEKDLNPVWNEVFYFNISNPNNLPNLT 178

+L+P D G S YV+LK ++T T + LNPVWNE F FN+ + L+

Sbjct: 167

NLIPMDPNGLSDPYVKLKLIPDPRNLTKQKTRTVKATLNPVWNETFVFNLKP
GDVERRLS 226Query: 179 LEAVVYSYNQSTNAKDFLGKVCISGSSFVTYP

45

274

+E V+ +++ T+ DF+G + S + P

Sbjct: 227 VE--VWDWDR-TSRNDFMGAMSGVSELLKAP 255

RANK 17 ITERATION 0>gb|AAA60102.1| M13977 protein kinase C-gamma
[Homo sapiens]

5 Length = 317

Score = 48.0 bits (112), Expect = 3e-005

Identities = 30/87 (34%), Positives = 48/87 (54%), Gaps = 5/87 (5%)

Frame = +2Query: 14 DLVPKDGE GSSSAYVELKFDDQ-----

10 RYRTSTKEKDLNPVWNEVFYFNISNPNNLPNLT 178

+L+P D G S YV+LK ++T T + LNPVWNE F FN+ + L+

Sbjct: 182

NLIPMDPNGLSDPYVKLKLIPDPRNLTKQKTRTVKATLNPVWNETFVFNLP

GDVERRLS 241Query: 179 LEAVVYSYNQSTNAKDFLGKVCISGSSSFVTYP

15 274

+E V+ +++ T+ DF+G + S + P

Sbjct: 242 VE--VWDWDR-TSRNDFMGAMSGVSELLKAP 270

RANK 18 ITERATION 0>emb|CAA78820.1| Z15114 protein kinase C gamma
[Homo sapiens]

20 Length = 536

Score = 48.0 bits (112), Expect = 3e-005

Identities = 30/87 (34%), Positives = 48/87 (54%), Gaps = 5/87 (5%)

25 Frame = +2Query: 14 DLVPKDGE GSSSAYVELKFDDQ-----

RYRTSTKEKDLNPVWNEVFYFNISNPNNLPNLT 178

+L+P D G S YV+LK ++T T + LNPVWNE F FN+ + L+

Sbjct: 21

NLIPMDPNGLSDPYVKLKLIPDPRNLTKQKTRTVKATLNPVWNETFVFNLP

30 GDVERRLS 80Query: 179 LEAVVYSYNQSTNAKDFLGKVCISGSSSFVTYP

274

+E V+ +++ T+ DF+G + S + P

Sbjct: 81 VE--VWDWDR-TSRNDFMGAMSGVSELLKAP 109

35 RANK 19 ITERATION 0>sp|P05129|KPCG_HUMAN PROTEIN KINASE C,
GAMMA TYPE (PKC-GAMMA)

>gi|2117775|pir||D24664 protein kinase C (EC 2.7.1.-)

gamma - human

Length = 697

40

Score = 48.0 bits (112), Expect = 3e-005

Identities = 30/87 (34%), Positives = 48/87 (54%), Gaps = 5/87 (5%)

Frame = +2Query: 14 DLVPKDGE GSSSAYVELKFDDQ-----

RYRTSTKEKDLNPVWNEVFYFNISNPNNLPNLT 178

45 +L+P D G S YV+LK ++T T + LNPVWNE F FN+ + L+

Sbjct: 182
NLIPMDPNGLSDPYVKLKLIPDPRNLTKQKTRTVKATLNPVWNETFVFNLPK
GDVERRLS 241Query: 179 LEAVVYSYNQSTNAKDFLGKVCISGSSFVTYP
274

5 +E V+ +++ T+ DF+G + S + P

Sbjct: 242 VE--VWDWDR-TSRNDFMGAMSFGVSELLKAP 270

RANK 20 ITERATION 0>sp|P10829|KPCG_RABIT PROTEIN KINASE C,
GAMMA TYPE (PKC-GAMMA) (DELTA)

10 >gi|66728|pir||KIRBGC protein kinase C (EC 2.7.1.-) gamma
- rabbit >gi|165652|gb|AAA31449.1| (M19338) protein
kinase delta [Oryctolagus cuniculus]
Length = 697

15 Score = 48.0 bits (112), Expect = 3e-005
Identities = 30/87 (34%), Positives = 48/87 (54%), Gaps = 5/87 (5%)
Frame = +2Query: 14 DLVPKDGEGSSSAYVELKFDDQ-----
RYRTSTKEKDLNPVWNEVFYFNISNPNNLPNLT 178

+L+P D G S YV+LK ++T T + LNPVWNE F FN+ + L+

20 Sbjct: 182
NLIPMDPNGLSDPYVKLKLIPDPRNLTKQKTRTVKATLNPVWNETFVFNLPK
GDVERRLS 241Query: 179 LEAVVYSYNQSTNAKDFLGKVCISGSSFVTYP
274

+E V+ +++ T+ DF+G + S + P

25 Sbjct: 242 VE--VWDWDR-TSRNDFMGAMSFGVSELLKAP 270
[END
ALIGNMENTS]

30 Job DetailsReturn to top

[BEGIN JOB STATUS][BEGIN SEARCH TIME]

[END SEARCH TIME]

[VERSION]

[SEARCH ID]

35 [EOL] CRLF

[COMMENT] /Comment=NCBI BLASTX Translated Search

[COMMENT]

[ALGORITHM] BLASTX

[MATRIX] D:\DECYPHER\MATRIX\BLOSUM62.MAA

40 [QUERY FORMAT] FASTA/PEARSON

[QUERY TYPE] NT

[QUERY FILTER] T

[QUERY SEARCH] -1 -2 -3 1 2 3

[QUERY PATH] d:\decypher\query

45 [QUERY SET]

[TARGET TYPE] AA

[TARGET FRAMES] 1

A: 40

X1: 16 (7.3 bits)

X2: 38 (14.8 bits)

X3: 64 (24.9 bits)

5 S1: 41 (21.7 bits)

S2: 65 (29.7 bits)[JOB MESSAGES] [END JOB STATUS]

DeCypher Results for: NCBI TBLASTX Similarity Search

Results by Query

Click on a query below to view its search results.

10 Your_Query starting with: CACTGCANCACATGATCTTG

Search Details

Results for: Your_Query starting with:

15 **CACTGCANCACATGATCTTG; (Length=297)**

[Return to query summary](#)

	RANK	Sequences producing significant alignments:	(bits)	Value
	<u>1</u>	CL008746.206.147	123	7e-031
20	<u>2</u>	CL038882.184	121	7e-027
	<u>3</u>	CL007196.224	83	2e-015
	<u>4</u>	CL015365.122	73	1e-012
	<u>5</u>	CL037124.12	71	8e-012
	<u>6</u>	CL011286.38	63	1e-009
25	<u>7</u>	CL012497.54	56	2e-007
	<u>8</u>	CL027507.179	48	4e-005
	<u>9</u>	CL038154.109	44	7e-004
	<u>10</u>	CL028291.55	39	0.017
	<u>11</u>	CL000466.566	38	0.031
30	<u>12</u>	CL012497.49	38	0.042
	<u>13</u>	CL015365.137	37	0.057
	<u>14</u>	CL016730.47.52	37	0.057
	<u>15</u>	CL026569.111	37	0.057
	<u>16</u>	CL015430.119	37	0.078
35	<u>17</u>	CL029186.110	36	0.11
	<u>18</u>	CL036710.61	34	0.69
	<u>19</u>	CL039132.67	34	0.69
	<u>20</u>	CL025356.146	34	0.69
	21	CL009499.126	33	0.95
40	22	CL017909.225.155	32	1.2
	23	CL013983.133	33	1.3
	24	CL010998.39	33	1.3
	25	CL043753.68.71	32	1.6
	26	CL047053.157.1	32	1.6

Frame = -1 / +3
Query: 279 ASG*VTKDDPLIHTLPRKSL 220
ASG T + P I TLPRK L
Sbjct: 8859 ASNGTNEVPAILTLPRKDL 8918
5 Score = 61.5 bits (128), Expect(2) = 2e-011
Identities = 35/67 (52%), Positives = 39/67 (57%)
Frame = -1 / +3
Query: 213
VD*L*L*TTASRVRLGRLFGLDILK*NTSFQTGFKSFSFVLVRYXXXXXXXXXST
10 *ALDEPS 34
+D L L *T AS GRL G + LK* SF TGF+S S + VR ST AL EP
Sbjct: 8928
MDLLML*TYASSASSGRLDGSETLK*KRSFHTGFRSLSLIAVRNRWPSNVSS
TQALAEPC 9107
15 Query: 33 PSLGTRS 13
PSLG RS
Sbjct: 9108 PSLGIRS 9128
Score = 41.4 bits (84), Expect = 0.002
Identities = 23/62 (37%), Positives = 34/62 (54%)
20 Frame = -3 / +2
Query: 196
IDNCFKGKIGKIVWIGYIEIYLIPNRVQVFFFRASTISLIKLELYIGTR*AFTVF
RHK 17
+D FK K+ KI I +E+E LIP+ VQ+ + L IK +L GT * + H+
25 Sbjct: 8945
VDVRFKRKLRRIRNVEVEALIPHVVQILVLDSRAEPLAIKRKLDTGTC*T
LPILGHQ 9124
Query: 16 IM 11
+M
30 Sbjct: 9125 VM 9130

RANK 2 ITERATION 0>CL038882.184
Length = 8464

35 Score = 20.8 bits (39), Expect(2) = 0.14
Identities = 6/10 (60%), Positives = 9/10 (90%)
Frame = +2 / +1
Query: 2 TAXHDLVPKD 31
T+ HDL+PK+
40 Sbjct: 6487 TSAHDLLPKE 6516
Score = 33.6 bits (67), Expect(2) = 0.14
Identities = 11/29 (37%), Positives = 20/29 (68%)
Frame = +1 / +3
Query: 52 LCRAQV**SKISY*HERKRLEPCLE*GIL 138
45 LCR ++ * +++ H+R+ +PCLE +L
Sbjct: 6534 LCRDRIR*PEVPHSHQREGYQPCLERAVL 6620

L+H+ +L IG
Sbjct: 6573 CAELLVIEFDLDIG 6532

RANK 3 ITERATION 0>CL007196.224

5 Length = 5351

Score = 83.1 bits (175), Expect = 2e-015
Identities = 31/55 (56%), Positives = 44/55 (79%)
Frame = +2 / +3

10 Query: 5
AXHDLVPKDGEGSSSAYVELKFDDQRYRTSTKEKDLNPVWNEVFYFNISNP
NNLP 169

A +L+PKDG+GSSSAYVE++F+ QR RT + K+LNPVWNE F +++P++LP
Sbjct: 4743

15 AAXNLMPKDGQGSSSAYVEVEFEHQRRRTRARPKELNPVWNERLVFAVAD
PDDL 4907

Score = 38.2 bits (77), Expect = 0.019
Identities = 21/51 (41%), Positives = 23/51 (44%)
Frame = -1 / -2

20 Query: 168
GRLFGLDILK*NTSFQTGFKSFSFVLVRYXXXXXXXXST*ALDEPSPSLGTR 16

GR G K SFQTG S VR ST A ++P PSLG R

Sbjct: 4906
GRSSGSATAKTRRSFQTGLSSLGLARVRRLWCSNSTSTYADEDPCPSLGMR

25 4754

RANK 4 ITERATION 0>CL015365.122

Length = 851

30 Score = 73.5 bits (154), Expect = 1e-012
Identities = 26/61 (42%), Positives = 42/61 (68%)
Frame = +2 / +1

Query: 14
DLVPKDGEGSSSAYVELKFDDQRYRTSTKEKDLNPVWNEVFYFNISNPNNL
35 PNLTLEAVV 193

+L PKDG G+ +A+VE++FD Q+ RT TK D +P WN F++ +P+ LP+L ++ V
Sbjct: 358
ELAPKDGAGACNAFVEVEFDGQKQRTPTKPADRSPQWNHTLVFDVRDPSR
LPSLPVDVSV 537

40 Query: 194 Y 196
+

Sbjct: 538 H 540
Score = 32.2 bits (64), Expect = 1.2
Identities = 22/60 (36%), Positives = 24/60 (39%)
45 Frame = -1 / -1

Query: 192
TTASRVRLGRLFGDLILK*NTSFQTGFKSFSFVLVRYXXXXXXXXST*ALDEPS
PSLGTRS 13

T S R GR G F G +S V VR ST AL P+PSLG S

5 Sbjct: 536
TETSTGREGRREGSRTSNTRVWFHCGERSAGLVGVRCFCPSNSTSTNALQA
PAPSLGASS 357

RANK 5 ITERATION 0>CL037124.12

10 Length = 1672

Score = 70.7 bits (148), Expect = 8e-012
Identities = 28/62 (45%), Positives = 43/62 (69%)
Frame = +2 / +2

15 Query: 14
DLVPKDGEGSSSAYVELKFDDQRYRTSTKEKDLNPVWNEVFYFNISNPNNL
PNLTLEAVV 193

+L+PKDG+G++SAY + FD QR RT+T++DLNP W E F ++P++ TLE +

Sbjct: 278
20 NLMPKDGQGTASAYAVVDFDGQRRRTATRPRDLNPQWGERLEFLVHDPDA
MCAETLELNL 457

Query: 194 YS 199

Y+

Sbjct: 458 YN 463
25

RANK 6 ITERATION 0>CL011286.38

Length = 1478

Score = 63.4 bits (132), Expect = 1e-009
30 Identities = 27/61 (44%), Positives = 38/61 (62%)
Frame = +2 / +2

Query: 14
DLVPKDGEGSSSAYVELKFDDQRYRTSTKEKDLNPVWNEVFYFNISNPNNL
PNLTLEAVV 193

35 DLVPKDG G+SSA+ + FD QR RT T +DL+P W+E F ++P + L+ +

Sbjct: 1040
DLVPKDGGLGTSSAFVDFDGQRKRTRTVPRDLSPQWHERLEFAVHDPAA
MHAEALDVSL 1219

Query: 194 Y 196

40 Y

Sbjct: 1220 Y 1222

Score = 37.3 bits (75), Expect = 0.036
Identities = 18/39 (46%), Positives = 21/39 (53%)
Frame = -1 / -3

45 Query: 129 SFQTGFKSFSFVLVRYXXXXXXXXST*ALDEPSPSLGTRS 13
S G+S V VR+ + ALD PSPSLGTRS

Sbjct: 1155 SCHCGLRSRGTVRVRFRCPSTTAKALDVPSPLGTRS 1039

RANK 7 ITERATION 0>CL012497.54

Length = 2888

5

Score = 55.6 bits (115), Expect = 2e-007
Identities = 21/46 (45%), Positives = 29/46 (62%)
Frame = +2 / -2

Query: 14

10 DLVPKDGEGSSSAYVELKFDDQRYRTSTKEKDLNPVWNEVFYFNIS 151
+L+PKDG G SS ++FD QR +T T ++LNP WNE F +

Sbjct: 835

NLLPKDGTGKSSP*ARVEFDGQRRKTHTVPRELNPAWNEALEFKFA 698

15 RANK 8 ITERATION 0>CL027507.179

Length = 8490

Score = 47.8 bits (98), Expect = 4e-005
Identities = 17/49 (34%), Positives = 30/49 (60%)

20 Frame = +2 / +1

Query: 29

DGEGSSSAYVELKFDDQRYRTSTKEKDLNPVWNEVFYFNISNPNL 175
D G S YV+L+ QR++T +K+LNP W++ F F++ + ++ L

Sbjct: 3688

25 DSNGFSDPYVKLQLGKQRFKTKVVKKNLNPAPWDQEFSSVGDVRDVLKL
3834

RANK 9 ITERATION 0>CL038154.109

Length = 8044

30

Score = 43.7 bits (89), Expect = 7e-004
Identities = 20/44 (45%), Positives = 24/44 (54%)
Frame = +2 / +1

Query: 14

35 DLVPKDGEGSSSAYVELKFDDQRYRTSTKEKDLNPVWNEVFYFN 145
DL KD GS YVE+K + T EK NP WN+VF F+

Sbjct: 3673

DLPSKDITGSCDPYVEVKLGNYXGTTRHFEKKTNPENQVFAFS 3804

Score = 39.1 bits (79), Expect = 0.017

40 Identities = 15/44 (34%), Positives = 23/44 (52%)
Frame = +2 / +1

Query: 26 KDGE GSSSAYVELKFDDQRYRTSTKEKDLNPVWNEVFYFNISNP
157

KDG G++ AY K+ + RT T P WNE + + + +P

45 Sbjct: 4663

KDGRGTTDAYCVAKYGQKWVRTRTIIDSFTPKWNEQYTWEVYDP 4794

[illegible]

5 Score = 39.1 bits (79), Expect = 0.017
 Identities = 14/44 (31%), Positives = 24/44 (53%)
 Frame = +2 / -2
 Query: 26 KDGE GSSSAYVELKFDDQRYRTSTKEKDLNPVWNEVFYFNISNP
 157
 10 +DG G++ AY K+ + RT T +P WNE + + + +P
 Sbjct: 274
 RDGRGTTDAYCVAKYGQKWVRTRTMLGTFSPTWNEQYTWVEVFD 143

15 Length = 716

20 Query: 38 GSSSAYVELKFDDQRYRTSTKEKDLNPVWNEVFYFNISNP 157
GS+ AYW LK+ + RT T NP WNE + ++P
Sbjct: 540 GSTDAYVVLKYGPKWARTRTILDQFNPRWNEQYALEVFDP 659

25 Length = 977

30 Query: 29 DGE GSSSAYVELKFDDQRYRTSTKEKDLNPVWNEVFYFNISNP
157
DG+G + AY K+ + RT T +P WNE + + + +P
Sbjct: 660
DGKGCTDAYAVAKYGPKWARTRTISDSFDPAWNEQYTWPVYDP 788

Length = 750

Query: 14
DLVPKDGEGSSSAYVELKFDDQRYRTSTKEKDLNPVWNEVFYFN 145
DL D G+ YVE++ ++ T EK+ NPVW +VF F+
45 Shjct: 651 DLPNMDITGALDPYVEVRLGNFKGVTRHLEKNPNPVWRQVFAFS
520

RANK 14 ITERATION 0>CL016730.47.52

Length = 4302

- 5 Score = 37.3 bits (75), Expect = 0.057
 Identities = 12/27 (44%), Positives = 19/27 (69%)
 Frame = +2 / +1
 Query: 77 QRYRTSTKEKDLNPVWNEVFYFNISNP 157
 Q+ +TS K+K +NP+W+E +I NP
10 Sbjct: 1846 QKVKTSVKKKSVNPIWHEELTLSIMNP 1926

RANK 15 ITERATION 0>CL026569.111

Length = 2843

- 15 Score = 37.3 bits (75), Expect = 0.057
 Identities = 12/26 (46%), Positives = 19/26 (72%)
 Frame = +2 / -1
 Query: 80 RYRTSTKEKDLNPVWNEVFYFNISNP 157
 + +TS ++K+ NPVWNEV ++NP
20 Sbjct: 1067 KVKTSVQKKNSNPVWNEVLQLAVTNP 990

RANK 16 ITERATION 0>CL015430.119

Length = 5715

- 25 Score = 36.8 bits (74), Expect = 0.078
 Identities = 15/31 (48%), Positives = 20/31 (64%)
 Frame = +2 / +3
 Query: 170 NLTLEAVVYSYNQSTNAKDFLGKVCISGSSF 262
 NL LEA VY ++Q +N+K LGKV + F
30 Sbjct: 2544 NLILEAAVYCFDQMSNSKSLLGKVLLPEKYF 2636

RANK 17 ITERATION 0>CL029186.110

Length = 3185

- 35 Score = 36.3 bits (73), Expect = 0.11
 Identities = 17/45 (37%), Positives = 24/45 (52%)
 Frame = +2 / +2
 Query: 146
 ISNPNNLPNLTLEAVVYSYNQSTNAKDFLGKVCISGSSFVTYPEA 280
40 I N N PN + V+++Y FLG V ISG+S +T P +
 Sbjct: 1721 IFNRNRPPNRSFPRVIHAYRIILPINYFLGGVIISGTSCITIPRS 1855

RANK 18 ITERATION 0>CL036710.61

Length = 3050

- 45 Score = 33.6 bits (67), Expect = 0.69

Identities = 14/28 (50%), Positives = 19/28 (67%)

Frame = +2 / -2

Query: 143 NISNPNNLPNLTLEAVVYSYNQSTNAKD 226

N SNPNN+P+LT+ AVV +S +D

5 Sbjct: 2167 NCSNPNNIPDLTVAAVVTCTSTSLASMD 2084

RANK 19 ITERATION 0>CL039132.67

Length = 912

10 Score = 33.6 bits (67), Expect = 0.69

Identities = 11/24 (45%), Positives = 17/24 (70%)

Frame = +2 / -3

Query: 86 RTSTKEKDLNPVWNEVFYFNISNP 157

+T+ K +LNP WNE F F +++P

15 Sbjct: 667 KTTVKRSNLNPEWNEDFKFVVTD P 596

RANK 20 ITERATION 0>CL025356.146

Length = 1565

20 Score = 33.6 bits (67), Expect = 0.69

Identities = 12/41 (29%), Positives = 24/41 (58%)

Frame = +2 / -1

Query: 26 KDGE GSSSAYVELKFDDQRYRTSTKEKDLNPVWNEVFYFNI 148

+DG GS AY K+ +YRT T ++P +++ +++ +

25 Sbjct: 455 RDGRGSCDAYCVAKYGVK WYRTRTVTDSISPRFHQQYHWEV
333

[END

ALIGNMENTS]

30 Job DetailsReturn to top

[BEGIN JOB STATUS][BEGIN SEARCH TIME]

[END SEARCH TIME]

[VERSION]

35 [SEARCH ID]

[EOL] CRLF

[COMMENT] /Comment=NCBI TBLASTX Similarity Search

[COMMENT] /CGI

[ALGORITHM] TBLASTX

40 [MATRIX] D:\DECYPHER\MATRIX\BLOSUM62.MAA

[QUERY FORMAT] FASTA/PEARSON

[QUERY TYPE] NT

[QUERY FILTER] T

[QUERY SEARCH] -1 -2 -3 1 2 3

45 [QUERY PATH] d:\decypher\query

[QUERY SET]

[TARGET TYPE] NT

```

[TARGET FRAMES] -1 -2 -3 1 2 3
[TARGET PATH] d:\decypher\target\blast
[TARGET SET] rice_contigs_
[MAX SCORES] 30
5  [MAX ALIGNMENTS] 20
   [THRESHOLD] 1
   [RESULT PATH] d:\decypher\output
   [OUTPUT FORMAT] TEXT EXTRACTALIGNED[SHOW GI] F
   [EXPECTATION] 10
10  [GAPPED ALIGNMENT] TTBLASTX
    TBLASTX
    Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
    Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
    "Gapped BLAST and PSI-BLAST: a new generation of protein database search
15  programs", Nucleic Acids Res. 25:3389-3402.Query= Your_Query starting with:
    CACTGCANCACATGATCTTG /QuerySize=297
        (297 letters)Database:
            154,797 sequences; 359,911,975 total letters Database:
            Posted date:
20  Number of letters in database: 359,911,975
    Number of sequences in database: 154,797

    Lambda  K  H
        0.318 0.135 0.401
25  Matrix: BLOSUM62.MAA
    Number of Hits to DB: 219582214
    Number of Sequences: 154797
    Number of extensions: 2512235
    Number of successful extensions: 120342
30  Number of sequences better than 10.0: 201
    length of query: 99
    length of database: 119,970,658
    effective HSP length: 50
    effective length of query: 48
35  effective length of database: 112,230,808
    effective search space: 5387078784
    effective search space used: 5387078784
    frameshift window, decay const: 50, 0.1
    T: 13
40  A: 40
    X1: 16 ( 7.3 bits)
    X2: 0 ( 0.0 bits)
    S1: 41 (21.7 bits)
    S2: 57 (29.0 bits)[JOB MESSAGES]
45  [END JOB STATUS]

```

DESCA12 Blast result against nonredundant proteins

DeCypher Results for: NCBI BLASTX Translated Search

Results by Query

Click on a query below to view its search results.

5 Your_Query starting with: TGATGAGTCCTGAGTAAACC

Search Details

Results for: Your_Query starting with:

10 **TGATGAGTCCTGAGTAAACC; (Length=322)**

[Return to query summary](#)

RANK		Sequences producing significant alignments:		(bits)	Value
15	<u>1</u>	dbj <u>BAB09184.1</u> <u>AB008264</u>	N-hydroxycinnamoyl/benzoyltransferas...	127	5e-029
	<u>2</u>	pir <u>T45610</u>	proanthranilate N-benzoyltransferase-like protein -...	109	1e-023
	<u>3</u>	gb <u>AAB95283.1</u> <u>AF002109</u>	putative anthocyanin 5-aromatic acylt...	107	4e-023
20	<u>4</u>	pir <u>T45961</u>	anthranilate N-benzoyltransferase-like protein - Ar...	107	5e-023
	<u>5</u>	pir <u>T45611</u>	N-hydroxycinnamoyl/benzoyltransferase-like protein ...	106	8e-023
	<u>6</u>	pir <u>T45612</u>	N-hydroxycinnamoyl/benzoyltransferase-like protein ...	98	2e-020
25	<u>7</u>	dbj <u>BAA93453.1</u> <u>AB026495</u>	acyltransferase homolog [Petunia x h...	73	8e-013
	<u>8</u>	dbj <u>BAB10949.1</u> <u>AB020742</u>	anthranilate N-hydroxycinnamoyl/benz...	73	1e-012
	<u>9</u>	dbj <u>BAB10067.1</u> <u>AB005244</u>	acyltransferase [Arabidopsis thaliana]	63	1e-009
30	<u>10</u>	pir <u>T45574</u>	anthranilate N-hydroxycinnamoyl/benzoyltransferase-...	59	2e-008
	<u>11</u>	pir <u>T45576</u>	anthranilate N-hydroxycinnamoyl/benzoyltransferase-...	54	6e-007
	<u>12</u>	pir <u>T45573</u>	anthranilate N-hydroxycinnamoyl/benzoyltransferase-...	52	2e-006
35	<u>13</u>	dbj <u>BAB10950.1</u> <u>AB020742</u>	anthranilate N-hydroxycinnamoyl/benz...	50	8e-006
	<u>14</u>	dbj <u>BAB11280.1</u> <u>AB005247</u>	anthranilate N-hydroxycinnamoyl/benz...	45	3e-004
	<u>15</u>	dbj <u>BAA93475.1</u> <u>AB029340</u>	anthocyanin acyltransferase [Perilla...	35	0.32
40	<u>16</u>	gb <u>AAF56962.1</u> <u>AE003771</u>	CG15512 gene product [alt 1] [Drosoph...	34	0.71
	<u>17</u>	pir <u>T40256</u>	hypothetical protein SPBC337.03 - fission yeast (S...	34	0.71

18	emb CAB63877.1 AL034358	hypothetical protein L4830.02 [Leish...	34
0.71			
19	gb AAD22971.1 AF124335_1 AF124335	kappa casein precursor [Tri...	33
1.2			
5	20 dbj BAB10831.1 AB016892	anthocyanin acyltransferase-like pro...	32 1.6
21	gb AAC70926.1 AF063018	homeodomain protein [Danio rerio]	32
1.6			
22	pir B72698	hypothetical protein APE1002 - Aeropyrum pernix (st...	32 2.1
23	pir T51029	related to pathway-specific nitrogen regulator [imp...	32 2.8
10	24 pir S42886	collagen - silkworm >gi 457769 emb CAA83002.1 (Z30...	32
2.8			
25	gb AAF36387.1 AF220656_1 AF220656	apoptosis-associated nuclea...	31
3.6			
26	ref NP_031376.1	pleckstrin homology-like domain, family A, mem...	31
15	3.6		
27	pir S74461	ABC transporter slr1494 - Synechocystis sp. (strain...	31 3.6
28	gb AAC25822.1 AF038608	contains similarity to Mus musculus t...	31
4.7			
29	gb AAF75279.1 AF265353_1 AF265353	byssal protein Dpfp1 precu...	31
20	4.7		
30	pir D83554	hypothetical protein PA0732 [imported] - Pseudomona...	31
4.7			

RANK 1 ITERATION 0>dbj|BAB09184.1| AB008264 N-
25 hydroxycinnamoyl/benzoyltransferase-like
protein [Arabidopsis thaliana]
Length = 450

Score = 127 bits (315), Expect = 5e-029
30 Identities = 58/103 (56%), Positives = 80/103 (77%), Gaps = 1/103 (0%)
Frame = +2Query: 5 ES*VNHSDKVVRDFVNKWLQSPYVYPMG-
MFDSSSVMMGSSSPGFDMYGNEFGLGKAIALR 181
++ H+ + V +++WL+SPY+Y + +F+ SVMMGSSP F+ YG EFGLGK +
LR
35 Sbjct: 342
QAVAEHTSEKVSQMIDQWLKSPYIYHIDRLFEPMSVMMGSSPRFNKYGCEF
GLGKGVTLR 401Query: 182
SGYANKFVGKVTSYEGYEGGGSVDLEICLPPDSMKALESDEELV 313
SGYA+KF GKV++Y G EGGGS+DLE+CL P+ M+ALESDEE +
40 Sbjct: 402 SGYAHKFDGKVSAYPGREGGGSIDLEVCLVPEFMEALESDEEFM
445

RANK 2 ITERATION 0>pir|T45610 proanthranilate N-benzoyltransferase-like protein -

45 Arabidopsis thaliana >gi|6562299|emb|CAB62597.1|
(AL133421) proanthranilate N-benzoyltransferase-like

protein [Arabidopsis thaliana]
 >gi|10176719|dbj|BAB09949.1| (AB005249) anthranilate
 N-hydroxycinnamoyl/benzoyltransferase-like protein
 [Arabidopsis thaliana]
 5 Length = 456

Score = 109 bits (269), Expect = 1e-023
 Identities = 50/103 (48%), Positives = 76/103 (73%), Gaps = 1/103 (0%)
 Frame = +2Query: 5 ES*VNHSDKVVRDFVNKWLQSPYVYPMG-
 10 MFDSSSVMMGSSPGFDMYGNEFGLGKAIALR 181
 E+ + + + VV + + WL+S YV+ + + + V +GSSP F MY EFG+GKA+A+R
 Sbjct: 346
 EAVIGNTSEVVSETIKNWLKSSYVFHLEKLLGAMVVHIGSSPRFKMYECEFG
 MGKAVAVR 405Query: 182
 15 SGYANKFVGKVTSEYEGYEGGGSVDLEICLPPDSMKALESDEELV 313
 SGY KF GK+++Y G EGGG++DLE+CL P+ M+ALES D+E +
 Sbjct: 406 SGYGGKFDGKISAYAGREGGGTIDLEVCLLPEFMEALES DQEFM
 449

20 RANK 3 ITERATION 0>gb|AAB95283.1| AF002109 putative anthocyanin 5-
 aromatic
 acyltransferase [Arabidopsis thaliana]
 Length = 482

25 Score = 107 bits (265), Expect = 4e-023
 Identities = 49/105 (46%), Positives = 71/105 (66%)
 Frame = +2Query: 2
 DES*VNHSDKVVRDFVNKWLQSPYVYPMGMFDDSSSVMMGSSPGFDMYGN
 EFGLGKAIALR 181
 30 ++S HD +R V W +P +P+G D +SV MGSSP F MY N+FG G+ +A+R
 Sbjct: 373
 NQSVAAHQDGRIRSVVADWEANPRCFPLGNADGASVTMGSSPRFPMYDND
 FGWGRPVAVR 432Query: 182
 SGYANKFVGKVTSEYEGYEGGGSVDLEICLPPDSMKALESDEELVR 316
 35 SG +NKF GK++++ G EG G+VDLE+ L P++M +ESD E +R
 Sbjct: 433 SGRSNKFDGKISAFPGREGNGTV DLEVVLSPETMAGIESDGEFMR
 477

40 RANK 4 ITERATION 0>pir|[T45961] anthranilate N-benzoyltransferase-like protein
 -
 Arabidopsis thaliana >gi|6759444|emb|CAB69849.1|
 (AL137189) anthranilate N-benzoyltransferase-like protein
 [Arabidopsis thaliana]
 Length = 475

45 Score = 107 bits (264), Expect = 5e-023

Identities = 49/101 (48%), Positives = 69/101 (67%)

Frame = +2Query: 14

VNHSDKVVRDFVNKWLQSPYVYPMGMFDSSSVMMGSSPGFDMYGNFGL
GKAIALRSGYA 193

5 V H D VR + W P ++P+G D +S+ MGSSP F MY N+FG GK +A+RSG A

Sbjct: 366

VAHDDATVRRGIAAWESDPRLFPLGNPDGASITMGSSPRFPMYDNDFGWG
KPLAVRSGGA 425Query: 194

NKFVGVKVTSEGYEGGGSDLEICLPDMSMKALESDEELVR 316

10 NKF GK++++ G EG GSVDLE+ L P++M +E+D E ++

Sbjct: 426 NKFDGKISAFPGREGNGSVDLEVVLAPETMTGIENDAEFMQ 466

RANK 5 ITERATION 0>pir|[T45611] N-hydroxycinnamoyl/benzoyltransferase-like
protein -

15 Arabidopsis thaliana >gi|6562300|emb|CAB62598.1|
(AL133421) N-hydroxycinnamoyl/benzoyltransferase-like
protein [Arabidopsis thaliana]

>gi|10176720|dbj|BAB09950.1| (AB005249)
N-hydroxycinnamoyl/benzoyltransferase-like protein
20 [Arabidopsis thaliana]
Length = 454

Score = 106 bits (262), Expect = 8e-023

Identities = 48/103 (46%), Positives = 75/103 (72%)

25 Frame = +2Query: 5

ES*VNHSDKVVRDFVNKWLQSPYVYPMGMFDSSSVMMGSSPGFDMYGNF
FGLGKAIALRS 184

++ H+ ++ + ++WL++ ++ G F + V MGSSP F+ YG+EFG+GKA+A+RS
Sbjct: 344 QAVTEHTGEKISADMDRWLKA-

30 HLKLDGFFSPNIVHMGSSPRFNKYGSEFGMGKAVAVRS 402Query: 185
GYANKFVGVKVTSEGYEGGGSDLEICLPDMSMKALESDEELV 313

GY K+ GKV++Y G EGG S+DLE+CLPP+ M+ALE D+E +
Sbjct: 403 GYGGKYDGKVSAYPGREGGASIDLEVCLPPECMEALELDQEFM
445

35 RANK 6 ITERATION 0>pir|[T45612] N-hydroxycinnamoyl/benzoyltransferase-like
protein -

Arabidopsis thaliana >gi|6562301|emb|CAB62599.1|
(AL133421) N-hydroxycinnamoyl/benzoyltransferase-like
40 protein [Arabidopsis thaliana]
>gi|10176721|dbj|BAB09951.1| (AB005249)
N-hydroxycinnamoyl/benzoyltransferase-like protein
[Arabidopsis thaliana]
Length = 464

45

Score = 98.3 bits (241), Expect = 2e-020

RANK 9 ITERATION 0>dbj|BAB10067.1| AB005244 acyltransferase
[Arabidopsis thaliana]
Length = 484

5 Score = 62.8 bits (150), Expect = 1e-009
Identities = 34/98 (34%), Positives = 53/98 (53%)
Frame = +2Query: 20
HSDKVVRDFVNKWLQSPYVYPMGMFDSSSVMMGSSPGFDMYGNEFGLGK
AIALRSGYANK 199
10 H V+ ++W +SP ++ + V +GSSP F +Y +FG GK +RSG N+
Sbjct: 351
HDASVIDARNDEWEKSPKIFQFKDAGVNCVAVGSSPRFRVYEVDGFGKPE
TVRSGSNR 410Query: 200
FVGKVTSEYEGYEGGGSVDLEICLPPDSMKALESDEELV 313
15 F G + Y+G GG S+D+EI L M+ L +E +
Sbjct: 411 FNGMMYLYQKGAGGISIDVEITLEASVMEKLVKSKEFL 448

RANK 10 ITERATION 0>pir|[T45574 anthranilate N-
hydroxycinnamoyl/benzoyltransferase-like
protein - Arabidopsis thaliana
>gi|6523039|emb|CAB62307.1| (AL132976) anthranilate
N-hydroxycinnamoyl/benzoyltransferase-like protein
[Arabidopsis thaliana]
Length = 443

25 Score = 58.9 bits (140), Expect = 2e-008
Identities = 32/92 (34%), Positives = 53/92 (56%), Gaps = 3/92 (3%)
Frame = +2Query: 38 RDFVNKWLQSPYVYPMGM---
FDSSSVMMGSSPGFDMYGNEFGLGKAIALRSGYANKFVG 208
30 R + W+++ + G+ SV++ SSP F++Y N+FG GK IA+R+G +N G
Sbjct: 346
RIYAENWVRNMKIQKSGLGSKMTRDSVIVSSSPRFEVYDNDGFGWKPIAVR
AGPSNSISG 405Query: 209
KVTSYEGYEGGGSVDLEICLPPDSMKALESDEELV 313
35 K+ + G E G +D+ L PD + L +D E +
Sbjct: 406 KLVFFRGIE-EGCIDVHAFLLPDVLVKLLADVEFL 439

RANK 11 ITERATION 0>pir|[T45576 anthranilate N-
hydroxycinnamoyl/benzoyltransferase-like
protein - Arabidopsis thaliana
>gi|6523041|emb|CAB62309.1| (AL132976) anthranilate
N-hydroxycinnamoyl/benzoyltransferase-like protein
[Arabidopsis thaliana]
Length = 459
45 Score = 53.9 bits (127), Expect = 6e-007

Identities = 29/83 (34%), Positives = 47/83 (55%), Gaps = 3/83 (3%)
 Frame = +2Query: 20 HSDKVVRDFVNKWLQS---
 PYVYPMGMFDDSSVMMGSSPGFDMYGNEFGLGKAIALRSGY 190
 H+++ R F W+++ P + M+ +SP F +Y N+FGLGK +A+R+G

5 Sbjct: 340
 HTNENFRTFSENWVRNGKIPRIDVRSRMGDHGFMSVNSPWFQVYDNDNDFGL
 GKPM AVRAGP 399Query: 191 ANKFVGKVTSEYEGYEGGGSVDLEICL 268
 AN GK+ + G E GS+D+ L
 Sbjct: 400 ANGIGGKLVVFRGIE-EGSIDVHAIL 424

10 RANK 12 ITERATION 0>pir|[T45573 anthranilate N-
hydroxycinnamoyl/benzoyltransferase-like
protein - Arabidopsis thaliana
>gi|6523038|emb|CAB62306.1| (AL132976) anthranilate
 15 N-hydroxycinnamoyl/benzoyltransferase-like protein
 [Arabidopsis thaliana]
 Length = 450

Score = 51.9 bits (122), Expect = 2e-006
 20 Identities = 28/99 (28%), Positives = 58/99 (58%), Gaps = 2/99 (2%)
 Frame = +2Query: 17 NHSDKVVRDFVNKWLQSPYVYPMGMFDS--
 SSVMMGSSPGFDMYGNEFGLGKAIALRSGY 190
 + +++ + F W+++ G+ +++++ SSP F++Y +FG GK IA+R+G
 Sbjct: 345
 25 SQTNETCKSFAEDWVRNIKNLNSGIGSKVGN TIV IASSPRFEVYNKDFGWGK
 PIAIRAGP 404Query: 191
 ANKFVGKVTSEYEGYEGGGSVDLEICLPPDSMKALESD EELV 313
 +N GK++ ++G GS+D++ L D + L +D E +
 Sbjct: 405 SNSINGKLSVFQGI-SEGSIDVQAILWGDVIVKLLADLEFL 444

30 RANK 13 ITERATION 0>dbj|[BAB10950.1| AB020742 anthranilate
N-hydroxycinnamoyl/benzoyltransferase-like protein
[Arabidopsis thaliana]
Length = 434

35 Score = 50.0 bits (117), Expect = 8e-006
 Identities = 31/99 (31%), Positives = 57/99 (57%), Gaps = 2/99 (2%)
 Frame = +2Query: 11
 *VNHSDKVVRDFVNKWLQSPYVYPMGMFDDSSVMMGSSPGFDMYGNEFG
 40 LGKAIALRSG- 187
 ++ +D+ + F W+++ + P++ S +++ +S FD+Y N+FG GK IA R+G
 Sbjct: 332 ELSQTDEKAKAFAENWVKNIKI-PVSV-
 GSKDLVVTNSHRFDVYCND FGWGKPIAARAGP 389Query: 188 -
 YANKFVGKVTSEYEGYEGGGSVDLEICLPPDSMKALESD EEE 307
 45 Y N G++ ++G G S+D + CL P ++ L D E
 Sbjct: 390 PYLN---GRLVVFKGI-GEASLDFQACLLPQVVEKLVKDAE 426

Sbjct: 100 DVPTAKPRDSMTSVVTVNRHNSISVIGSTPQTTPRKDTRL--
 SLGKVDFERAGLQPASQP 157Query: 147
 LPYMSNPGEPIITLELSNIPIGYT*GDCNHLTKSRTTL 28
 LP ++P+ TL++ +IP+ N L +S+TTL

5 Sbjct: 158 LPRPRKIVQVPVATLDVEDIPVVAPSPSSNGLFRRSKTTL 197

RANK 17 ITERATION 0>pir|T40256 hypothetical protein SPBC337.03 - fission
 yeast

10 (Schizosaccharomyces pombe) >gi|3738180|emb|CAA21273.1|
 (AL031854) hypothetical protein [Schizosaccharomyces
 pombe]
 Length = 387

Score = 33.6 bits (75), Expect = 0.71
 15 Identities = 19/54 (35%), Positives = 28/54 (51%)
 Frame = -2Query: 276
 SGGKHISKSTLPPPSYPS*EVTFTNLFAYPELRRAIAFPSPNSLPYMSNPGEPI
 115

+ GKH ++T PP S P+ + + +Y PS NS+PY SN E P
 20 Sbjct: 273 TAGKHNVETTSPSSSPNSDDAYSPQVDSYS-----
 PSINSVPYTSNIVENP 319

RANK 18 ITERATION 0>emb|CAB63877.1| AL034358 hypothetical protein
 L4830.02 [Leishmania
 25 major]
 Length = 501

Score = 33.6 bits (75), Expect = 0.71
 Identities = 19/76 (25%), Positives = 37/76 (48%)
 30 Frame = +1Query: 64
 VSLCIPNGDVR*FQCDDGKFAGV*HVW**IWTRKSYSSSKWVCK*VCWEGD
 FL*RI*GWR 243

VS +P+G++ ++DG + G R +++++ V W + R G +
 Sbjct: 424 VSDAVPDGNLLDRKFEDGIYPGCEQDRQQ---RIELTAMEEIQRNV-
 35 WRKEKAKRKEGGQ 479Query: 244 KCGFGNMFATGFDEGS 291
 +CG G++ A D+GS
 Sbjct: 480 QCGRGDVTAVEDDDGS 495

RANK 19 ITERATION 0>gb|AAD22971.1|AF124335_1 AF124335 kappa casein
 40 precursor
 [Trichosurus vulpecula]
 Length = 178

Score = 32.8 bits (73), Expect = 1.2
 45 Identities = 21/54 (38%), Positives = 30/54 (54%), Gaps = 3/54 (5%)

Frame = -2Query: 243 PPSY-PS*EVTFTNLFAAYPLRRAIAFPSPN--
SLPYMSNPGELPIITLELSNIPI 82

P PSY P +P +++ L A AF P+ LP S+P P T++ +NIPI

Sbjct: 85

5 PYPSYMPDLLPSIYPWSVSRNLHPAFAFNPPHYAQLPVPSSPTNSPTTTTIQTTN
IPI 141

RANK 20 ITERATION 0>dbj|BAB10831.1| AB016892 anthocyanin
acyltransferase-like protein

10 [Arabidopsis thaliana]
Length = 448

Score = 32.5 bits (72), Expect = 1.6

Identities = 22/72 (30%), Positives = 32/72 (43%), Gaps = 1/72 (1%)

15 Frame = +2Query: 77 YPMGMFDSSSVMMGSSPGFDMYGNEFGLGKAI-
ALRSGYANKFVGKVTSEYEGYEGGSVD 253

Y DS V+ S F+YG+FG GK +L + GK++ E +G G V+

Sbjct: 369 YEKAPVDSQFVSVAGSTRFGIYGLDFGWGKPFKSLVLSIDQR--
GKISIAESRDGSGGVE 426Query: 254 LEICLPPDSMKAL 292

20 + L M L
Sbjct: 427 IGFSLLKKQEMNVL 439
[END
ALIGNMENTS]

25 Job DetailsReturn to top

[BEGIN JOB STATUS][BEGIN SEARCH TIME]

[END SEARCH TIME]

[VERSION]

30 [SEARCH ID]

[EOL] CRLF

[COMMENT] /Comment=NCBI BLASTX Translated Search

[COMMENT] /

[ALGORITHM] BLASTX

35 [MATRIX] D:\DECYPHER\MATRIX\BLOSUM62.MAA

[QUERY FORMAT] FASTA/PEARSON

[QUERY TYPE] NT

[QUERY FILTER] T

[QUERY SEARCH] -1 -2 -3 1 2 3

40 [QUERY PATH] d:\decypher\query

[QUERY SET]

[TARGET TYPE] AA

[TARGET FRAMES] 1

[TARGET PATH] d:\decypher\target\blast

45 [TARGET SET] nr

[MAX SCORES] 30

[MAX ALIGNMENTS] 20

[THRESHOLD] 1
 [RESULT PATH] d:\decypher\output
 [OUTPUT FORMAT] TEXT EXTRACTALIGNED[SHOW GI] F
 [EXPECTATION] 10
 5 [GAPPED ALIGNMENT] TBLASTX
 BLASTX
 Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
 Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
 "Gapped BLAST and PSI-BLAST: a new generation of protein database search
 10 programs", Nucleic Acids Res. 25:3389-3402.Query= Your_Query starting with:
 TGATGAGTCCTGAGTAAACC /QuerySize=322
 (322 letters)Database: Nonredundant Proteins
 598,029 sequences; 189,012,571 total letters Database: Nonredundant
 Proteins
 15 Posted date:
 Number of letters in database: 189,012,571
 Number of sequences in database: 598,029

 Lambda K H
 20 0.318 0.135 0.401 Gapped
 Lambda K H
 0.270 0.0470 0.230
 Matrix: BLOSUM62.MAA
 Gap Penalties: Existence: 11, Extension: 1
 25 Number of Hits to DB: 133516101
 Number of Sequences: 598029
 Number of extensions: 2998397
 Number of successful extensions: 13427
 Number of sequences better than 10.0: 74
 30 Number of HSP's better than 10.0 without gapping: 19
 Number of HSP's successfully gapped in prelim test: 46
 Number of HSP's that attempted gapping in prelim test: 13378
 Number of HSP's gapped (non-prelim): 85
 length of query: 107
 35 length of database: 189,012,571
 effective HSP length: 52
 effective length of query: 54
 effective length of database: 157,915,063
 effective search space: 8527413402
 40 effective search space used: 8527413402
 frameshift window, decay const: 50, 0.1
 T: 12
 A: 40
 X1: 16 (7.3 bits)
 45 X2: 38 (14.8 bits)
 X3: 64 (24.9 bits)

S1: 41 (21.7 bits)
 S2: 65 (29.7 bits)[JOB MESSAGES]
 [END JOB STATUS]

DeCypher Results for: NCBI TBLASTX Similarity Search

5 Results by Query

Click on a query below to view its search results.

Your Query starting with: TGATGAGTCCTGAGTAAACC

Search Details

10 Results for: Your Query starting with:

TGATGAGTCCTGAGTAAACC; (Length=322)

[Return to query summary](#)

15	RANK	Sequences producing significant alignments:	(bits)	Value
	<u>1</u>	CL002872.88	123	5e-028
	<u>2</u>	CL025601.82.101	115	1e-025
	<u>3</u>	CL007466.48	97	4e-020
	<u>4</u>	CL023826.92	95	2e-019
20	<u>5</u>	CL029578.37.46	93	6e-019
	<u>6</u>	CL011486.47	78	1e-018
	<u>7</u>	CL032764.243	79	1e-018
	<u>8</u>	CL000914.59.74	86	1e-016
	<u>9</u>	CL012237.69	85	1e-016
25	<u>10</u>	CL003422.136	56	1e-014
	<u>11</u>	CL033768.113	58	3e-013
	<u>12</u>	CL032764.163	52	6e-010
	<u>13</u>	CL018865.84	55	2e-007
	<u>14</u>	CL024779.52.46	36	0.11
30	<u>15</u>	CL018266.130.51	36	0.11
	<u>16</u>	HTC084560-A01.R.75.110	28	0.13
	<u>17</u>	CL004816.157.53	35	0.15
	<u>18</u>	CL003911.66	35	0.15
	<u>19</u>	CL036945.61	35	0.20
35	<u>20</u>	CL031215.110	35	0.20
	21	CL009258.284	35	0.20
	22	CL009192.67	35	0.28
	23	CL006163.148	34	0.38
	24	CL003188.61	34	0.38
40	25	CL019614.57	34	0.38
	26	CL018419.53	34	0.38
	27	CL006309.333	34	0.38
	28	CL016897.178.190	34	0.38
	29	CL031069.149	34	0.53

RANK 1 ITERATION 0>CL002872.88

Length = 5276

5

Score = 123 bits (263), Expect = 5e-028
Identities = 53/97 (54%), Positives = 62/97 (63%)
Frame = +2 / +3

Query: 20

10 HSDKVVRDFVNKWLQSPYVYPMGMFDSSSVMMGSSPGFDMYGNEFGLGK
AIALRSGYANK 199

H+D +R V W P+Y FD S VMMGSSP FDMYG +FG GKA+A RSG

ANK

Sbjct: 3021

15 HTDADIRARVAAWEVKPIIYTARYFDPSGVMGSSPRFDMYGCDFGWGKA
LAARSGKANK 3200

Query: 200 FVGKVTSYEGYEGGGSVDLEICLPDMSMKALESDEEL 310

GK + Y G EGGGS+D E+ L P M AL+ D EL

Sbjct: 3201 MDGKASLYPGREGGGSIDAEVVLTPHHMAALDDDHEL 3311

20 Score = 81.7 bits (172), Expect = 2e-015
Identities = 43/96 (44%), Positives = 52/96 (53%)
Frame = -2 / -2

Query: 309

Query: 509
 NSSSDSRAFIESGGKHISKSTLPPPSYPS*EVTFPTNLFAYPLRRAIAFPSPNSLP
 YMSN 130

+S S S A + G S S L P P S P P + L A P L R A A F P P S P Y M S N

Sbjct: 3310

SSWSSSSAAMWCGVSTTSASMLPPPSRPGYSDALPSILLALPLRAASAFHPK
SOPYMSN 3131

30 Query: 129 PGELPIITLELSNIPIGYT*GDCNHLTKSRTTSL 22
GELPIIT+S Y G +H T++ +S+

Sbjct: 3130 RGELPIITPDGSKYLAVYIIGFTSHAATRALMSASV 3023

Score = 47.3 bits (97), Expect = 4e-005
Identities = 21/79 (26%), Positives = 37/79 (46%)

35 Frame = -1 / -1

Query: 310

QFLI*FKSLHRIRWQTYFQIHTSSTLISFIRSHLPNKLICPTSKSYSFSESKFITIH
VK 131

$$O^{++} + H^{+} + I^{+} + SS L^{++} L^{++} + K^{+} + HV^{+}$$

40 Sbict: 3311

QLVVVVQRRHVWSEHHLRIYASSALPPRVQRR LAVHLVGLAAPRRQRLPP
PKVA AVHVE 3132

Query: 130 PRRTSHHHTGTIEHPHWVY 74

PRR HHH +E P VY

45 Sbjct: 3131 PRRAPHHHPRRVEVPRRVY 3075

RANK 2 ITERATION 0>CL025601.82.101

Length = 7440

Score = 115 bits (245), Expect = 1e-025

5 Identities = 51/96 (53%), Positives = 61/96 (63%)

Frame = +2 / +3

Query: 20

HSDKVVRDFVNKWLQSPYVYPMGMFDSSSVMMGSSPGFDMYGNEFGLGK

AIALRSGYANK 199

10 H+D +R V W P VY FD+S VM+GSSP FDMYG +FG GKA+A RSG

ANK

Sbjct: 5079

HTDAGIRARVAAWGARPTVYTARCFDASGVMVGSSPRFDMYGCDGFGWGK

AVAARSGKANK 5258

15 Query: 200 FVGKVTSEGYEGGGSVLDLEICLPPDSMKALESDDEE 307

GK + Y +GGG VD E+ L P+ M ALE D E

Sbjct: 5259 SDGKASLYPARDGGGGVDAEVVLAPEHMAALELDGE 5366

Score = 95.5 bits (202), Expect = 1e-019

Identities = 47/96 (48%), Positives = 55/96 (56%)

20 Frame = -2 / -3

Query: 309

NSSSDSRAFIESGGKHISKSTLPPPSYPS*EVTFTNLFA YPLRRAIAFPSPNSLP

YMSN 130

NS S S A + SG S ST PPPS FP++LFA+PLR A AFP P S PYMSN

25 Sbjct: 5368

NSPSSSSAAMCSGASTTSASTPPPPSRAGYSDAFPSDLFAFPLRAATAFPHPK

SHPYMSN 5189

Query: 129 PGELPIITLELSNIPIGYT*GDCNHLLTKSRTTSL 22

GELP IT + S YT G H T++R S+

30 Sbjct: 5188 RGELPTITPDASKHLAVYTVGLAPHAATRARMASV 5081

Score = 52.4 bits (108), Expect = 1e-006

Identities = 19/79 (24%), Positives = 39/79 (49%)

Frame = -1 / -2

Query: 310

35 QFLI*FKSLHRIRWQTYFQIHTSSTLISFIRSHLPNKLICPTSKSYSFSESKFITIH

VK 131

+ + + H +R Q + + + +S + ++ LP L + +P + + + +HV+

Sbjct: 5369

ELAVELQRRHVLRRQHHLRVDAASAVPRRVQRRLPVGLVRLPAPRRHRLPP

40 PEVAPVHVE 5190

Query: 130 PRRTSHHHTGTIEHPHWVY 74

PRR HHH +E P V+

Sbjct: 5189 PRRAPHHHPRRVEAPRRVH 5133

45 RANK 3 ITERATION 0>CL007466.48

Length = 2719

Score = 97.3 bits (206), Expect = 4e-020
Identities = 37/77 (48%), Positives = 55/77 (71%)
Frame = +2 / +1

5 Query: 83
MGMFDSSSVMMGSSPGFDMYGNEFGLGKAIALRSGYANKFVGKVTSEYEGY
EGGGSVDLEI 262

++ ++++ GSSP FD++GN+FG G+ +RSG ANKF GKVT YEG +G GS+
LE+

10 Sbjct: 1369
LSLLGGAAIITGSSPRFDVFGNDFGWGRPATVRSGGANKFDGKVTVEYEGPD
GAGSMSLEV 1548

Query: 263 CLPPDSMKALESDEELV 313
CL P ++ L +DEE +

15 Sbjct: 1549 CLTPAALAKLVADEEFM 1599
Score = 74.4 bits (156), Expect = 3e-013
Identities = 34/67 (50%), Positives = 40/67 (58%)
Frame = -2 / -3

Query: 309
20 NSSSDSRAFIESGGKHISKSTLPPPSYPS*EVTFPTNLFAYPLRRAIAFPSPNSLP
YMSN 130

NSSS + +G + S LP PS PS VTFP+NLFA PLR P P SLP SN

Sbjct: 1595
NSSSATSFASAAGVRQTSSDMLPAPSGPSYTVTFPSNLFAPPLRTVAGLPHPK
25 SLPNTSN 1416

Query: 129 PGELPII 109
GELP++

Sbjct: 1415 RGELPVM 1395

30 RANK 4 ITERATION 0>CL023826.92
Length = 7907

Score = 94.5 bits (200), Expect = 2e-019
Identities = 34/70 (48%), Positives = 53/70 (75%)

35 Frame = +2 / +2
Query: 104
SVMMGSSPGFDMYGNEFGLGKAIALRSGYANKFVGKVTSEYEGYEGGGSVD
LEICLPPDSM 283

+++ GSSP FD++GN+FG G+ +A+RSG NK GK T +EG +G GS+ LE+C+
40 PD++
Sbjct: 2018
ALITGSSPRFDVFGNDFGWGRPVAVRSGAGNKIDGKATVFEGPDGAGMSL
EVCIPDAL 2197

Query: 284 KALESDEELV 313
45 + L +DEE +
Sbjct: 2198 RRLVADEEFM 2227

- Score = 68.9 bits (144), Expect = 1e-011
 Identities = 33/68 (48%), Positives = 37/68 (53%)
 Frame = -2 / -3
 Query: 309
 5 NSSSDSRAFIESGGKHISKSTLPPPSYPS*EVTFPTNLFAYPLRRAIAFPSPNSLP
 YMSN 130
 NSSS + SG S LP PS PS V FP+ LF PL A P P SLP SN
 Sbjct: 2223
 NSSSATSLRSASGAMQTSSDMLPAPSGPSNTVAFPSILFPAPLLTATGLPHPKS
 10 LPNTSN 2044
 Query: 129 PGELPIIT 106
 GELP+I+
 Sbjct: 2043 RGELPVIS 2020
- 15 RANK 5 ITERATION 0>CL029578.37.46
 Length = 3483
- Score = 93.2 bits (197), Expect = 6e-019
 Identities = 38/71 (53%), Positives = 52/71 (72%)
 20 Frame = +2 / +3
 Query: 101
 SSVMMGSSPGFDMYGNEFGLGKAIALRSGYANKFVGKVTSEYEGYEGGGSV
 DLEICLPDS 280
 ++V GSSP FD++GN+FG G+ ++RSG ANKF GKVT YEG G GS+ LE+CL
 25 P +
 Sbjct: 1842
 TAVHTGSSPRFDVFGNDFGWGRPASVRSGGANKFDGKVTVEGPGGAGSM
 SLEVCLAPAA 2021
 Query: 281 MKALESDEELV 313
 30 + L +DEE +
 Sbjct: 2022 LGKLVADEEFM 2054
 Score = 69.8 bits (146), Expect = 7e-012
 Identities = 33/68 (48%), Positives = 38/68 (55%)
 Frame = -2 / -3
 35 Query: 309
 NSSSDSRAFIESGGKHISKSTLPPPSYPS*EVTFPTNLFAYPLRRAIAFPSPNSLP
 YMSN 130
 NSSS + +G + S LP P PS VT P+NLFA PLR P P SLP SN
 Sbjct: 2050
 40 NSSSATSFPSAAGARQTSSDMLPAPPGPSYTVTLPSNLFAPPLRTLGLPHPK
 SLPNTSN 1871
 Query: 129 PGELPIIT 106
 GELP+ T
 Sbjct: 1870 RGELPVWT 1847
- 45 RANK 6 ITERATION 0>CL011486.47

Length = 2925

Score = 35.0 bits (70), Expect(2) = 1e-018
Identities = 14/41 (34%), Positives = 21/41 (51%)

5 Frame = +2 / -1

Query: 20 HSDKVVRDFV NKWLQSPYVYPMGMFDSSSVMMGSSPGFDMY
142

+ D +R W +P +P+G D + + MGSS F MY

10 Sbjct: 1218 YDDGAIRRAAAWQGAPRCFPLGNPDGAVITMGSSNRFP MY
1096

Score = 78.0 bits (164), Expect(2) = 1e-018
Identities = 30/58 (51%), Positives = 43/58 (73%)
Frame = +2 / -1

Query: 143

15 GNEFGLGKAIALRSGYANKFVGKVTSEGYEGGGSV DLEICLPPDSMKALE
SDEELVR 316

GN+FG G+ +A+RSG ANKF GK++++ G GSVD+E+CL PD+M AL D E
++

Sbjct: 1092

20 GNDFGWGRPLAVRSGRANKFDGKMSAFPARAGDGSVDIEVCLAPDTMAAL
LRDSEFMQ 919

Score = 56.0 bits (116), Expect = 9e-008
Identities = 27/56 (48%), Positives = 31/56 (55%)
Frame = -2 / +2

25 Query: 309

NSSSDSRAFIESGGKHISKSTLPPPSYPS*EVTFPTNLFA YPLRRAIAFPSPNSLP
142

NS S S A + SG +H S STL P P+ P+NL A PLR A P P SLP

Sbjct: 926

30 NSLSRSSAAMVSGARHTSMSTLPSPARAGNADILPSNLLARPLRTARGRPHP
KSLP 1093

RANK 7 ITERATION 0>CL032764.243

Length = 3158

35

Score = 79.0 bits (166), Expect(2) = 1e-018
Identities = 32/60 (53%), Positives = 42/60 (69%)
Frame = +2 / -3

Query: 65

40 SPYVYPMGMFDSSSVMMGSSPGFDMY GNEFGLGKAIALRSGYANKFVGKV
TSYEGYEGGG 244

+P V +FD+S V + SSP FDMYG +FG GKA+A RSG NK+ GKV+ + G
+GGG

Sbjct: 342

45 APSVSAFRLFDASGVFVSSSPRFDMYG CDFGWGKAVAARS GKG NKYDGKV
SLFPGRDGGG 163

Score = 33.6 bits (67), Expect(2) = 1e-018
Identities = 13/24 (54%), Positives = 16/24 (66%)
Frame = +2 / -3

5 GGG +D E+ L P+ M ALE D E

Score = 63.4 bits (132), Expect = 6e-010
Identities = 35/80 (43%), Positives = 38/80 (46%)
Frame = -2 / +2

SSSDSRAFIESGGKHISKSTLPPPSYPS*EVTFPTNLFAYPLRRAIAFPSPNSLPY
MSNP 127

Sbjct: 101

Query: 126 GELPIITLELSNIPIGYT*G 67

Sbjct: 281 GELLTNTPLASNSLNADTDG 340

Query: 214 HLPNKLICPTSKSYSFSESKFITIHVKPRRTSHHHTGTIEHP 86

25 Sbjct: 193 HLPVVLVPLAAPRRHRLPPPEVAPVHVPEPRRAAHEHAARVEQP
321

Length = 5439

Score = 85.8 bits (181), Expect = 1e-016
Identities = 34/71 (47%), Positives = 49/71 (68%)
Frame = +2 / -1

35 SSVMMGSSPGFDMYGNEFGLGKAIALRSGYANKFVGKVTSYEGYEGGGSV
DLEICLPDS 280

+

40 TAINTGSSPRFDVFGKDFGWGRPATVRSGGTDKFDGKVTVEGPTGAGSMS
LEVCLTPVA 2326

+ L +DEE +

45 Score = 63.8 bits (133), Expect = 4e-010
Identities = 30/67 (44%), Positives = 36/67 (52%)

Frame = -2 / +2

Query: 309

NSSSDSRAFIESGGKHISKSTLPPPSYPS*EVTFTNLFA YPLRRAIAFPSPNSLP
YMSN 130

5 NSSS + +G + S L P P PS V T P+NL PLR P P SLP SN

Sbjct: 2297

NSSSATSFASATGVRQTSSDMLPAPVGPSYTVTLPSNLSVPPLRTVAGLPHPK
SLPNTSN 2476

Query: 129 PGELPII 109

10 GELP++

Sbjct: 2477 RGELPVL 2497

RANK 9 ITERATION 0>CL012237.69

Length = 2991

15

Score = 85.4 bits (180), Expect = 1e-016

Identities = 33/81 (40%), Positives = 53/81 (64%)

Frame = +2 / -2

Query: 71

20 YVYPMGMFDSSSVMMGSSPGFDMYGNFGLGKAIALRSGYANKFVGKVTS
YEGYEGGGSV 250

+V +++ V++ SP FD++GN+FG G+ ++RSG NK GK+T YE GGG +

Sbjct: 1289

FVTVASLQNAAGVVVISGSPRFDVFGNDFGWGRPVGVRSGAGNKMDGKITV

25 YERRGGGGGM 1110

Query: 251 DLEICLPPDSMKALESDEELV 313

+EICL P+++ L +DEE +

Sbjct: 1109 AVEICLAPEALARLVADEEFM 1047

Score = 35.4 bits (71), Expect = 0.15

30 Identities = 17/70 (24%), Positives = 31/70 (44%)

Frame = -1 / +3

Query: 316

AYQFLI*FKSLHRIRWQTYFQIHTSSTLISFIRSHLPNKLICIPTSKSYSFSESKFI
TIH 137

35 A++ L+ + R+R Q H++ + +LP LI ++ ++ H

Sbjct: 1044

AHELLVGDQPRERLRCQANLHRHAAAAASPLVHRNLPVHLIPGAAPDAHRP
PPPEVVAEH 1223

Query: 136 VKPRRTSHHH 107

40 V+PRR HH

Sbjct: 1224 VEPRRARDHH 1253

Score = 59.7 bits (124), Expect(2) = 3e-010

Identities = 31/68 (45%), Positives = 35/68 (50%)

Frame = -2 / +1

096677-062201

Query: 309
NSSSDSRAFIESGGKHISKSTLPPPSYPS*EVTFTNLFAAYPLRRAIAFPSPNSLP
YMSN 130

NSSS + SG + IS + PPP S V FP+ LF PLR P P SLP SN

5 Sbjct: 1051
NSSSATSLASASGARQISTAMPPPPRLSYTVIFPSILFPAPLRTPTGLPHPKSL
PNTSN 1230

Query: 129 PGELPIIT 106

GE I T

10 Sbjct: 1231 RGEPEITT 1254
Score = 24.4 bits (47), Expect(2) = 3e-010
Identities = 10/31 (32%), Positives = 14/31 (44%)
Frame = -1 / +3

Query: 127 RRTSHHHTGTIEHPHWVYIGRLQPFIDKIAH 35

15 R HHH G ++ H RL+P + H

Sbjct: 1236 RARDHHHAGVLQARHRHEPRRLRPRRQRAPH 1328

RANK 10 ITERATION 0>CL003422.136

Length = 6688

20 Score = 42.8 bits (87), Expect(3) = 1e-014
Identities = 17/43 (39%), Positives = 23/43 (52%)
Frame = +2 / +2

Query: 14

25 VNHS DKVVRDFVNKWLQSPYVYPMGMF DSSSVMMGSSPGFDMY 142

V H D +R W P +P+G D +++ MGSSP F MY

Sbjct: 2582
VAHEDGAIRRAAADWEAXPRCFPLGNPDGAALTMGSSPRFPMY 2710

30 Score = 19.8 bits (37), Expect(3) = 1e-014
Identities = 7/11 (63%), Positives = 9/11 (81%)
Frame = +2 / +2

Query: 143 GNEFGLGKAIA 175

GN+FG +AIA

Sbjct: 2714 GNDFGWXRAIA 2746

35 Score = 56.0 bits (116), Expect(3) = 1e-014
Identities = 22/46 (47%), Positives = 31/46 (66%)
Frame = +2 / +3

Query: 179

RSGYANKFVGKVTSEYEGYEGGGSVDLEICLPPDSMKALESDEELVR 316

40 R+G ANKF GK++++ G GSVD+E CL PD+M L D E ++

Sbjct: 2751
RTGRANKFDGKMSAFPSQAGDGSVDVEFCLAPDTMARLLGDHEFLQ 2888

Score = 40.0 bits (81), Expect(2) = 1e-005
Identities = 19/44 (43%), Positives = 25/44 (56%)
45 Frame = -2 / -1

Query: 309 NSSSDSRAFIESGGKHISKSTLPPPSYPS*EVTFTNLFAAYPLR 178

NS S SR + SG + S STLP P++ P+NL A P+R
 Sbjct: 2881 NSWSPSRRAMVSGARQNSTSTLPSPAWLGNADILPSNLLARPVR
 2750
 Score = 28.6 bits (56), Expect(2) = 1e-005
 5 Identities = 11/25 (44%), Positives = 15/25 (60%)
 Frame = -2 / -2
 Query: 141 YMSNPGE LPIITL ELSNIPIGYT*G 67
 Y+ N GELPI++ S +P G G
 Sbjct: 2709 YIGNRGELPIVSAAPSGLPSGKHRG 2635
 10
RANK 11 ITERATION 0>CL033768.113
 Length = 6217

 Score = 57.9 bits (120), Expect(2) = 3e-013
 15 Identities = 22/45 (48%), Positives = 31/45 (68%)
 Frame = +2 / -3
 Query: 107
 VMMGSSPGFD MYGNEFGLGKAIALRSGYANKFVGKVT SYEGYEGG 241
 +++ SP FD+ GN+FG G+ + +RSG NK GK+T YEG GG
 20 Sbjct: 2354
 MVISGSPRFDVLGNDFGWGRPVGVRSGAGNKVDGKMTVYEGRGGG 2220
 Score = 36.3 bits (73), Expect(2) = 3e-013
 Identities = 13/26 (50%), Positives = 20/26 (76%)
 Frame = +2 / -3
 25 Query: 236 GGGSV DLEICLPPDSMKALE SDEELV 313
 GGG S+ +EICL P+++ L +DEE +
 Sbjct: 2228 GGG SMAVEICLAPEALARLVADEEFM 2151
 Score = 27.6 bits (54), Expect(2) = 0.24
 Identities = 12/25 (48%), Positives = 15/25 (60%)
 30 Frame = -2 / +1
 Query: 309 NSSSDSRAFIESGGKHISKSTLPPP 235
 NSS S + SG + IS + LPPP
 Sbjct: 2155 NSSSATSLASASGARQISTAMLPPP 2229
 Score = 25.8 bits (50), Expect(2) = 0.24
 35 Identities = 11/39 (28%), Positives = 18/39 (45%)
 Frame = -1 / +3
 Query: 223 IRSHLPNKLIC IPTSKSYSFSESKFITIHVKPRRTSHHH 107
 + HLP L+ ++ ++ HV+PRR HH
 Sbjct: 2238 VHRHLPVHLVPGAAPDAHRPPPPEVVAQHVEPRRA*DHH 2354
 40 Score = 53.3 bits (110), Expect = 6e-007
 Identities = 24/62 (38%), Positives = 31/62 (49%)
 Frame = -2 / +1
 Query: 306
 SSSDSRAFIESGGKHISKSTLPPPSYPS*EVTFTP TNLFA YPLRRRAIAFPSPNSLPY
 45 MSNP 127
 +SS ++ + G ++ PP PS V FP+ LF PLR P P SLP SN

Sbjct: 2155
NSSSATSLASGARQISTAMLPPRPSYTVIFPSTLFPAPLRTPTGLPHPKSLP
NTSNR 2334

Query: 126 GE 121

5 GE

Sbjct: 2335 GE 2340

RANK 12 ITERATION 0>CL032764.163

Length = 3123

10

Score = 51.9 bits (107), Expect(2) = 6e-010

Identities = 20/35 (57%), Positives = 26/35 (74%)

Frame = +2 / +1

Query: 140 YGNEFGLGKAIALRSGYANKFVGKVTSEGYEGGG 244

15 YG +FG GKA+A RSG NK+ GKV+ + G +GGG

Sbjct: 1 YGCDGFWGKAVAARSGKGNKYDGKVSLEPGRDGGG 105

Score = 31.3 bits (62), Expect(2) = 6e-010

Identities = 12/24 (50%), Positives = 15/24 (62%)

Frame = +2 / +1

20 Query: 236 GGGSDLEICLPPDSMKALESDEE 307

GGG +D E+ L P+ M AL D E

Sbjct: 103 GGGGIDAEVELAPEHMXALXEDXE 174

Score = 46.0 bits (94), Expect = 1e-004

Identities = 19/34 (55%), Positives = 20/34 (57%)

25 Frame = -2 / -2

Query: 243 PPPSYPS*EVTFPTNLFAYPLRRAIAFPSPNSLP 142

PPPS P TFP+ LF PL A AFP P S P

Sbjct: 104 PPPSRPGNSDTFPSYLFPLPLLAATAFPHPKSHP 3

30 RANK 13 ITERATION 0>CL018865.84

Length = 1436

Score = 54.7 bits (113), Expect = 2e-007

Identities = 23/58 (39%), Positives = 32/58 (54%)

35 Frame = +2 / +1

Query: 128

GFDMYGNEFGLGKAIALRSGYANKFVGKVTSEGYEGGGSDLEICLPPDS
MKALESD 301

GF +Y G G+ +RSG NKF G V Y G G G +D+ + L P+ M+ L+ D

40 Sbjct: 97

GFQVYDVXXGFGRPERVRSGANNKFDGMVXLYPGRGGXGGIDVXLSLQPE
PMQRDKD 270

Score = 34.5 bits (69), Expect = 0.28

Identities = 21/56 (37%), Positives = 22/56 (38%)

45 Frame = -2 / -1

Query: 294
SRAFIESGGKHISKSTLPPSYPS*EVTFTNLFAAYPLRRAIAFPSPNSLPYMSN
P 127

S ISG S P P P * T P+NL PLR P P S NP

5 Sbjct: 263
SNLCIGSGCSESXTSMPPXPPRPG*RXTIPSNLLLAPLRTRSGRPKPXSTSXT*
NP 96

10 RANK 14 ITERATION 0>CL024779.52.46
Length = 3598

Score = 35.9 bits (72), Expect = 0.11
Identities = 14/31 (45%), Positives = 20/31 (64%)
Frame = -2 / -3

15 Query: 243 PPPSYPS*EVTFTNLFAAYPLRRAIAFPSPN 151
PPPS+PS ++ P+ L RRA A+P P+
Sbjct: 374 PPPSFPSLLSLPSLL*RQRRRAAAYPPPD 282

20 RANK 15 ITERATION 0>CL018266.130.51
Length = 3544

Score = 35.9 bits (72), Expect = 0.11
Identities = 14/31 (45%), Positives = 20/31 (64%)
Frame = -2 / +2

25 Query: 243 PPPSYPS*EVTFTNLFAAYPLRRAIAFPSPN 151
PPPS+PS ++ P+ L RRA A+P P+
Sbjct: 605 PPPSFPSLLSLPSLL*RQRRRAAAYPPPD 697

30 RANK 16 ITERATION 0>HTC084560-A01.R.75.110
Length = 6345

Score = 26.7 bits (52), Expect(2) = 0.13
Identities = 11/30 (36%), Positives = 15/30 (49%)
Frame = -3 / -2

35 Query: 314 VPIPHLIQEPSSNPVANIFPNPHFLHPHIL 225
VP + P P+ P+P+ LHPH L
Sbjct: 1190 VPQCFPLPHPHFQPLHQDHPDPYHLHPHDL 1101

Score = 27.6 bits (54), Expect(2) = 0.13
Identities = 11/20 (55%), Positives = 12/20 (60%)

40 Frame = -3 / -2
Query: 248 HFLHPHILHKKSPSQQTYLH 189
HF H H LH+ QQT LH
Sbjct: 1010 HFPHLHHLHQHSLQQTRLH 951

45 RANK 17 ITERATION 0>CL004816.157.53
Length = 3135

[END
ALIGNMENTS]

5 Job DetailsReturn to top

[BEGIN JOB STATUS][BEGIN SEARCH TIME]

[END SEARCH TIME]

[VERSION]

[SEARCH ID]

10 [EOL] CRLF

[COMMENT] /Comment=NCBI TBLASTX Similarity Search

[COMMENT] /

[ALGORITHM] TBLASTX

[MATRIX] D:\DECYPHER\MATRIX\BLOSUM62.MAA

15 [QUERY FORMAT] FASTA/PEARSON

[QUERY TYPE] NT

[QUERY FILTER] T

[QUERY SEARCH] -1 -2 -3 1 2 3

[QUERY PATH] d:\decypher\query

20 [QUERY SET]

[TARGET TYPE] NT

[TARGET FRAMES] -1 -2 -3 1 2 3

[TARGET PATH] d:\decypher\target\blast

[TARGET SET] rice_contigs

25 [MAX SCORES] 30

[MAX ALIGNMENTS] 20

[THRESHOLD] 1

[RESULT PATH] d:\decypher\output

[OUTPUT FORMAT] TEXT EXTRACTALIGNED[SHOW GI] F

30 [EXPECTATION] 10

[GAPPED ALIGNMENT] TTBLASTX

TBLASTX

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),

35 "Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs", Nucleic Acids Res. 25:3389-3402.Query= Your_Query starting with:
TGATGAGTCCTGAGTAAACC /QuerySize=322

(322 letters)Database:

154,797 sequences; 359,911,975 total letters Database:

40 Posted date:

Number of letters in database: 359,911,975

Number of sequences in database: 154,797

Lambda K H

45 0.318 0.135 0.401

Matrix: BLOSUM62.MAA

Number of Hits to DB: 322374408

Number of Sequences: 154797
 Number of extensions: 5099001
 Number of successful extensions: 274443
 Number of sequences better than 10.0: 619
 5 length of query: 107
 length of database: 119,970,658
 effective HSP length: 51
 effective length of query: 55
 effective length of database: 112,076,011
 10 effective search space: 6164180605
 effective search space used: 6164180605
 frameshift window, decay const: 50, 0.1
 T: 13
 A: 40
 15 X1: 16 (7.3 bits)
 X2: 0 (0.0 bits)
 S1: 41 (21.7 bits)
 S2: 58 (29.5 bits)[JOB MESSAGES]
 [END JOB STATUS]

20 DESCA13 Blast result against swissprot
DeCypher Results for: NCBI BLASTX Translated Search

Results by Query

25 *Click on a query below to view its search results.*
 Your_Query starting with: GATGAGTCCTGAGTAACAAT

Search Details

Results for: Your_Query starting with:

30 **GATGAGTCCTGAGTAACAAT; (Length=215)**

[Return to query summary](#)

RANK	Sequences producing significant alignments:	(bits)	Value
1	sp P26949 CAFA_YERPE F1 CAPSULE ANCHORING PROTEIN		
35	35 PRECURSOR 29 1.6		
2	sp P28582 CDPK_DAUCA CALCIUM-DEPENDENT PROTEIN KINASE (CDPK) 28 3.6		
3	sp P17971 CIKL_DROME VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN SH... 27 4.7		
40	4 sp THYG_RAT_2 [Segment 2 of 2] THYROGLOBULIN PRECURSOR 27 6.2		
5	sp P44526 ZNUA_HAEIN HIGH-AFFINITY ZINC UPTAKE SYSTEM PROTEIN Z... 27 8.1		

6 sp|O30408|TYCB_BACBR TYROCIDINE SYNTHETASE II [INCLUDES:
ATP-DE... 27 8.1

7 sp|P19888|MTBA_BACAR MODIFICATION METHYLASE BANI
(CYTOSINE-SPEC... 27 8.1

5

RANK 1 ITERATION 0>sp|P26949|CAFA_YERPE F1 CAPSULE ANCHORING
PROTEIN PRECURSOR

Length = 833

10 Score = 29.0 bits (63), Expect = 1.6

Identities = 15/43 (34%), Positives = 25/43 (57%)

Frame = +2Query: 65

TTSSFALYINHVFSYYHRLTLHNYKHEHIQLYDK*TSALHESV 193

+T+SF++ NH F LTL+ K ++I Y + TS L ++

15 Sbjct: 513 STTSFSVGYNHFFRNGMSLTLNLSKTQNINKYGEKTSSELLSNI 555

RANK 2 ITERATION 0>sp|P28582|CDPK_DAUCA CALCIUM-DEPENDENT
PROTEIN KINASE (CDPK)

Length = 532

20

Score = 27.8 bits (60), Expect = 3.6

Identities = 10/30 (33%), Positives = 17/30 (56%)

Frame = +2Query: 86 YINHVFSYYHRLTLHNYKHEHIQLYDK*TS 175

Y+ ++ HR L +Y+H+ Q +DK S

25 Sbjct: 440 YLEFITATMHRHKLESYEHQAFQYFDKDNS 469

RANK 3 ITERATION 0>sp|P17971|CIKL_DROME VOLTAGE-GATED
POTASSIUM CHANNEL PROTEIN SHAL

(SHAL2)

30 Length = 490

Score = 27.4 bits (59), Expect = 4.7

Identities = 10/25 (40%), Positives = 14/25 (56%)

Frame = +2Query: 95 HVFSYYHRLTLHNYKHEHIQLYDK* 169

35 H+ +YY LH KHE + YD+

Sbjct: 94 HILNYYRTGKLHYPKHECLTSYDEE 118

RANK 4 ITERATION 0>sp||THYG_RAT_2 [Segment 2 of 2] THYROGLOBULIN
PRECURSOR

40 Length = 967

Score = 27.0 bits (58), Expect = 6.2

Identities = 16/46 (34%), Positives = 23/46 (49%), Gaps = 2/46 (4%)

Frame = +2Query: 17 QSRFSVKYIIFHSHYFTTS--

45 SFALYINHVFSYYHRLTLHNYKHEHIQ 154

Q F ++ + YF+T S +L + H FS + R NY HE Q

Sbjct: 829

QYAFGLPFYSAYQGYFSTEEQSLSLKVMHYFSNFIRSGNPNYPHEFSQ 876

5 RANK 5 ITERATION 0>sp|P44526|ZNUA_HAEIN HIGH-AFFINITY ZINC
UPTAKE SYSTEM PROTEIN ZNUA
Length = 337

Score = 26.6 bits (57), Expect = 8.1

Identities = 9/27 (33%), Positives = 15/27 (55%)

10 Frame = +2Query: 128 HNYKHEHIQLYDK*TSALHESVLRNWY 208
H++KHEH ++ HE + NW+

Sbjct: 145 HDHKHEHKHDHEHHDHDHHEGLTTNWH 171

15 RANK 6 ITERATION 0>sp|O30408|TYCB_BACBR TYROCIDINE
SYNTHETASE II [INCLUDES:
ATP-DEPENDENT PROLINE ADENYLASE (PROA) (PROLINE
ACTIVASE); ATP-DEPENDENT PHENYLALANINE ADENYLASE
(PHEA)
(PHENYLALANINE ACTIVASE); ATP-DEPENDENT D-
20 PHENYLALANINE
ADENYLASE (D-PHEA) (D-PHENYLALANINE ACTIVASE);
PHENYLALA>
Length = 3587

25 Score = 26.6 bits (57), Expect = 8.1

Identities = 9/23 (39%), Positives = 15/23 (65%)

Frame = +2Query: 113 HRLTLHNYKHEHIQLYDK*TSAL 181
H+ TL + +EH+ LYD T ++

Sbjct: 322 HKRTLQSQPYEHVPLYDIQTQSV 344

30 RANK 7 ITERATION 0>sp|P19888|MTBA_BACAR MODIFICATION
METHYLASE BANI (CYTOSINE-SPECIFIC
METHYLTRANSFERASE BANI) (M.BANI)
Length = 428

35 Score = 26.6 bits (57), Expect = 8.1

Identities = 17/62 (27%), Positives = 33/62 (52%), Gaps = 11/62 (17%)

Frame = +2Query: 2 MSPE*QSRFSVKYIIFHSHYFTT--
SSFALYINHVFSSYYHRLTL-----HNYKHEH 148

40 +S + + V Y++ +S F + +YI + +LTL H YK+E

Sbjct: 132

ISKLEELGYGVSYLLLNSTFGVPQNRVRIYILGILGSKPKLTLTSNVGAADSH
KYKNEQ 191Query: 149 IQLYDK*TSALHE 187

I L+D+ + + +

45 Sbjct: 192 ISLFDESYATVKD 204

[END
ALIGNMENTS]

5 Job DetailsReturn to top

[BEGIN JOB STATUS][BEGIN SEARCH TIME]

[END SEARCH TIME]

[VERSION]

[SEARCH ID]

10 [EOL] CRLF

[COMMENT] /Comment=NCBI BLASTX Translated Search

[COMMENT] /

[ALGORITHM] BLASTX

[MATRIX] D:\DECYPHER\MATRIX\BLOSUM62.MAA

15 [QUERY FORMAT] FASTA/PEARSON

[QUERY TYPE] NT

[QUERY FILTER] T

[QUERY SEARCH] -1 -2 -3 1 2 3

[QUERY PATH] d:\decypher\query

20 [QUERY SET]

[TARGET TYPE] AA

[TARGET FRAMES] 1

[TARGET PATH] d:\decypher\target\blast

[TARGET SET] swissprot

25 [MAX SCORES] 30

[MAX ALIGNMENTS] 20

[THRESHOLD] 1

[RESULT PATH] d:\decypher\output

[OUTPUT FORMAT] TEXT EXTRACTALIGNED[SHOW GI] F

30 [EXPECTATION] 10

[GAPPED ALIGNMENT] TBLASTX

BLASTX

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),

35 "Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs", Nucleic Acids Res. 25:3389-3402.Query= Your_Query starting with:
GATGAGTCCTGAGTAACAAT /QuerySize=215

(215 letters)Database: Swissprot

90,939 sequences; 32,775,839 total letters Database: Swissprot

40 Posted date:

Number of letters in database: 32,775,839

Number of sequences in database: 90,939

Lambda K H

45 0.318 0.135 0.401 Gapped

Lambda K H

0.270 0.0470 0.230

	CL000907.152	32 0.75
	CL030748.133	32 0.75
	CL013238.182.102	31 1.0
	CL021640.548	31 1.0
5	CL008701.295	31 1.0
	CL039143.85.80	31 1.0
	CL011897.131	31 1.4
	HTC222996-A01.F.7.7	31 1.4
	HTC140759-A01.F.1.1	31 1.4
10	CL013070.129	31 1.4
	CL016632.74	31 1.4
	CL017276.121.116	31 1.4
	CL027354.30	25 1.7
	CL029257.249	30 2.0
15	CL000573.169	30 2.0
	CL003050.594	30 2.0
	CL032991.79	30 2.0
	CL041306.42.54	30 2.0
	CL004450.336.103	30 2.0
20	HTC103515-B01.2	30 2.0
	CL027240.80	30 2.0
	CL006985.101	30 2.0
	CL001724.118.57	30 2.0
	CL017598.98	30 2.7
25	CL058111.36.39	30 2.7
	CL030408.190	30 2.7
	CL029590.113	30 2.7
	CL037100.68	30 2.7
	CL002781.172	30 2.7
30	CL030121.112.46	30 2.7
	CL026181.44	30 2.7
	CL003219.62	30 2.7
	CL041218.61.72	30 2.7
	CL007392.90	30 2.7
35	CL006561.63	30 2.7
	CL013804.259.117	29 3.7
	CL000700.140	29 3.7
	CL036777.130.75	29 3.7
	CL009930.195	29 3.7
40	CL003696.51	29 3.7
	HTC010450-A01.68.70	29 3.7
	CL004350.130	29 3.7
	CL012370.233	29 3.7
	CL015238.128	29 3.7
45	CL048705.9.11	29 3.7
	CL004350.86	29 3.7

	CL017617.110	29 3.7
	CL022355.23.24	29 3.7
	CL031257.47	29 3.7
	CL000837.187	24 5.0
5	CL022460.132	29 5.1
	CL019716.54.54	29 5.1
	CL011892.326	29 5.1
	CL002499.62	29 5.1
	CL017893.131	29 5.1
10	CL002960.289.124	29 5.1
	CL020552.74	29 5.1
	CL051837.247.109	29 5.1
	CL009821.366	29 5.1
	CL012765.61	29 5.1
15	CL020107.145	29 5.1
	CL012555.130	29 5.1
	CL010294.81	29 5.1
	CL031523.251	29 5.1
	CL016618.17	29 5.1
20	CL028523.83	29 5.1
	CL022778.208	29 5.1
	CL016666.156	29 5.1
	CL004147.92	29 5.1
	CL031016.170	29 5.1
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	CL025083.95	29 5.1
	CL001289.1	29 5.1
	CL000788.96	29 5.1
	CL027007.80	29 5.1
30	CL023620.9	29 5.1
	CL015505.101	29 7.0
	CL001000.115	29 7.0
	CL004309.285	29 7.0
	CL037926.43.106	29 7.0
35	CL008211.67.66	29 7.0
	CL033040.102.117	29 7.0
	CL007815.435.115	29 7.0
	CL027201.140	29 7.0
	CL018364.160	29 7.0
40	CL004982.64	29 7.0
	CL012309.127	29 7.0
	CL030385.125	29 7.0
	CL021783.161	29 7.0
	HTC173438-B01.1.1	29 7.0
45	CL006559.88	29 7.0
	HTC116902-B01.3.3	29 7.0

	CL049599.40.47	29 7.0
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	CL004796.97	29 7.0
	CL045033.123.90	29 7.0
5	CL023309.206	29 7.0
	CL022675.100.116	29 7.0
	CL039468.25	29 7.0
	CL015070.134	29 7.0
	CL013130.138	29 7.0
10	CL022518.77	29 7.0
	CL016302.54	29 7.0
	CL016069.84	29 7.0
	CL024742.78.93	29 7.0
	CL041015.65.73	29 7.0
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	CL002315.115	29 7.0
	CL000524.112	29 7.0
	CL000010.563	29 7.0
	CL033960.122	27 8.8
20	CL020019.187.155	28 9.6
	CL015024.73.93	28 9.6
	CL001454.110.87	28 9.6
	CL023863.132	28 9.6
	CL006886.36.48	28 9.6
25	CL026159.182	28 9.6
	CL045948.68.76	28 9.6
	CL036120.80	28 9.6
	CL003524.284	28 9.6
	CL001192.315	28 9.6
30	CL030608.177	28 9.6
	CL028747.80	28 9.6
	CL010012.129	28 9.6
	CL002094.156	28 9.6
	CL037622.30	28 9.6
35	CL011449.115	28 9.6
	CL045949.45.39	28 9.6
	CL024514.44	28 9.6
	CL008946.78	28 9.6
	CL005457.176.95	28 9.6
40	CL004955.166.14	28 9.6
	CL055536.104.102	28 9.6
	CL033774.62	28 9.6
	CL029927.74	28 9.6
	CL025840.126	28 9.6
45	CL016295.51	28 9.6
	CL016184.165	28 9.6

CL037520.86.85 28 9.6
 CL036436.56 28 9.6
 CL018956.125 28 9.6
 CL011570.96 28 9.6
 5 CL006202.71 28 9.6
 CL036480.61 28 9.6
 CL035154.52 28 9.6
 CL027148.8 28 9.6
 CL000155.221 28 9.6
 10 CL040660.40.37 28 9.6
 CL038470.59 28 9.6
 CL037498.92 28 9.6
 CL020533.77 28 9.6
 HTC129722-A01.R.1.1 28 9.6
 15 CL011665.156.144 28 9.6
 CL000771.165.129 28 9.6
 CL006748.56 28 9.6
 CL043873.84.90 28 9.6
 CL024871.73 28 9.6>CL029313.20
 20 Length = 1953

 Score = 35.0 bits (70), Expect = 0.082
 Identities = 13/41 (31%), Positives = 22/41 (52%)
 Frame = +2 / +2
 25 Query: 38 YIIFHSHYFTTSSFALYINHVFSYYHRLTLHNYKHEHIQLY 160
 YI F+ H+T S +Y H++ Y H + Y +++I Y
 Sbjct: 1823 YICFYMHVYTFSIM*YFVHIYIYIHMHLHNIYMYKYIYXY 1945
 >CL052353.71.5
 Length = 735
 30
 Score = 28.1 bits (55), Expect(2) = 0.11
 Identities = 10/22 (45%), Positives = 13/22 (58%)
 Frame = +2 / +2
 Query: 77 FALYINHVFSYYHRLTLHNYKH 142
 35 F LY+ SY+HR L N +H
 Sbjct: 137 FRLYVEQWISYHHR*LLQNVQH 202
 Score = 24.4 bits (47), Expect(2) = 0.11
 Identities = 8/18 (44%), Positives = 14/18 (77%)
 Frame = +3 / +1
 40 Query: 141 TNTFNCMTSKLRHSTNQS 194
 T+TFNC+T +++ T+ S
 Sbjct: 382 THTFNCITPRVKILTSNS 435
 >CL005975.59
 Length = 3299
 45
 Score = 33.6 bits (67), Expect = 0.21

Identities = 12/33 (36%), Positives = 19/33 (57%)

Frame = +2 / +2

Query: 23 RFSVKYIIFHSHYFTTSSFALYINHVFSYYHRL 121

+F V + IFH F T +F H+ ++YH+L

5 Sbjct: 1250 KFEVYFKIFHQSLFFTLTFKSLRTHISNFYHKL 1348

>CL062271.7.18

Length = 3126

Score = 33.1 bits (66), Expect = 0.29

10 Identities = 12/40 (30%), Positives = 22/40 (55%)

Frame = +2 / -1

Query: 38 YIIFHSHYFTTSSFALYINHVFSYYHRLTLHNYKHEHIQL 157

YI F+ H +T S +Y H++ Y H + Y +++I +

Sbjct: 3018 YICFYMHVYTFSIM*IYFVHIYIYIHMHLHNIYMYKYIYI 2899

15 >CL005228.40

Length = 810

Score = 33.1 bits (66), Expect = 0.29

Identities = 12/40 (30%), Positives = 22/40 (55%)

20 Frame = +2 / -3

Query: 38 YIIFHSHYFTTSSFALYINHVFSYYHRLTLHNYKHEHIQL 157

YI F+ H +T S +Y H++ Y H + Y +++I +

Sbjct: 148 YICFYMHVYTFSIM*IYFVHIYIYIHMHLHNIYMYKYIYI 29

>CL024445.151

25 Length = 7862

Score = 33.1 bits (66), Expect = 0.29

Identities = 17/45 (37%), Positives = 22/45 (48%)

Frame = +1 / +1

30 Query: 19 ITF*RQIYNLSFTLLYYKQFCTLYKPCIQLLSPPYIT*LQARTHS 153

+T+ RQ YNL FTL + FC L + PP R+HS

Sbjct: 6007 LTYSRQ*YNLPFTLSFVLSFCQLIAFASVAILPPA*NSYCTRS

6141

>CL006638.68

35 Length = 4450

Score = 32.7 bits (65), Expect = 0.40

Identities = 13/38 (34%), Positives = 20/38 (52%)

Frame = +2 / -3

40 Query: 47 FHSYFTTSSFALYINHVFSYYHRLTLHNYKHEHIQLY 160

F+H +S ALYI++ YYH + H K+ + Y

Sbjct: 398 FITHCLAFNSLALYIRYISIIYHIVYTHTNKYTPVPGY 285

>CL020882.57

Length = 3883

45

Score = 32.7 bits (65), Expect = 0.40

Identities = 15/40 (37%), Positives = 21/40 (52%)

Frame = +2 / -1

Query: 2 MSPE*QSRFSVKYIIFHSHYFTTSSFALYINHVFSYYHRL 121

M E S S+ YI+ F FT +F L++ +YYH L

5 Sbjct: 2479 MCSEQSSMLSLSYILFLICLFTFPNFQLFLQIYSTYYHTL 2360
>CL005125.328

Length = 1915

Score = 32.7 bits (65), Expect = 0.40

10 Identities = 12/27 (44%), Positives = 18/27 (66%)

Frame = +2 / -2

Query: 68 TSSFALYINHVFSYYHRLTLHNYKHEH 148

T+ F+L +NH+ SY H T+ KH+H

Sbjct: 927 TNCFSLSLNHLTSYNHFATVPLIKHQH 847

15 >CL050075.54.29

Length = 2752

Score = 32.7 bits (65), Expect = 0.40

Identities = 11/24 (45%), Positives = 15/24 (61%)

20 Frame = -1 / +3

Query: 197 EGLIRGVPKFTCHTVECVRACSYV 126

EG + VP H V+CVR C++V

Sbjct: 2013 EGAVNRVPHLPSHKVDCVRLCTHV 2084

>CL028201.135

25 Length = 3946

Score = 32.2 bits (64), Expect = 0.55

Identities = 12/41 (29%), Positives = 22/41 (53%)

Frame = +2 / -3

30 Query: 41 IIFHSHYFTTSSFALYINHVFSYYHRLTLHNYKHEHIQLYD 163

II+H +++T+ + IN + Y H + Y E IQ ++

Sbjct: 2789 IYHEYFYTIAENYISINVIKKYQHSFDQYYYSERIQHHE 2667

>CL056443.95.113

Length = 7393

35

Score = 32.2 bits (64), Expect = 0.55

Identities = 13/34 (38%), Positives = 21/34 (61%)

Frame = +3 / +3

Query: 51 IHITLLQAVLHSI*TMYSVIITALHYITTSTNTF 152

40 IH L A LH+I T YS +++ HY + + ++F

Sbjct: 4479 IHRMLCNAKLHAIITCYCTLSSSTHYHSNTNSSF 4580

>CL002731.164.116

Length = 9528

45 Score = 32.2 bits (64), Expect = 0.55

Identities = 8/15 (53%), Positives = 14/15 (93%)

Frame = +2 / +2
 Query: 119 LTLHNYKHEHIQLYD 163
 +T+HNY+H H+++YD
 Sbjct: 7835 MTIHNYEHSBMRIYD 7879
 5 >CL011281.91.31
 Length = 2627

 Score = 32.2 bits (64), Expect = 0.55
 Identities = 10/23 (43%), Positives = 17/23 (73%)
 10 Frame = +1 / +2
 Query: 82 TLYKPCIQLLSPPYIT*LQARTH 150
 T+YK CIQ L PP++ ++ ++H
 Sbjct: 398 TIYKACIQSLEPPHLRPIRQKSH 466
 >CL030809.82
 15 Length = 5282

 Score = 32.2 bits (64), Expect = 0.55
 Identities = 13/24 (54%), Positives = 15/24 (62%)
 Frame = +3 / +2
 20 Query: 108 IITALHYITTSTNTFNCMTSKLRH 179
 I T L H T S T F + C M S + R H
 Sbjct: 3128 IFTILHLFYTSTIPFHCMQSRQRH 3199
 >CL000907.152
 Length = 9396
 25
 Score = 31.8 bits (63), Expect = 0.75
 Identities = 18/59 (30%), Positives = 26/59 (43%)
 Frame = +2 / +1
 Query: 29
 30 SVKYIIFHSHYFTTSSFALYINHVFSYYHRLTLHNYKHEHIQLYDK*TSALHES
 VLRNW 205
 S+ I H ++TSS ++ HV +Y+ T N +LY A H S NW
 Sbjct: 5893
 SISIIFLHISRYSTSSSFVSGHVCNYFVCRTSSNKGKML*ELYSSRVMKHHIS
 35 R*NW 6069
 >CL030748.133
 Length = 3324

 Score = 31.8 bits (63), Expect = 0.75
 40 Identities = 17/53 (32%), Positives = 26/53 (48%)
 Frame = +3 / -1
 Query: 24
 VLASNI*SFIHITLLQAVLHSI*TMYSVIITALHYITTSTNTFNCMTSKLRHS 182
 V L S I * + H I + H + I + I H + + + T F N T K + + S

Sbjct: 3090
 VLYSKI*NIRHIYYFSYIFHNIRRACMHVINY*HFLSTKLLFFNSFTLKISNS
 2932
 >CL013238.182.102
 5 Length = 7209

Score = 31.3 bits (62), Expect = 1.0
 Identities = 12/36 (33%), Positives = 22/36 (60%)
 Frame = +2 / -2
 10 Query: 50 HSHYFTTSSFALYINHVFSYYHRLTLHNYKHEHIQL 157
 HS + S+F L+ N +FS + + + NY H+ ++L
 Sbjct: 6899 HSFPISTFHLFTNAIFSSTYHILV*NYAHQLLKL 6792
 >CL021640.548
 Length = 20530

15 Score = 31.3 bits (62), Expect = 1.0
 Identities = 11/24 (45%), Positives = 16/24 (65%)
 Frame = +2 / +2
 Query: 32 VKYIIFHSHYFTTSSFALYINHV 103
 20 +KY +FH + F TS++ L NH F
 Sbjct: 6329 IKYKLFHLNSFYTSTYPLCTNHAF 6400
 >CL008701.295
 Length = 6101

25 Score = 31.3 bits (62), Expect = 1.0
 Identities = 14/29 (48%), Positives = 16/29 (54%)
 Frame = +2 / +1
 Query: 47 FHSYFTTSSFALYINHVFSYYHRLTLHN 133
 F S TT F L NHV SYY L ++N
 30 Sbjct: 370 FSSRGETTFEFLKYNHVISYYKDLIINN 456
 >CL039143.85.80
 Length = 5495

35 Score = 31.3 bits (62), Expect = 1.0
 Identities = 12/25 (48%), Positives = 17/25 (68%)
 Frame = +2 / +1
 Query: 41 IIFHSHYFTTSSFALYINHVFSYYH 115
 +IF T +SFA YI+HVF ++H
 Sbjct: 2686 VIFDFSTNTRTSFADYIHHVFCFFH 2760
 40 >CL011897.131
 Length = 9620

45 Score = 30.8 bits (61), Expect = 1.4
 Identities = 12/41 (29%), Positives = 20/41 (48%)
 Frame = +2 / +1
 Query: 38 YIIFHSHYFTTSSFALYINHVFSYYHRLTLHNYKHEHIQLY 160

YI H Y +++++I Y H +H Y +HI Y
 Sbjct: 868 YIYMHCIYICINTYSVHIYACV*YIHL YIMHIYVFKHIYAY 990
 >HTC222996-A01.F.7.7
 Length = 708

5

Score = 30.8 bits (61), Expect = 1.4
 Identities = 11/37 (29%), Positives = 20/37 (53%)
 Frame = +2 / -1

Query: 38 YIIFHSHYFTTSSFALYINHVFSYYHRLTLHNYKHEH 148

10 YI F+ H +T S +Y H++ Y H + Y +++

Sbjct: 177 YICFYMHVYTFSIM*YFVHIYIYIHMHLHNIYMYKY 67

>HTC140759-A01.F.1.1

Length = 570

15

Score = 30.8 bits (61), Expect = 1.4
 Identities = 11/40 (27%), Positives = 21/40 (52%)
 Frame = +2 / -3

Query: 38 YIIFHSHYFTTSSFALYINHVFSYYHRLTLHNYKHEHIQL 157

YI F+ H + S +Y H++ Y H + Y +++I +

20

Sbjct: 148 YICFYMHVYXFSIM*YFVHIYIYIHMHLHNIYMYKYIYI 29

>CL013070.129

Length = 5406

25

Score = 30.8 bits (61), Expect = 1.4
 Identities = 12/33 (36%), Positives = 19/33 (57%)
 Frame = +2 / +2

Query: 44 IFHSHYFTTSSFALYINHVFSYYHRLTLHNYKH 142

IFH+ FT F +I+H F+Y+ ++ N H

Sbjct: 560 IFHTTIFTEHLF*SHISHPFTYFTSIHIFNIFH 658

30

>CL016632.74

Length = 2149

35

Score = 30.8 bits (61), Expect = 1.4
 Identities = 10/34 (29%), Positives = 18/34 (52%)
 Frame = +2 / -1

Query: 50 HSHYFTTSSFALYINHVFSYYHRLTLHNYKHEHI 151

H Y +S +++++ + Y R H+YKH H+

Sbjct: 433 HGGYLLSSKIYMFLSIFYGYS*RAHTHSYKHIHV 332

>CL017276.121.116

40

Length = 7981

45

Score = 30.8 bits (61), Expect = 1.4
 Identities = 12/34 (35%), Positives = 17/34 (49%)
 Frame = +2 / -2
 Query: 44 IFHSHYFTTSSFALYINHVFSYYHRLTLHNYKHE 145
 ++H F S F L + H F Y + L +H HE

Sbjct: 4200 VYHLFQFFLSLFDLILQHFFVYIYCLQIHYKMHE 4099
>CL027354.30
Length = 769

5 Score = 25.3 bits (49), Expect(2) = 1.7
Identities = 10/18 (55%), Positives = 11/18 (60%)
Frame = +1 / +3

Query: 37 IYNLSFTLLYYKQFCTLY 90
I L F LLY +FC LY

10 Sbjct: 447 INRLFFLLLYINRFCLLY 500
Score = 23.1 bits (44), Expect(2) = 1.7
Identities = 6/13 (46%), Positives = 10/13 (76%)
Frame = +1 / +3

Query: 85 LYKPCIQLLSPPY 123

15 LY PC++ + PP+
Sbjct: 684 LY*PCLETMKPPH 722
>CL029257.249
Length = 6264

20 Score = 30.4 bits (60), Expect = 2.0
Identities = 11/34 (32%), Positives = 19/34 (55%)
Frame = +2 / -1

Query: 53 SHYFTTSSFALYINHVFSYYHRLTLHNYKHEHIQ 154
+H T+ +++ +V +Y R H YKH H+Q

25 Sbjct: 6222 AHLSTMAVMSISMLYVCTYPPRRNFHRYKMHMVQ 6121
>CL000573.169
Length = 4370

Score = 30.4 bits (60), Expect = 2.0
30 Identities = 11/28 (39%), Positives = 16/28 (56%)
Frame = +2 / -2

Query: 59 YFTTSSFALYINHVFSYYHRLTLHNYKH 142
YF TS F +Y V+ L+++ YKH

Sbjct: 2614 YFVTSGFVIYSYIVYIVLDTLSMYKYKH 2531
35 >CL003050.594
Length = 2396

Score = 30.4 bits (60), Expect = 2.0
Identities = 12/33 (36%), Positives = 16/33 (48%)
40 Frame = +2 / +2

Query: 23 RFSVKYIIFHSHYFTTSSFALYINHVFSYYHRL 121
R S YI++ S Y +Y H SYY+ L

Sbjct: 1490 RISPSYIVY*SDYMLLILAKIYSTHTISYYYNL 1588
>CL032991.79
45 Length = 5185

- Identities = 14/40 (35%), Positives = 16/40 (40%)
 Frame = +2 / +3
 Query: 44 IFHSHYFTTSSSFALYINHVFSYYHRLTLHNYKHEHIQLYD 163
 IFH H F S + Y H S YH H + Q D
 5 Sbjct: 390 IFHHHIFLLSIYKNYSKHNDISKYHFFNFSRDLHNDLQHND 509
 >CL041218.61.72
 Length = 4965
- Score = 29.9 bits (59), Expect = 2.7
 10 Identities = 9/25 (36%), Positives = 14/25 (56%)
 Frame = +2 / +2
 Query: 74 SFALYINHVFSYYHRLTLHNYKHEH 148
 + +YI +F YH + H YK+ H
 Sbjct: 2390 TIVIIYITDLFDIYHNVRAHLYKYTH 2464
 15 >CL007392.90
 Length = 1161
- Score = 29.9 bits (59), Expect = 2.7
 Identities = 9/21 (42%), Positives = 15/21 (70%)
 20 Frame = +2 / +3
 Query: 59 YFTTSSSFALYINHVFSYYHRL 121
 YFTT +F L I H++ +Y ++
 Sbjct: 438 YFTTFTFELPITHIYKFYSKI 500
 >CL006561.63
 25 Length = 3535
- Score = 29.9 bits (59), Expect = 2.7
 Identities = 11/23 (47%), Positives = 16/23 (68%)
 Frame = +2 / -1
 30 Query: 11 E*QSRFSVKYIIFHSHYFTTSSF 79
 E Q R S+++++F HY TTS F
 Sbjct: 1969 EIQIRTSIQHVLFRMHYSTTSHF 1901
 >CL013804.259.117
 Length = 6864
- 35 Score = 29.5 bits (58), Expect = 3.7
 Identities = 19/59 (32%), Positives = 28/59 (47%)
 Frame = -2 / -1
 Query: 184
 40 VECRSLLVIQLNVFVLVVM*CKAVIITEYMVYIECKTACSKVM*MKDYIFDA
 KT*LLLR 8
 V C S + +L + L V C A I I Y++ E K+ + K I F + LLL+
 Sbjct: 672
 VHCCSFVTNKLILVYLFVSCCSATHVAYLMRTEQKSLEGSTIPTKWVIFQSL
 45 WLLLQ 496
 >CL000700.140

Length = 6255

Score = 29.5 bits (58), Expect = 3.7
Identities = 10/30 (33%), Positives = 18/30 (59%)

5 Frame = +2 / +1

Query: 35 KYIIFHSHYFTTSSFALYINHVFSYYHRLT 124

KY++FH+H F TS ++ ++ Y + T

Sbjct: 5206 KYLVFHAHNF*TSKGSFF*KIIYKSYFKKT 5295

>CL036777.130.75

10 Length = 8551

Score = 29.5 bits (58), Expect = 3.7
Identities = 12/33 (36%), Positives = 18/33 (54%)
Frame = +2 / +3

15 Query: 44 IFHSHYFTTSSFALYINHVFSYYHRLTLHNYKH 142

IFH FT F +I+H F+Y+ ++ N H

Sbjct: 7758 IFHITTFTEHPF*SHISHPFTYFTSIHIFNIFH 7856

>CL009930.195

Length = 12162

20

Score = 29.5 bits (58), Expect = 3.7
Identities = 9/40 (22%), Positives = 22/40 (54%)
Frame = +2 / +1

Query: 38 YIIFHSHYFTTSSFALYINHVFSYYHRLTLHNYKHEHIQL 157

25 YI+ + ++ F +I+H++ Y + T+ ++ +QL

Sbjct: 7888 YILDEGSSYVSNKFIFHISHIYQYKKKTTISSFYQTPMQL 8007

>CL003696.51

Length = 14805

30 Score = 29.5 bits (58), Expect = 3.7
Identities = 10/30 (33%), Positives = 17/30 (56%)
Frame = +2 / +1

Query: 56 HYFTTSSFALYINHVFSYYHRLTLHNYKHE 145

H +++ Y H +YY+R+ H YKH+

35 Sbjct: 8392 HQIYSTNILQYWLHKLAYYNRICKHVYKHK 8481

>HTC010450-A01.68.70

Length = 4228

Score = 29.5 bits (58), Expect = 3.7
Identities = 8/16 (50%), Positives = 14/16 (87%)
Frame = +2 / +2

Query: 110 YHRLTLHNYKHEHIQL 157

++RL+ HNY H+H+Q+

Sbjct: 3851 FNRLSSHNYAHQHLQV 3898

45 >CL004350.130

Length = 3579

- Score = 29.5 bits (58), Expect = 3.7
Identities = 10/24 (41%), Positives = 16/24 (66%)
Frame = +2 / -1
Query: 65 TTSSFALYINHVFSYYHRLTLHNY 136
5 TT+S L+ +++ Y+H LHNY
Sbjct: 2488 TTTSKVLFSSSLYHYFHHHLHNY 2417
>CL022355.23.24
Length = 2656
- 10 Score = 29.5 bits (58), Expect = 3.7
Identities = 11/18 (61%), Positives = 12/18 (66%)
Frame = +1 / +1
Query: 37 IYNLSFTLLYYKQFCTLY 90
IY L F LLY +FC LY
15 Sbjct: 520 IYRLFFLLLYINRFCLLY 573
>CL031257.47
Length = 3663
- 20 Score = 29.5 bits (58), Expect = 3.7
Identities = 11/30 (36%), Positives = 18/30 (59%)
Frame = +2 / +2
Query: 26 FSVKYIIFHSHYFTTSSFALYINHVFSYYH 115
F VKYI +++ FT F+ ++ H Y+H
Sbjct: 1769 FIVKYIFIYTYSTYLFSSYHLIHC*IYFH 1858
25 >CL000837.187
Length = 3569
- 30 Score = 23.5 bits (45), Expect(2) = 5.0
Identities = 9/22 (40%), Positives = 14/22 (62%)
Frame = +1 / -3
Query: 37 IYNLSFTLLYYKQFCTLYKPCI 102
IY+L F L+Y K + + K C+
Sbjct: 1731 IYHLPFFFLMYCK*YFSTCKSCL 1666
Score = 24.0 bits (46), Expect(2) = 5.0
35 Identities = 9/29 (31%), Positives = 17/29 (58%)
Frame = +2 / -1
Query: 77 FALYINHVFSYYHRLTLHNYKHEHIQLYD 163
F LYI+H++S + + KH H +++
Sbjct: 1559 FDLYISHLYSLTYI*IWTHIKHNHGSMHE 1473
40 >CL022460.132
Length = 4776
- 45 Score = 29.0 bits (57), Expect = 5.1
Identities = 12/34 (35%), Positives = 19/34 (55%)
Frame = +2 / +2
Query: 38 YIIFHSHYFTTSSFALYINHVFSYYHRLTLHNYK 139

Y++FH F SF ++HFS++L+L K
 Sbjct: 2486 YLVFHFLNFNYHSFQEFKHHFFSFSYILSLSKAK 2587
 >CL019716.54.54
 Length = 3564

5

Score = 29.0 bits (57), Expect = 5.1
 Identities = 13/39 (33%), Positives = 25/39 (63%)
 Frame = +2 / -1

Query: 17 QSRFSVKYIIFHSHYFTTSSFALYINHVFSYYHRLTLHN 133
 +SR+ I+ +Y ++SF +YI+ V+S +LTL++

10

Sbjct: 2112 RSRYLNRNSIVLDINYGMSNSFLIYIS*VYSEPYPLTLYS 1996
 >CL011892.326
 Length = 5954

15

Score = 29.0 bits (57), Expect = 5.1
 Identities = 10/25 (40%), Positives = 16/25 (64%)
 Frame = +3 / -1

Query: 102 SVIITALHYITTSTNTFNCMTSKLR 176
 ++I+ +HY TT+ N C+TS R

20

Sbjct: 3017 NLILDMIHYSTTNLNILECVTSSPR 2943
 >CL002499.62
 Length = 3562

25

Score = 29.0 bits (57), Expect = 5.1
 Identities = 13/35 (37%), Positives = 22/35 (62%)
 Frame = +3 / -2

Query: 54 HITLLQAVLHSI*TMYSVIITALHYITTSTNTFNC 158
 +I+ Q +L +T++S I T+LH T +TF+C

30

Sbjct: 3150 YIIVNQ*LLEKLDTVHSPITTS LHCPITRQSTFSC 3046
 >CL017893.131
 Length = 8961

35

Score = 29.0 bits (57), Expect = 5.1
 Identities = 12/42 (28%), Positives = 22/42 (51%)
 Frame = +2 / -3

Query: 32 VKYIIFHSHYFTTSSFALYINHVFSYYHRLTLHNYKHEHIQL 157
 +K +H Y T SFA+ HV+++ +H YK+ ++

Sbjct: 3706 LKCCLVHYKY*TACSF AIM*LH VYTHVCHTHIHIYKYATVTI
 3581

40

>CL002960.289.124
 Length = 9214

45

Score = 29.0 bits (57), Expect = 5.1
 Identities = 13/48 (27%), Positives = 23/48 (47%)
 Frame = +2 / -1

- Query: 47
FHSYFTTSSFALYINHVFSYYHRLTLHNYKHEHIQLYDK*TSALHES 190
F SH T + + +HV F L + + H H + + SA + H + +
Sbjct: 7594
- 5 FPSHLSVTHQTSFHHDHVFPLETNLLSIHHPHCHLNHFPSHLSAIHQT 7451
>CL020552.74
Length = 4420
- Score = 29.0 bits (57), Expect = 5.1
Identities = 14/45 (31%), Positives = 27/45 (59%)
Frame = +3 / +3
- 10 Query: 24 VLASNI*SFIHITLLQAVLHSI*TMYSVIITALHYITTSTNTFNC 158
+ + S + + IH + + + H + I T Y + + II L Y T + T + C
Sbjct: 1035 LIVSQLLALIHL*PI**LIHTIVT*YTHIPGLTYHTHTTSWSPC 1169
>CL051837.247.109
Length = 8364
- Score = 29.0 bits (57), Expect = 5.1
Identities = 9/40 (22%), Positives = 21/40 (52%)
Frame = +2 / +3
- 20 Query: 35 KYIIFHSYFTTSSFALYINHVFSYYHRLTLHNYKHEHIQ 154
KY + + YF + SF L + + + Y + + + + + Q
Sbjct: 5658 KYVVVECRYFSVISFMLFTDYCICYFSAHKIFSRLERQWLQ 5777
>CL009821.366
Length = 3912
- Score = 29.0 bits (57), Expect = 5.1
Identities = 12/31 (38%), Positives = 15/31 (47%)
Frame = +2 / -2
- 30 Query: 47 FHSYFTTSSFALYINHVFSYYHRLTLHNYK 139
FH H + F T Y + NH + TLH K
Sbjct: 1613 FHYHFFLTIFLYSYLNHMQE*TTTYTLHGLK 1521
>CL012765.61
Length = 5494
- Score = 29.0 bits (57), Expect = 5.1
Identities = 8/19 (42%), Positives = 15/19 (78%)
Frame = +2 / -2
- 35 Query: 83 LYINHVFSYYHRLTLHNYK 139
LY + N + + + + + TLH YK
Sbjct: 1263 LYVNSIYNFFYIFTLHVYK 1207
>CL020107.145
Length = 5153
- Score = 29.0 bits (57), Expect = 5.1
Identities = 15/39 (38%), Positives = 20/39 (50%)
- 45

- ++IF H+F+ ++ L + +FSY R+ N
Sbjct: 503 FVIFFIHHFSPAPYDLVLLIFSIEQRIPAPN 408
>CL015505.101
Length = 5969
- 5 Score = 28.6 bits (56), Expect = 7.0
Identities = 8/17 (47%), Positives = 13/17 (76%)
Frame = +2 / +1
Query: 98 VFSYYHRLTLHNYKHEH 148
- 10 +F+YY R+ +HN + EH
Sbjct: 829 IFTYYFRMLVHNIQKEH 879
>CL001000.115
Length = 7356
- 15 Score = 28.6 bits (56), Expect = 7.0
Identities = 9/20 (45%), Positives = 15/20 (75%)
Frame = +1 / +3
Query: 34 QIYNLSFTLLYYKQFCTLYK 93
Q++N S TLL+Y+ CT+ +
- 20 Sbjct: 6534 QVHNASMTLLFYQPGCTIVR 6593
>CL004309.285
Length = 3763
- Score = 28.6 bits (56), Expect = 7.0
25 Identities = 10/25 (40%), Positives = 14/25 (56%)
Frame = +2 / -1
Query: 47 FHSYFTTSSFALYINHVFSYYHRL 121
FH +F S+F L + YYH+L
Sbjct: 949 FHRSFLLASTFRLLRISI*KYYHKL 875
- 30 >CL037926.43.106
Length = 8639
- Score = 28.6 bits (56), Expect = 7.0
Identities = 9/23 (39%), Positives = 16/23 (69%)
35 Frame = -2 / -3
Query: 124 CKAVIITEYMYIECKTACSKVM 56
CK++IITE+ + ++CK K +
Sbjct: 4575 CKSIITEWYLRRLQCKLDSEKYL 4507
>CL008211.67.66
- 40 Length = 6231
- Score = 28.6 bits (56), Expect = 7.0
Identities = 13/45 (28%), Positives = 19/45 (41%)
Frame = +2 / +3
45 Query: 23 RFSVKYIIFHSYFTTSSFALYINHVFSYYHRLTLHNYKHEHIQL
157

F SH F SS++ Y+N H L H +H
Sbjct: 257 FFSHMFDHSSYSKYLNKYIFXCHGLIYH*MNFKH 156
>CL012309.127
Length = 4264

5
Score = 28.6 bits (56), Expect = 7.0
Identities = 9/22 (40%), Positives = 13/22 (58%)
Frame = +2 / +3

Query: 83 LYINHVFSYYHRLTLHNYKHEH 148
10 +Y +H +SY H T + Y H H
Sbjct: 429 IYTSHTYSYKHTYTSYFYDHLH 494
>CL030385.125
Length = 2535

15
Score = 28.6 bits (56), Expect = 7.0
Identities = 10/30 (33%), Positives = 16/30 (53%)
Frame = +2 / +3

Query: 26 FSVKYIIFHSHYFTTSSFALYINHVFSYYH 115
F V ++ H F + LY++ VF+Y H
20 Sbjct: 2172 FFVLFFVCQHNNFFVAHLFLYVSSVFNYIH 2261
>CL021783.161
Length = 4314

Score = 28.6 bits (56), Expect = 7.0
25 Identities = 16/51 (31%), Positives = 23/51 (44%)
Frame = +2 / +1

Query: 56
HYFTTSSFALYINHVFSYYHRLTLHNYKHEHIQLYDK*TSALHESVLRNWWY
208
30 H +S A Y NH SY L +K H+QL + L S +++Y
Sbjct: 3343
HLDNCNSSANYYNHHASYSSHLVPSHQKSYHLQLSQLKSRHLQSSHSKHYY
3495
>HTC173438-B01.1.1
35 Length = 556

Score = 28.6 bits (56), Expect = 7.0
Identities = 12/38 (31%), Positives = 19/38 (49%)
Frame = +2 / -3

40 Query: 26 FSVKYIIFHSHYFTTSSFALYINHVFSYYHRLTLHNYK 139
FSVK++ +H+ A IN Y H ++H Y+
Sbjct: 200 FSVKFSVSWHAQSVHNKLVA*SINSKHIYLHDTSIHPYR 87
>CL006559.88
Length = 3043

45
Score = 28.6 bits (56), Expect = 7.0

- Identities = 12/28 (42%), Positives = 19/28 (67%)
 Frame = +3 / -2
 Query: 6 VLSNNHVLASNI*SFIHITLLQAVLHSI 89
 +LSN+ ++ASNI F ++L V HS+
 5 Sbjct: 171 LLSNSFLIASNICQFCSMAMLLPVRHSL 88
 >CL022518.77
 Length = 1572
- Score = 28.6 bits (56), Expect = 7.0
 10 Identities = 8/20 (40%), Positives = 13/20 (65%)
 Frame = +1 / -2
 Query: 40 YNLSFTLLYYKQFCTLYKPC 99
 YN+S +++ Y CT+ PC
 Sbjct: 167 YNISLSIMLYSTRCTISSPC 108
 15 >CL016302.54
 Length = 3779
- Score = 28.6 bits (56), Expect = 7.0
 Identities = 10/23 (43%), Positives = 17/23 (73%)
 20 Frame = -2 / -1
 Query: 178 CRSLLVIQLNVFVLVVM*CKAVI 110
 C+S+L+ L+VF L+ CKA++
 Sbjct: 1301 CKSILISSLDVFFLLTDICKALV 1233
 >CL016069.84
 25 Length = 5201
- Score = 28.6 bits (56), Expect = 7.0
 Identities = 12/30 (40%), Positives = 16/30 (53%)
 Frame = +2 / -1
 30 Query: 62 FTTSSFALYINHVFSYYHRLTLHNYKHEHI 151
 F S YI+ V + + LH+YKH HI
 Sbjct: 2276 FNKSKPITYIDPVCEFE*NIPLHSYKHYHI 2187
 >CL024742.78.93
 Length = 6147
- 35 Score = 28.6 bits (56), Expect = 7.0
 Identities = 9/16 (56%), Positives = 13/16 (81%)
 Frame = +1 / +1
 Query: 82 TLYKPCIQLLSPPYIT 129
 TL+KP ++L PPY+T
 40 Sbjct: 4747 TLHKPPLELFPPPYVT 4794
 >CL041015.65.73
 Length = 5315
- 45 Score = 28.6 bits (56), Expect = 7.0
 Identities = 10/17 (58%), Positives = 12/17 (69%)

Frame = +2 / +1
 Query: 20 SRFSVKYIIFHSHYFTT 70
 SRF V ++FHSF T
 Sbjct: 625 SRFQVSPLVFHSHVFQT 675
 5 >CL015505.97
 Length = 2688

 Score = 28.6 bits (56), Expect = 7.0
 Identities = 8/17 (47%), Positives = 13/17 (76%)
 10 Frame = +2 / -3
 Query: 98 VFSYYHRLTLHNYKHEH 148
 +F+YY R+ +HN + EH
 Sbjct: 94 IFTYYFRMLVHNIQKEH 44
 >CL002315.115
 15 Length = 4856

 Score = 28.6 bits (56), Expect = 7.0
 Identities = 9/22 (40%), Positives = 16/22 (71%)
 Frame = +1 / +1
 20 Query: 22 TF*RQIYNLSFTLLYYKQFCTL 87
 TF* ++NL ++ Y+ QFC++
 Sbjct: 226 TF*LEYFNLLYAVCYFLQFCSM 291
 >CL000524.112
 Length = 2269
 25
 Score = 28.6 bits (56), Expect = 7.0
 Identities = 9/22 (40%), Positives = 16/22 (71%)
 Frame = +1 / +3
 Query: 22 TF*RQIYNLSFTLLYYKQFCTL 87
 30 TF* ++NL ++ Y+ QFC++
 Sbjct: 1275 TF*LEYFNLLYAVCYFLQFCSM 1340
 >CL000010.563
 Length = 19521

 35 Score = 28.6 bits (56), Expect = 7.0
 Identities = 11/37 (29%), Positives = 18/37 (47%)
 Frame = +2 / -1
 Query: 38 YIIFHSHYFTTSSFALYINHVFSYYHRLTLHNYKHEH 148
 +I++ HY + V Y+H LTL N+ + H
 40 Sbjct: 12102 HIVYC*HY*NLKHAVNYFA*AVICYFHNLTLDNHSNNH 11992
 >CL033960.122
 Length = 4244

 45 Score = 19.8 bits (37), Expect(2) = 8.8
 Identities = 6/19 (31%), Positives = 10/19 (52%)
 Frame = +2 / -2

Query: 56 HYFTTSSFALYINHVFSYY 112
 HY+ S +NH F ++
 Sbjct: 3070 HYYALSFQRSFSNHTFFFH 3014
 Score = 26.7 bits (52), Expect(2) = 8.8
 5 Identities = 9/15 (60%), Positives = 12/15 (80%)
 Frame = +3 / -1
 Query: 114 TALHYITTSTNTFNC 158
 T++HY TTS N+F C
 Sbjct: 2936 TSIHYTTTSGNSF*C 2892
 10 >CL020019.187.155
 Length = 10271

 Score = 28.1 bits (55), Expect = 9.6
 Identities = 8/28 (28%), Positives = 21/28 (74%)
 15 Frame = -2 / -3
 Query: 172 SLLVIQLNVFVLVVM*CKAVIITEYMVY 89
 SLL ++N+ ++V++ C+++ + + M+Y
 Sbjct: 1368 SLLTKKVNIIVIIISCRSLKLEDMMIY 1285
 >CL015024.73.93
 20 Length = 5954

 Score = 28.1 bits (55), Expect = 9.6
 Identities = 11/38 (28%), Positives = 18/38 (46%)
 Frame = +2 / +2
 25 Query: 35 KYIIFHSHYFTTSSFALYINHVFSYYHRLTLHNYKHEH 148
 +YII HS + S Y +FS+++ H E+
 Sbjct: 4907 RYIILHSQ LWHNKS AIYYTEQIFS FVYTIQ*HEICSEN 5020

 >CL001454.110.87
 30 Length = 4770

 Score = 28.1 bits (55), Expect = 9.6
 Identities = 11/27 (40%), Positives = 15/27 (54%)
 Frame = +1 / +2
 35 Query: 31 RQIYNLSFTLLYYKQFCTLYKPCIQLL 111
 RQI + S TL YY + LY+ Q +
 Sbjct: 3695 RQILSFSITLFYYMAYFVLYRASQQFI 3775
 >CL023863.132
 Length = 3344
 40
 Score = 28.1 bits (55), Expect = 9.6
 Identities = 11/33 (33%), Positives = 18/33 (54%)
 Frame = +2 / -1
 Query: 59 YFTTSSFALYINHVFSYYHRLTLHNYKHEHIQL 157
 45 +FT F + H +S +++ LHN +H H L
 Sbjct: 878 FFTLLCFYWHWIIHSYSLHYII*LHNIRHNHFFL 780

>CL006886.36.48

Length = 8844

Score = 28.1 bits (55), Expect = 9.6

5 Identities = 8/20 (40%), Positives = 14/20 (70%)

Frame = +1 / -1

Query: 67 YKQFCTLYKPCIQLLSPPYI 126

YK+ C++YK C ++L P +

Sbjct: 3225 YKKLCSVYKVC TRVLDQPVL 3166

10 >CL026159.182

Length = 11269

Score = 28.1 bits (55), Expect = 9.6

Identities = 12/34 (35%), Positives = 15/34 (43%)

15 Frame = +2 / +2

Query: 89 INHVFSYYHRLTLHNYKHEHIQLYDK*TSALHES 190

INH F YYHR + H Y K + H +

Sbjct: 3698 INHQFYYYHRFWDQYFNTPHFFFY*KKCTKYHHT 3799

>CL045948.68.76

20 Length = 5134

Score = 28.1 bits (55), Expect = 9.6

Identities = 11/33 (33%), Positives = 16/33 (48%)

Frame = +2 / +3

25 Query: 50 HSHYFTTSSFALYINHVFSYYHRLTLHNYKHEH 148

HSF S ++ Y+ S+Y L H +H

Sbjct: 684 HSHIFDHSFYSKYLCKYISFYRGLIYH*MNFKH 782

>CL036120.80

Length = 5338

30

Score = 28.1 bits (55), Expect = 9.6

Identities = 9/23 (39%), Positives = 15/23 (65%)

Frame = +2 / +1

Query: 38 YIIFHSHYFTTSSFALYINHVFS 106

35 Y ++H +TT F +Y+N+V S

Sbjct: 1525 YCVYH*FIYTTPVFIVYLN YVLS 1593

>CL003524.284

Length = 9636

40 Score = 28.1 bits (55), Expect = 9.6

Identities = 9/20 (45%), Positives = 13/20 (65%)

Frame = +2 / -1

Query: 92 NHVFSYYHRLTLHNYKHEHI 151

N +YHRLTLH + + H+

45 Sbjct: 2058 NRHHC FYHRLTLHCFPY YHV 1999

>CL001192.315

- Score = 28.1 bits (55), Expect = 9.6
 Identities = 7/21 (33%), Positives = 16/21 (75%)
 Frame = -2 / +3
 5 Query: 106 TEYMVYIECKTACSKVM*MKD 44
 TE ++++EC+ CS+++ + D
 Sbjct: 663 TEVLIWVECEVCSEIVVLSD 725
 >CL004955.166.14
 Length = 1205
- 10
 Score = 28.1 bits (55), Expect = 9.6
 Identities = 13/37 (35%), Positives = 18/37 (48%)
 Frame = +2 / +3
 Query: 86 YINHVFSYYHRLTLHNYKHEHIQLYDK*TSALHESVL 196
 15 Y N + +YH LT +KH LY *T H ++
 Sbjct: 417 YTNKMLYHYHPLTTIKFKHHANMLYYL*TYI*HVIII 527
 >CL055536.104.102
 Length = 7720
- 20 Score = 28.1 bits (55), Expect = 9.6
 Identities = 10/21 (47%), Positives = 12/21 (56%)
 Frame = +2 / +3
 Query: 50 HSHYFTTSSFALYINHVFSYY 112
 H HY T F L++ H SYY
 25 Sbjct: 3579 HFHYQTNMLFFLFLYHSISYY 3641
 >CL033774.62
 Length = 5196
- 30 Score = 28.1 bits (55), Expect = 9.6
 Identities = 10/28 (35%), Positives = 18/28 (63%)
 Frame = +3 / -3
 Query: 99 YSVIITALHYITTSTNTFNCMTSKLRHS 182
 Y ++ ++ITTS + +C TS +RH+
 Sbjct: 3928 YLLLPYLFYHITTSLSKHDCCTSSVRHT 3845
 35 >CL029927.74
 Length = 2913
- 40 Score = 28.1 bits (55), Expect = 9.6
 Identities = 10/24 (41%), Positives = 16/24 (66%)
 Frame = +2 / -2
 Query: 32 VKYIIFHSHYFTTSSFALYINHVF 103
 +KY FH + + TS+++L NH F
 Sbjct: 1796 IKYKPFHLNSYLTSTYSLCTNHSF 1725
 >CL025840.126
 45 Length = 938

- Score = 28.1 bits (55), Expect = 9.6
Identities = 11/24 (45%), Positives = 16/24 (65%)
Frame = +2 / -1
Query: 131 NYKHEHIQLYDK*TSALHESVLRN 202
5 N + +H+QL+ K LH SVL+N
Sbjct: 110 NSQIDHLQLHHKLLKLLHHSVLKN 39
>CL016295.51
Length = 2200
- 10 Score = 28.1 bits (55), Expect = 9.6
Identities = 12/46 (26%), Positives = 22/46 (47%)
Frame = +2 / -1
Query: 29 SVKYIIFHSHYFTTSSFALYINHVFSYYHRLTLHNYKHEHIQLYDK
166
15 +VK ++FH Y + +FS+ + + L Y ++L DK
Sbjct: 223
NVKVVLFFHRYNIFICYNQINRKIFSHNYEMDLETY*SRWMKLQDK 86
>CL016184.165
Length = 7835
- 20 Score = 28.1 bits (55), Expect = 9.6
Identities = 7/21 (33%), Positives = 16/21 (75%)
Frame = -2 / +2
Query: 106 TEYMVYIECKTACSKVM*MKD 44
25 TE ++++EC+ CS+++ + D
Sbjct: 7433 TEVLIWVECECVCEIVVLSD 7495
>CL037520.86.85
Length = 6096
- 30 Score = 28.1 bits (55), Expect = 9.6
Identities = 9/24 (37%), Positives = 14/24 (57%)
Frame = -1 / -2
Query: 200 SEGLIRGVPKFTCHTVECVRACSY 129
S+G++ + TCHTVE C +
35 Sbjct: 5282 SKGILHEMVSVTCHTVESTVGCKF 5211
>CL036436.56
Length = 3020
- 40 Score = 28.1 bits (55), Expect = 9.6
Identities = 15/52 (28%), Positives = 26/52 (49%)
Frame = +3 / +1
Query: 45
SFIHITLLQAVLHSI*TMYSVIITALHYITTSTNTFNCMTSKLRHSTNQSFG 200
+F+ ITLL + + + S + +L+ STN T+ + H T +S G

Sbjct: 2452
AFVFITLLVVRVRILQSFISNL*LSLYIARVSTNRTQQTTTAIMHMTGESKG
2607
>CL018956.125

5 Length = 7421

Score = 28.1 bits (55), Expect = 9.6
Identities = 10/20 (50%), Positives = 12/20 (60%)
Frame = +2 / -2

10 Query: 89 INHVFSYYHRLTLHNYKHEH 148
INH+F H +L NYK H

Sbjct: 451 INHLFGNLHPFSLSNYKISH 392
>CL011570.96
Length = 5102

15

Score = 28.1 bits (55), Expect = 9.6
Identities = 10/18 (55%), Positives = 15/18 (82%)
Frame = -2 / -3

20 Query: 184 VECRSLVLIQLNVFVLVV 131
+ECR ++++Q N FVLVV

Sbjct: 4536 IECRDVILLQDNSFVLVV 4483
>CL006202.71
Length = 4872

25 Score = 28.1 bits (55), Expect = 9.6
Identities = 11/27 (40%), Positives = 16/27 (58%)
Frame = +2 / +3

Query: 62 FTTSSFALYINHVFSYYHRLTLHNYKH 142
F+ F YI+ SY HR+ LH+ +H

30 Sbjct: 2841 FSKFFLTYYHGSVSYVHRV*LHSCRH 2921
>CL036480.61
Length = 338

35 Score = 28.1 bits (55), Expect = 9.6
Identities = 10/35 (28%), Positives = 19/35 (53%)
Frame = +3 / +2

Query: 108 IITALHYITTSTNTFNCMTSKLRHSTNQSFQIGTQ 212
+I+ H++ T F C+ ++ HSTN + + Q

40 Sbjct: 68 LISYTHFVDYRTFFPCLCLQIYHSTNAAAALPPQ 172
>CL035154.52
Length = 3038

45 Score = 28.1 bits (55), Expect = 9.6
Identities = 12/25 (48%), Positives = 14/25 (56%)
Frame = +2 / -3

Query: 77 FALYINHVFSYYHRLTLHNYKHEHI 151

F YIN F Y H L T H N + + I
 Sbjct: 2679 FLFYINIRFMYKHS�TPHNSSNMNI 2605
 >CL027148.8
 Length = 647

5
 Score = 28.1 bits (55), Expect = 9.6
 Identities = 11/30 (36%), Positives = 16/30 (52%)
 Frame = +2 / -2
 Query: 50 HSHYFTTSSFALYINHVFSYYHRLTLHNYK 139
 ++ Y F L +NH+F YY T NY+

10
 Sbjct: 145 YAKYI*LLEFILILNHIFGYVVLST*INYR 56
 >CL000155.221
 Length = 2040

15
 Score = 28.1 bits (55), Expect = 9.6
 Identities = 13/35 (37%), Positives = 16/35 (45%)
 Frame = +2 / -1
 Query: 29 SVKYIIFHSHYFTTSSFALYINHVFSYYHRLTLHN 133
 SV++I H + S LYINHV HN

20
 Sbjct: 642 SVQFIFDHKQIYRKSLTYLYINHVIQNGTNFYKHN 538
 >CL040660.40.37
 Length = 3887

25
 Score = 28.1 bits (55), Expect = 9.6
 Identities = 9/35 (25%), Positives = 21/35 (59%)
 Frame = +2 / +3
 Query: 62 FTTSSFALYINHVFSYYHRLTLHNYKHEHIQLYDK 166
 F+ + +Y+N + S ++ +++N +H H+ Y K

30
 Sbjct: 2826 FSVYN*VIYVNFMSRIYQFSIYNSQHIHLFFYRK 2930
 >CL038470.59
 Length = 2137

35
 Score = 28.1 bits (55), Expect = 9.6
 Identities = 11/31 (35%), Positives = 21/31 (67%)
 Frame = +2 / +3
 Query: 29 SVKYIIFHSHYFTTSSFALYINHVFSYYHRL 121
 ++K ++F S + +FA +IN+V +Y+RL

40
 Sbjct: 1803 NLKNVLFISMCHSFYTFASFINNVVKHYYRL 1895
 >CL037498.92
 Length = 5442

45
 Score = 28.1 bits (55), Expect = 9.6
 Identities = 8/36 (22%), Positives = 19/36 (52%)
 Frame = +2 / +1
 Query: 35 KYIIFHSHYFTTSSFALYINHVFSYYHRLTLHNYKH 142
 +Y ++ +T+ F ++ +++ Y H L + Y H

Sbjct: 49 EYFVYMYIVYTSIYFGIHKKYIYKYTHILCISTYNH 156
>CL020533.77

Length = 5441

5 Score = 28.1 bits (55), Expect = 9.6
Identities = 10/26 (38%), Positives = 16/26 (61%)
Frame = +2 / -2

Query: 50 HSHYFTTSSFALYINHVFSYYHRLTL 127

H+H+ S+FALY H ++LT+

10 Sbjct: 1213 HAHFLDRSAFALYCMHATLHVYILTV 1136
>HTC129722-A01.R.1.1

Length = 748

Score = 28.1 bits (55), Expect = 9.6
15 Identities = 11/28 (39%), Positives = 16/28 (56%)
Frame = +2 / +1

Query: 59 YFTTSSFALYINHVFSYYHRLTLHNYKH 142

YFT+S F+L+ FSY + H+ H

Sbjct: 187 YFTSSCFLSIRCFSDIHVVWHHVAH 270
20 >CL011665.156.144

Length = 9674

Score = 28.1 bits (55), Expect = 9.6
Identities = 10/25 (40%), Positives = 14/25 (56%)
25 Frame = +2 / -1

Query: 35 KYIIFHSHYFTTSSFALYINHVFSY 109

KY +F H + T Y+NHV+ Y

Sbjct: 4856 KYXVFQ*HIYNTQ**RKYLNHVYIY 4782
30 >CL000771.165.129

Length = 9580

Score = 28.1 bits (55), Expect = 9.6
Identities = 12/26 (46%), Positives = 14/26 (53%)
Frame = +2 / -2

35 Query: 44 IFHSHYFTTSSFALYINHVFSYYHRL 121

+H H F S F L+ HVFS H L

Sbjct: 2904 LLH*HIFLSEFCLFHIHVFSQTHIL 2827
>CL006748.56

Length = 2192

40 Score = 28.1 bits (55), Expect = 9.6
Identities = 9/22 (40%), Positives = 13/22 (58%)
Frame = +2 / +3

Query: 95 HVFSYYHRLTLHNYKHEHIQLY 160

45 H+ YHR HN++ H Q+Y

Sbjct: 1527 HIKLTYHRSNEHNHQQNHPQIY 1592

>CL043873.84.90
Length = 6156

Score = 28.1 bits (55), Expect = 9.6
5 Identities = 7/33 (21%), Positives = 19/33 (57%)
Frame = +2 / +1
Query: 59 YFTTSSFALYINHVFSYYHRLTLHNYKHEHIQL 157
Y+ S + + +FS+ L+++++ H+H +
Sbjct: 4708 YWIASFYVRFAKQIFSFLSLSIYSFSHQHFSM 4806

10 >CL024871.73
Length = 2050

Score = 28.1 bits (55), Expect = 9.6
Identities = 10/22 (45%), Positives = 15/22 (67%)
15 Frame = +1 / +2
Query: 22 TF*RQIYNLSFTLLYYKQFCTL 87
TF*++ YNLSF L+ + C +
Sbjct: 1859 TFRFYNLSFIYLFIQSCCN 1924

Database:
20 Posted date:
Number of letters in database: 359,911,985
Number of sequences in database: 154,797

Lambda K H
25 0.318 0.135 0.401
Matrix: BLOSUM62
Number of Hits to DB: 175183387
Number of Sequences: 154797
Number of extensions: 2093073
30 Number of successful extensions: 72243
Number of sequences better than 10.0: 345
length of query: 71
length of database: 119,970,661
effective HSP length: 49
35 effective length of query: 22
effective length of database: 112,385,608
effective search space: 2472483376
effective search space used: 2472483376
frameshift window, decay const: 50, 0.1
40 T: 13
A: 40
X1: 16 (7.3 bits)
X2: 0 (0.0 bits)
S1: 41 (21.7 bits)
45 S2: 55 (28.1 bits)

Table 28: Exemplary sequences of the invention

SEQ ID NO:50

5 atgggaggac atgtcttgct tactgttttc actctttgta tgctttgttc
aggggttagg 60

gcacagctaa gccctgacat ttatgctaaa tcgtgccccca atctagttca
aattgtccgt 120

10 aaacaagttg ccatcgccct gaaggccgag atacggatgg ctgcttctct
cattcgtctt 180

catttccacg actgctttgt taatgggtgt gatgcgtcgt tattgttgga
15 tggagctgac 240

agcgagaaac tcgcatccc aaacattaac tctgctagag gatttgaagt
aattgataca 300

20 atcaaagccg ctgtggaaaa cgcatgtcct ggtgttgttt cttgtgctga
taccctcact 360

ttggccgctc gtgactccgt tgtattgagt ggagggcctg ggtggagagt
ggcattagga 420

25 agaaaagatg gattggtggc aaatcagaac agtgcaaaca atctaccatc
tccttttgaa 480

ccttttagacg ccattatcgc caaatttgta gccgtaaacc ttaacatcac
30 cgacgtcgta 540

gctttatcag gagctcacac ctttggacaa gcgaagtgtg ctgtcttcag
caaccgtctg 600

35 ttcaacttta ccggcttggg aaatcccgac gcaacacttg agacatcact
cttgtctaata 660

ctgcaaacag tttgtccgct cggaggaaat agtaacataa cagcacctct
tgacaggagc 720

40 actacggaca ccttcgacaa caattatttc aagaacctgc ttgaaggaaa
aggtcttttg 780

agttctgatc agattctgtt ctcgagtgc ttagccgtga acaccacaaa
45 gaaactagt 840

gaggcttata gtcggagcca gagcttgttt ttcagggact tcacatgtgc
gatgatcaga 900

atgggaaaca tttcgaatgg agctagtggg gaggttagga caaactgcag
ggttatcaat 960

5 aattag
966

SEQ ID NO:139

10 atggcctttca caaaaatctc cttagtcctt cttctctgcc tcttaggttt
cttttctgaa 60

actgtcaagt ctcaaaactg cgggtgcgct ccaaacctct gttgcagtca
gttcggttac 120

15 tgtggtaccg acgatgcata ctgcggtggt ggatgccgat caggtccttg
tagaggtagt 180

20 ggaacccoga cgggagggtc ggtcggtagc attgtgacac aaggtttctt
taacaatatt 240

atcaaccaag ctggtaatgg ttgcgcgggg aaaagattct acaccgtga
ctctttcggt 300

25 aacgccgcta atactttccc caactttgcc aattctgtta ccagacgtga
aattgctacc 360

atgtttgctc atttcactca cgagaccgga catttctgct acatagaaga
gattaacgga 420

30 gcaacacgta actactgcca gagcagcaac acacaatacc catgtgcacc
gggaaaaggc 480

35 tacttcggtc gtggtccgat ccaactatca tggaactaca actacggagc
gtgtggtcaa 540

agtctcggtc ttgaccttct acgccagccc gaacttgtgg gtagcaaccc
aactgtagct 600

40 ttcaggacgg gtttgtgggt ttggatgaat agcgtaaggc cggttctgaa
ccaagggttt 660

ggagccacca ttagagctat taatggaatg gaatgtaacg gtggtaatc
cggtgcagtc 720

45 aacgcaagga ttggatacta tagagactat tgtggacagc ttggtgtgga
ccctggtcct 780

aaccttagtt gctaa
795

SEQ ID NO:609

5 atgccacttc accgtcaa atagttagat tcgcgccgga tccatcttat
tgtagatcgg 60

ttcttccaaa ccagcccgga gatatatatt cctacggacg tttgtctcta
cgaagatccc 120

10 tctcacgagc ccgccggggc tctcgaagac tgcaaattcc tagccagcct
gactatggac 180

tacctcctta gtagctcaca gacggctgat tccacaaaaa cactgtcgtt
15 atctagggcc 240

gaggatgttc atacatttct gagtgtgcc atcaccaatg agcagacttg
tcttgaagga 300

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 30 tccctaacca 1200

gaaattggct atctaaggag tcaattttta ttttctctaa gttcaaacaa
 acttattttt 1260

35 tttggggcga atgtacatct aacaggaccc acaggtagac gtgatttttt
 ctaaaaaaag 1320

atgttataaa attgcacctt gtatcaaaat actttgacat atatacattc
 caaagggaga 1380

40 atatgttgct agacacttgt aataattgat tggttcagaa attaatact
 aattgtccgt 1440

aaagggttta attaatcggt agtggttaca gttggatgat atatgccaaa
 45 atgaacggtg 1500

aatttcgaat ctttcttgca tctgggtggct attaattact ttaggagtaa
 atttaaaaaa 1560

ctatatgtat gttaatatca aactatcaca aactacttat ttgagacatt
gtattataaa 1620

5 ctatagattt cgcaccaaaa atatcacaaa actacatatt taaagcccaa
actcaaaaaa 1680

ctatggtttt gttatataaa cgttatatgt aaatatgtca accaaacgtc
gtcacatgga 1740

10 gaaaccagat aaaacagact gacagtctgg agaaccatta aaatcttaca
agatcacaca 1800

ctgcaaactg catgctctct ctccctctca acgcctatat aagcacatcc
atcccccta 1860

15 tgatcaaagc atcacagaaa ccataaacac acaggcatct gattagagaa
atcta 1920

The material on the CD-ROM (filed in duplicate herewith ; CD 010623_1108 , file
38236 created on June 23, 2001, size 12,203 KB) is hereby incorporated by
reference herein pursuant to 37 C.F.R. sec. 1.52(e)(5).

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All publications, patents and patent applications are incorporated herein by reference. While in the foregoing specification this invention has been described in relation to certain preferred embodiments thereof, and many details have been set forth for purposes of illustration, it will be apparent to those skilled in the art that the invention is susceptible to additional embodiments and that certain of the details described herein may be varied considerably without departing from the basic principles of the invention.

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